

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 13.2661 Seconds  
(without alignments)  
927.898 Million cell updates/sec

Title: US-10-019-455a-6  
Perfect score: 676  
Sequence: 1 MARILLFLPGLVAVCAVHG.....RVQEATKEVPTTIDIFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	257.5	38.1	131	2 I38019	melanoma-derived g
2	86.5	12.8	839	1 TVHUV	transforming prote
3	85.5	12.6	844	1 TVMSV	transforming prote
4	81.5	12.1	878	2 I51940	gene VAV2 protei
5	78.5	11.6	1589	1 RGYICS	cell division cont
6	76.5	11.3	295	2 F90113	cell division cycl
7	74.5	11.0	1215	2 T32734	myosin-IA - Acanth
8	74	10.9	308	2 T48525	hypothetical prote
9	71.5	10.6	541	2 C64439	asparagine synthas
10	71.5	10.6	671	1 C69621	fructose-bisphosph
11	71	10.5	283	2 A23516	Balbani ring 1 ch
12	71	10.5	585	2 G96995	ATP-dependent RNA
13	71	10.5	722	2 G86746	hypothetical prote
14	71	10.5	769	2 C90186	AAA family ATPase
15	70.5	10.4	84	2 AG0693	probable lipoprote
16	70.5	10.4	444	1 A64417	phosphoribosylamin
17	70.5	10.4	669	2 T72278	endo-1,4-beta-mann
18	70.5	10.4	578	2 C97114	recG helicase [imp
19	70	10.4	209	2 D86758	orotate phosphorib
20	70	10.4	259	2 C64427	hypothetical prote
21	69.5	10.3	1199	2 T47442	disease resistance
22	69	10.2	328	2 E86714	quinone oxidoreduc
23	69	10.2	392	2 I39521	rubredoxin-NAD+ re
24	69	10.2	670	2 S67383	probable signal tr
25	69	10.2	2193	2 S52919	polyprotein (IA, 1
26	69	10.2	2541	2 T29340	hypothetical prote
27	68.5	10.1	461	2 AF2340	sugar ABC transpor
28	68.5	10.1	505	1 S24550	protein-tyrosine k
29	68.5	10.1	506	1 S24553	protein-tyrosine k

30	68	10.1	162	2 B29662	Balbani ring 2 ch
31	68	10.1	234	2 AE3482	hypothetical prote
32	68	10.1	332	2 T04200	hypothetical prote
33	68	10.1	359	2 B29960	Balbani ring 2 ch
34	68	10.1	366	2 G90951	probable cytochrom
35	68	10.1	366	2 C85800	probable cytochrom
36	68	10.1	782	2 B83966	formate dehydrogen
37	67.5	10.0	374	2 B97258	glycosyltransferas
38	67.5	10.0	839	2 G96719	probable chromomet
39	67.5	10.0	1072	2 AD1280	SNF2-type helicase
40	67	9.9	142	2 C75325	methylmalonyl-CoA
41	67	9.9	373	2 T39655	VHS domain contain
42	67	9.9	383	2 S24156	polygalacturonase
43	67	9.9	509	2 G82104	glutaryl-L-TRNA synt
44	67	9.9	518	1 P2WL8	L2 protein - human
45	67	9.9	524	2 S36483	L2 protein - human

## ALIGNMENTS

### RESULT 1

I38019  
melanoma-derived growth regulatory protein MIA - human  
C;Species: Homo sapiens (man)  
C;Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000  
C;Accession: I38019; S40238  
R;Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hoesdoerfer, B.; Schmitt, A.; Jac  
Cancer Res. 54, 5695-5701, 1994  
A;Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA.  
A;Reference number: I38019; MUID:95007612; PMID:7923218  
A;Accession: I38019  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-131 <RES>  
A;Cross-references: EMBL:X75450; NID:g438057; PIDN:CAA53203.1; PID:g438058  
C;Genetics:  
A;Gene: mia  
C;Superfamily: human melanoma-derived growth regulatory protein MIA

Query Match	38.1%;	Score	257.5;	DB 2;	Length	131;			
Best Local Similarity	41.2%;	Pred. No.	4.7e-19;						
Matches	56;	Conservative	26;	Mismatches	41;	Indels	13;	Gaps	5;
Qy	1	MARILLFLPGLVAVCA-----VHGIFMDRLASKKLCADDECVCYTISLSAQEDYNAPD	54						
Db	1	MARSLVCL--GVIIILSAFSGPGVGRGPMFKLADRLKLCADQEGSHPTISMAVALQDYNAPD	58						
Qy	55	CRFINVKKGOIYVYVKLVKENGAGE-FMAGSVYVGQDDEMGV-VGYFPRNLVKEORVYQ	112						
Db	59	CRFLTTHRGQVYVFSKL---KGRGLFWGSGVQDYGDLAARLGFPPSSIVREDQTLK	115						
Qy	113	EATKEVPTTIDIFFCE	128						
Db	116	PGKVDVKTDRKDFYCQ	131						

### RESULT 2

TVHUV  
transforming protein vav - human (fragments)  
N;Alternate names: finger protein vav  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1991 #sequence\_revision 03-May-1996 #text\_change 18-Jun-1999  
C;Accession: B39576; S05382  
R;Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991  
A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene  
A;Reference number: A39576; MUID:91172176; PMID:2005887  
A;Accession: B39576  
A;Molecule type: mRNA  
A;Residues: 1-61 <KAT>  
A;Cross-references: GB:M59834; NID:g340189; PIDN:AAA63267.1; PID:g340190  
A;Note: the authors translated the codon CAA for residue 6 as Glu, CAG for residue 13

R;Katzav, S.; Martin-Zanca, D.; Barbacid, M.  
EMBO J. 8, 2283-2290, 1989  
A;Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in hematopoietic cells  
A;Reference number: S05382; MUID:90005432; PMID:2477241  
A;Accession: S05382  
A;Molecule type: mRNA  
A;Residues: 62-839 <KAT2>  
A;Cross-references: EMBL:X16316  
R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.  
Oncogene 7, 611-618, 1992  
A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl oncogene  
A;Reference number: S23669; MUID:92228488; PMID:1565462  
A;Contents: annotation  
A;Note: in the sequence from mouse the authors find three additional nucleotides that predicted to occur in the published human sequences  
C;Comment: In comparing these sequences with the mouse (see PIR:TWMSV), there appear to be differences in the sequence from mouse  
C;Genetics:  
A;Gene: GDB:VAV1; VAV  
A;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding  
A;Keywords: phosphoprotein; transforming protein; zinc finger  
F;126-170/Region: acidic  
F;188-452/Domain: CDC24 homology <CD24>  
F;509-557/Domain: protein kinase C zinc-binding repeat homology <K22>  
F;522-542/Region: zinc finger CCCC motif  
F;547-560/Region: zinc finger HCH motif  
F;598-648/Domain: SH3 homology <SH3A>  
F;664-756/Domain: SH2 homology <SH2>  
F;783-831/Domain: SH3 homology <SH3B>  
F;433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 12.8%; Score 86.5; DB 1; Length 839;  
Best Local Similarity 32.9%; Pred. No. 1;  
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;  
QY 44 ASAQEDYNAPDPCRFINVKKQOIIVYVSKLVKENGAGFVAGSGVGGQDEMGVGVYFPRN 103  
DB 781 AKARYDFCARDRLSLSKEDII----KILNKKGGQGWRRGEIYGR-----VGMFPAN 829  
QY 104 LVKEQRYVQE 113  
DB 830 YVEED--YSE 837

RESULT 3  
TWMSV  
C;Species: Mus musculus (house mouse)  
C;Date: 03-May-1994 #sequence revision 16-Feb-1996 #text\_change 18-Jun-1999  
C;Accession: A61187; A39576; S36941; S23669  
R;Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M.  
Cell Growth Differ. 2, 95-105, 1991  
A;Title: Mechanism of activation of the vav protooncogene.  
A;Reference number: A61187; MUID:91299578; PMID:2069873  
A;Accession: A61187  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-844 <COP>  
R;Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991  
A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene affects its transforming activity  
A;Reference number: A39576; MUID:91172176; PMID:2005887  
A;Accession: A39576  
A;Molecule type: mRNA  
A;Residues: 1-28, 'E', '30-93 <KAT>  
A;Cross-references: GB:M59833; NID:9202343; PIDN:AAA63402.1; PID:G202344  
R;Adams, J.M.  
submitted to the EMBL Data Library, January 1992  
A;Reference number: S36941  
A;Accession: S36941  
A;Molecule type: mRNA  
A;Residues: 1-323, 'DLLMVMQRLVKYHLLQLQELVK', 346-347, 'QDAT', 352, 'K', 354, 'N', 355-453, 'R', 45

A;Cross-references: EMBL:X64361; NID:955220; PIDN:CAA45713.1; PID:955221  
R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.  
Oncogene 7, 611-618, 1992  
A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the d oncogene  
A;Reference number: S23669; MUID:92228488; PMID:1565462  
A;Contents: annotation; the authors note the frameshift difference with sequence in A6  
A;Note: the complete sequence was submitted to Genbank; see S36941  
C;Genetics:  
A;Gene: vav  
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding  
A;Keywords: phosphoprotein; transforming protein; zinc finger  
F;132-102/Region: leucine-rich  
F;132-176/Region: acidic  
F;194-458/Domain: CDC24 homology <CD24>  
F;336-340/Region: nuclear location signal  
F;486-493/Region: protein kinase C zinc-binding repeat homology <K21>  
F;513-563/Domain: protein kinase C zinc-binding repeat homology  
F;528-548/Region: zinc finger CCCC motif  
F;553-566/Region: zinc finger HCH motif  
F;575-582/Region: nuclear location signal  
F;604-654/Domain: SH3 homology <SH3A>  
F;606-609/Region: proline-rich  
F;670-761/Domain: SH2 homology <SH2>  
F;788-836/Domain: SH3 homology <SH3B>  
F;433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 12.6%; Score 85.5; DB 1; Length 844;  
Best Local Similarity 31.4%; Pred. No. 1.3;  
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;  
QY 44 ASAQEDYNAPDPCRFINVKKQOIIVYVSKLVKENGAGFVAGSGVGGQDEMGVGVYFPRN 103  
DB 786 AKARYDFCARDRLSLSKEDII----KILNKKGGQGWRRGEIYGR-----IGWFPAN 834  
QY 104 LVKEQRYVQE 113  
DB 835 YVEED--YSE 842

RESULT 4  
IS1940  
gene VAV2 protein - human  
C;Species: Homo sapiens (man)  
C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 16-Jul-1999  
C;Accession: IS1940  
R;Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramakrishna, S.; Haines, J.L.; K.  
Ann. Hum. Genet. 59, 25-37, 1995  
A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis gene  
A;Reference number: IS1940; MUID:95283235; PMID:7762982  
A;Accession: IS1940  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-878 <RES>  
A;Cross-references: GB:S76992; NID:9913345; PIDN:AAB34377.1; PID:9913346  
C;Genetics:  
A;Gene: GDB:VAV2  
A;Cross-references: GDB:370880; OMIM:600428  
A;Map position: 9q34-9q34  
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding  
F;198-462/Domain: CDC24 homology <CD24>  
F;524-572/Domain: protein kinase C zinc-binding repeat homology <K22>  
F;673-764/Domain: SH2 homology <SH2>  
F;823-872/Domain: SH3 homology <SH3>

Query Match 12.1%; Score 81.5; DB 2; Length 878;  
Best Local Similarity 26.3%; Pred. No. 3.4;  
Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;  
QY 38 VVT---ISLASAODYNAPDPCRFINVKKQOIIVYVSKLVKENGAGFVAGSGVGGQDEM 94  
DB 812 VFTPRVIGTAVRYNFAARDRLSLSKEDII----KILNKKGGQGWRRGEIYGR-----ETN 861  
QY 95 GVGVYFPRNLVKEQRYV 110





Tue Dec 30 10:20:54 2003

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Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlo
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Ser
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpsira, P.; Tognoni, A.; Tosato, V.; Uchiyam
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Yumoto, K.; Yumoto, K.; Yumoto,
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C69621
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-671 <KUN>
A;Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16056.1; PID:g263656
A;Experimental source: strain 168
C;Genetics:
A;Gene: fbp; yydE
C;Function:
A;Description: catalyzes the hydrolysis of fructose-1,6-bisphosphate to fructose-6-ph
A;Pathway: gluconeogenesis
A;Note: requires manganese ion for stability and phosphoenolpyruvate for activation
C;Superfamily: Bacillus subtilis fructose-bisphosphatase; phosphoesterase core homolog
C;Keywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoe
Query Match 10.6%; Score 71.5; DB 1; Length 671;
Best Local Similarity 22.8%; Pred. No. 27; Mismatches 21; Indels 29; Gaps 4;
Matches 26; Conservative
Qy 22 FMDRLASKKLCADDEC-VYTTISLASAQEDYNAPDCRFINVKKGQIYVYS-----KLV 73
Db 35 YLDLLAQKYCEKVVTEINLKA-----ILNLPKGFHFVSLHGEYQAFQHV 83
Qy 74 KENGAG-----EFWAGSVYGGQDEMVGVGFFPN---LVKEQRYQVQATKE 117
Db 84 LRNGSGRVKEKIRDFISGVIYDREIDELAAALVYYPEDKLIKHKHDFDAKEALNE 137

RESULT 11
A23516
Balbiani ring 1 chain - midge (Chironomus tentans) (fragment)
C;Species: Chironomus tentans
C;Date: 23-Aug-1987 #sequence_revision 23-Aug-1987 #text_change 21-Jul-2000
C;Accession: A23516
R;Hoog, C.; Engberg, C.; Wieslander, L.
Nucleic Acids Res. 14, 703-719, 1986
A;Title: A BR 1 gene in Chironomus tentans has a composite structure: a large repetiti
A;Reference number: A23516; MUID:86120366; PMID:3003693
A;Accession: A23516
A;Molecule type: DNA
A;Residues: 1-383 <HOO>
A;Cross-references: GB:X03490; NID:g7043; PIDN:CAA27206.1; PID:g769785
A;Note: the authors translated the codon GAA for residue 118 as Gly and TTC for residu
C;Genetics:
A;Introns: 273/1
C;Superfamily: unassigned Balbiani ring proteins
Query Match 10.5%; Score 71; DB 2; Length 383;
Best Local Similarity 28.0%; Pred. No. 17; Mismatches 37; Indels 20; Gaps 3;
Matches 26; Conservative
Qy 24 DRLASKKLCADDEC-VYTTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKENGAGEFWA 83
Db 303 DKDCCKNCNCDGAKF-----PECESNSKQSGMDFILAKLFPQGG-GDFFA 348
Qy 84 GSVYGGQDEMVGVGFFPNLVKEQRYQVQATK 116
Db 349 GSVEVDGKK-----LSPEKKEKFGKALQDAVK 375

RESULT 12
G96995
ATP-dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

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C;Accession: G96995  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 193, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
C;Accession: G96995  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-585 <KUR>  
A;Cross-references: GB:AE001437; PIDN:AAK78754.1; PID:gl5023664; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0778

Query Match 10.5%; Score 71; DB 2; Length 585;  
Best Local Similarity 29.4%; Pred. No. 26;  
Matches 30; Conservative 13; Mismatches 37; Indels 22; Gaps 5;

QY 30 KLCADD----ECVYTISLASAQEDYNAPDCRFINVKGGQIYVYSK-----LVKENGAGE 80  
DB 272 KCDEVEIKYKRAIPLEVEDSEFNKD-----IKEGDAVVVFSKRVLEIAQSVSARG 326

QY 81 FWAGSVGCDQDGVGVGVPFRNLVKEQRYVQBATKEVPTTD 122  
DB 327 IKASIIYGDLPPEV-----RMLQVEQFIKKE-TKVLVITD 360

RESULT 13  
G86746  
hypothetical protein nrde [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C;Accession: G86746  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissensbach, J.; Ehrlich  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: G86746  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-722 <STO>  
A;Cross-references: GB:AE005176; PID:gl2723918; PIDN:AAK05073.1; GSPDB:GN00146  
A;Experimental source: strain IL1403  
C;Genetics:  
A;Gene: nrde  
C;Superfamily: Salmonella typhimurium ribonucleoside-diphosphate reductase

Query Match 10.5%; Score 71; DB 2; Length 722;  
Best Local Similarity 26.2%; Pred. No. 33;  
Matches 28; Conservative 21; Mismatches 52; Indels 6; Gaps 2;

QY 11 GLVAVCAVHGIFMDRLASKKLCADDEC-VYTISLASAQEDYNAPDCRFINVKGGQIYVY 69  
DB 249 GVVYLSLFPDIMEFLSTKKENADEKIRVKTSLG-----VTVPDKFVELVKKGTMVLF 303

QY 70 SKLVKENGAGFWAGSVGCDQDGVGVGVPFRNLVKEQRYVQBATK 116  
DB 304 EPYFVEKYGKPFADVDITAEYDKMVPANPEIRKTSINARELEQELSK 350

RESULT 14  
C90186  
AAA family ATPase [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
C;Accession: C90186  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.  
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139

A;Accession: C90186  
A;Status: Preliminary  
A;Molecule type: DNA  
A;Residues: 1-769 <KUR>  
A;Cross-references: GB:AE006641; NID:gl13813572; PIDN:AAK40746.1; GSPDB:GN00155  
C;Genetics:  
A;Gene: SSO0421  
C;Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bi

Query Match 10.5%; Score 71; DB 2; Length 769;  
Best Local Similarity 35.0%; Pred. No. 35;  
Matches 28; Conservative 10; Mismatches 20; Indels 22; Gaps 5;

QY 67 YVYSKLVKENG-----AGFWAGSVGCDG--QDEMVGVGYPFRNL-----VKE 107  
DB 51 YTISRLGIENGVDYVEIIGPSGSAQAALIGDGADEIRVDGIYRSIGVIGDEVTVKR 110

QY 108 QRVYQBATKEV--PTTDIDF 125  
DB 111 AQV-QDATKVLAPTQPISF 129

RESULT 15  
AG0693  
probable lipoprotein ydha [imported] - Salmonella enterica subsp. enterica serovar Typh  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C;Accession: AG0693  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farra  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica ser  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AG0693  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-84 <PAR>  
A;Cross-references: GB:AL513382; PIDN:CAD01920.1; PID:gl6502762; GSPDB:GN00176  
C;Genetics:  
A;Gene: ydha

Query Match 10.4%; Score 70.5; DB 2; Length 84;  
Best Local Similarity 26.8%; Pred. No. 3.8;  
Matches 22; Conservative 20; Mismatches 25; Indels 15; Gaps 4;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKL---CADDECYVTISLASAQEDYN-APDCR 56  
DB 3 MKKIAIMFLPVLITGCSVYQQFVERMQTDTLEYQC--DEKPLTVKANNPREEVSFYDNK 60

QY 57 FINVKG-----QQIYVY 69  
DB 61 LLTLKQGISASGARYTDGIYVF 82

Search completed: December 29, 2003, 16:10:38  
Job time : 15.2661 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 5.01961 Seconds  
(without alignments)  
1199,181 Million cell updates/sec

Title: US-10-019-455a-6

Perfect score: 676

Sequence: 1 MARILLFLPLGLVAVCAVHG.....RVYQEAKEVPTTIDFFCE 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	676	100.0	128	1	Q9nrc9 homo sapien
2	602	89.1	128	1	O9iie3 mus musculus
3	480	71.0	132	1	O9i8p5 gallus gall
4	390	57.7	133	1	O9i8p5 rana catesb
5	257.5	38.1	131	1	MIA_HUMAN
6	256.5	37.9	130	1	MIA_BOVIN
7	254	37.6	130	1	MIA_RAT
8	235.5	34.8	130	1	MIA_MOUSE
9	88.5	13.1	847	1	VAV3_MOUSE
10	86.5	12.8	845	1	VAV3_HUMAN
11	85.5	12.6	843	1	VAV3_MOUSE
12	85.5	12.6	845	1	VAV3_MOUSE
13	85.5	12.6	845	1	VAV3_MOUSE
14	82.5	12.2	868	1	VAV2_MOUSE
15	81.5	12.1	878	1	VAV2_HUMAN
16	78.5	11.6	1589	1	CC25_YEAST
17	78	11.5	625	1	TR11_MOUSE
18	75	11.1	1721	1	ITN1_MOUSE
19	74	10.9	2161	1	SHK1_HUMAN
20	73	10.8	1217	1	ITN1_RAT
21	71.5	10.6	541	1	ASNH_METJA
22	71	10.5	1714	1	ITN1_MOUSE
23	71	10.5	2167	1	SHK1_RAT
24	70.5	10.4	444	1	PUR2_METJA
25	70.5	10.4	905	1	ZO3_MOUSE
26	70	10.4	209	1	PYR2_LACLA
27	70	10.4	209	1	PYR2_STRP3
28	70	10.4	209	1	PYR2_STRPY
29	70	10.4	259	1	YAZO_METJA
30	70	10.4	1815	1	SHK3_RAT
31	69	10.2	392	1	RUBE_ACICA
32	69	10.2	670	1	YBV2_SCHPO
33	69	10.2	2193	1	POLG_EC09H

# ALIGNMENTS

## RESULT 1

ID	OTOT_HUMAN	STANDARD;	PRT;	128 AA.
AC	Q9NRC9;	2001 (Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, last sequence update)		
DT	28-FEB-2003	(Rel. 41, last annotation update)		
DE	Otoraplin precursor (Fibrocyte-derived protein)	(Melanoma inhibitory activity like protein).		
GN	OTOT OR FDP OR MIAL.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
EN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cochlea;			
RX	MEDLINE=20334619; PubMed=10873378;			
RA	Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;			
RT	"A novel conserved cochlear gene, OTOT: identification, expression analysis, and chromosomal mapping.";			
RL	Genomics 66:242-248 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=20568254; PubMed=10998416;			
RX	Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;			
RT	"Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme.";			
RL	J. Biol. Chem. 275:40036-40041 (2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain and Cochlea;			
RX	MEDLINE=21100875; PubMed=11161796;			
RT	Rendtorff N.D., Prodin M., Attie-Bitach T., Vekemans M., Tommerup N.;			
RT	"Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation.";			
RL	Genomics 71:40-52 (2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=21638749; PubMed=11780052;			
RX	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L., Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grahm D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			

34	69	10.2	2203	1	POLG_EC09B
35	68.5	10.1	505	1	SRK1_SPOLA
36	68.5	10.1	506	1	SRK4_SPOLA
37	68	10.1	162	1	BAR2_CHIPA
38	68	10.1	366	1	TORY_ECO57
39	68	10.1	534	1	VL2_HPV37
40	67	9.9	383	1	PGI3_ASPNG
41	67	9.9	474	1	SYE_VIBCH
42	67	9.9	518	1	VL2_HPV08
43	67	9.9	524	1	VL2_HPV17
44	67	9.9	809	1	DCML_OLICA
45	66.5	9.8	209	1	PYRE_LISMO

Q66577	e genome po
P42686	spongilla 1
P42690	spongilla 1
P08725	chironomus
P58361	escherichia
Q80905	human papil
Q12554	aspergillus
O31153	vibrio chol
P06419	human papil
P19919	oligotropa
Q85688	listeria mo

RA Leivaeslaiho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
RA Marsh V.L., Martin S.B., McConnachie L.J., McDay K., McMurray A.A.,  
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
RA Rogers J.;  
RT "The DNA sequence and comparative analysis of human chromosome 20.";  
RL Nature 414:865-871(2001).  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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CC -----  
DR EMBL; AF233261; AAP82078.1; -;  
DR EMBL; AF243505; AAG42356.1; -;  
DR EMBL; AF242552; CAC27443.1; -;  
DR EMBL; AJ252324; CAC28085.1; -;  
DR EMBL; AJ252325; CAC28085.1; JOINED.  
DR EMBL; AJ252326; CAC28085.1; JOINED.  
DR EMBL; AJ252327; CAC28085.1; JOINED.  
DR EMBL; AL034428; CAC16848.1; -;  
DR HSSP; Q16674; 111J.  
DR Genew; HGNC:8517; OTOR.  
DR MIM; 606067; -;  
DR GO; GO:0007605; P:hearing; TAS.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50002; SH3; 1.  
DR SIGNAL; SH3 domain. 18 POTENTIAL.  
FT CHAIN 19 128 OTORAPLIN.  
FT DOMAIN 39 110 SH3.  
FT DISULFID 32 37 BY SIMILARITY.  
FT DISULFID 55 127 BY SIMILARITY.  
SQ SEQUENCE 128 AA; 14332 MW; 9BB52C7F5D4FB700 CRC64;  
Query Match 100.0%; Score 676; DB 1; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5.4e-63;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPLGLVAVCAVHGIFMDRLASKKLCADDECYVITISLASAQEDYNAPDCRFINV 60  
DB 1 MARILLFLPLGLVAVCAVHGIFMDRLASKKLCADDECYVITISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYKLVKENGAGFWAGSVYGDQDENGWVGYGPPRNLVKQRYVQATKEVPT 120  
DB 61 KKGQIYVYKLVKENGAGFWAGSVYGDQDENGWVGYGPPRNLVKQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128  
RESULT 2  
ID OTOR MOUSE  
AC Q9UIE3; STANDARD; PRT; 128 AA.  
DT 16-Oct-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DE 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Otoraplin precursor (Melanoma inhibitory activity-like protein).  
GN OTOR OR MIAL.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20334619; PubMed=10973378;  
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,  
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;  
RT "A novel conserved cochlear gene, OTOR: identification, expression  
RT analysis, and chromosomal mapping.";  
RL Genomics 66:242-248(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Fetal;  
RC MEDLINE=21100875; PubMed=1161796;  
RA Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;  
RT "Identification and characterization of an inner ear-expressed human  
RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent  
RT polymorphism that abolishes translation.";  
RL Genomics 71:40-52(2001).  
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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CC -----  
DR EMBL; AF233333; AAP82079.1; -;  
DR EMBL; AJ243939; CAC27444.1; -;  
DR HSSP; Q16674; 111J.  
DR MGD; MGI:1888678; Otor.  
DR GO; GO:0001502; P:cartilage condensation; IMP.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50002; SH3; 1.  
DR SIGNAL; SH3 domain. 18 POTENTIAL.  
FT CHAIN 19 128 OTORAPLIN.  
FT DOMAIN 39 110 SH3.  
FT DISULFID 32 37 BY SIMILARITY.  
FT DISULFID 55 127 BY SIMILARITY.  
SQ SEQUENCE 128 AA; 14328 MW; 3DD47D4C77C4A7FD CRC64;  
Query Match 89.1%; Score 602; DB 1; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.4e-55;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MARILLFLPLGLVAVCAVHGIFMDRLASKKLCADDECYVITISLASAQEDYNAPDCRFINV 60  
DB 1 MARILLFLPLGLVAVCAVHGIFMDRLASKKLCADDECYVITISLASAQEDYNAPDCRFIDV 60  
QY 61 KKGQIYVYKLVKENGAGFWAGSVYGDQDENGWVGYGPPRNLVKQRYVQATKEVPT 120  
DB 61 KKGQIYVYKLVKENGAGFWAGSVYGDQDENGWVGYGPPRNLVKQRYVQATKEIPT 120  
QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128  
RESULT 3

```
OTOR_CHICK STANDARD; PRT; 132 AA.
AC Q918P6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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-----
DR EMBL; AF233518; AAF82727.1; -.
DR HSP; Q16674; I11J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW Signal; SH3 domain.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 132 OTORAPLIN.
FT DOMAIN 42 114 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 131 BY SIMILARITY.
SQ SEQUENCE 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;

Query Match 71.0%; Score 480; DB 1; Length 132;
Best Local Similarity 73.8%; Pred. No. 1e-42; Mismatches 20; Indels 2; Gaps 2;
Matches 93; Conservative 11;

QY 4 ILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKG 63
DB 8 IVLFLCGLMNPFT-GIFMDKLSKLCADDDCVYTTISLVRABEDYNAPDCRFINIKKG 66

QY 64 QOIYVYKLVKNGAGFVAGSVYDGG-QDEMGVVGVEPRNLVKEQRYQVQATKEVPTD 122
DB 67 QLIYVYKLVKKEGSEGFVAGSVYGEYEDHMGTVGFFPSRLSVSQHVYQANKTIPTD 126

QY 123 IDFCFCE 128
DB 127 IDFCFCE 132

RESULT 4
OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q918P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN Otoraplin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosscherhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
RL Cancer Res. 54:5695-5701(1994).
```

```
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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-----
DR EMBL; AF233519; AAF82728.1; -.
DR HSP; Q16674; I11J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
KW Signal; SH3 domain.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 133 OTORAPLIN.
FT DOMAIN 48 115 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 132 BY SIMILARITY.
SQ SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;

Query Match 57.7%; Score 390; DB 1; Length 133;
Best Local Similarity 58.9%; Pred. No. 2.1e-33;
Matches 66; Conservative 26; Mismatches 18; Indels 2; Gaps 2;

QY 19 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQOIYVYKLVKEN-G 77
DB 22 YGVYKQLSKDKLCADDECVYTTISFGRAEDDYNAPDCRFVNLKKGELVYITKLKEND 81

QY 78 AGEFWAGSVYDGG-QDEMGVVGVEPRNLVKEQRYQVQATKEVPTDIDFCFCE 128
DB 82 AGEFWAGSVYDQYRDQQLGVGFPSSLVTETLVYKQLBELPTTAVDFYCD 133

RESULT 5
MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosscherhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
RL Cancer Res. 54:5695-5701(1994).
```

FT	CHAIN	25	131	MELANOMA DERIVED GROWTH REGULATORY PROTEIN. SH3.
FT	DOMAIN	43	113	
FT	DISULFID	36	41	
FT	DISULFID	59	130	
FT	STRAND	33	36	
FT	TURN	39	40	
FT	STRAND	46	50	
FT	STRAND	54	54	
FT	TURN	59	60	
FT	STRAND	61	61	
FT	STRAND	64	64	
FT	TURN	66	67	
FT	STRAND	69	76	
FT	HELIX	78	80	
FT	TURN	81	82	
FT	STRAND	83	89	
FT	TURN	93	94	
FT	STRAND	96	96	
FT	STRAND	101	104	
FT	HELIX	105	107	
FT	STRAND	108	113	
FT	STRAND	119	122	
FT	HELIX	126	128	
SQ	SEQUENCE	131 AA; 14509 MW; 4D3BB30BD6008BDC CRC64;		
Query Match 38.1%; Score 257.5; DB 1; Length 131;				
Best Local Similarity 41.2%; Pred. No. 1.1e-19;				
Matches 56; Conservative 26; Mismatches 41; Indels 13; Gaps 5;				
QY	1	MARILLFLPOLVAVCA-----VHGIFMDRLASKKLCADDECVTITISLASAQEDYNAPD	54	
DB	1	MARSIVCL--GVILLSAFSGPGVGGPWPKLADRLCADQCSHPISMAVALQDYNAPD	58	
QY	55	CRFINVKKGQIYYVSKLVKENAGE--FWAGSVYGDGQDEMGV-VGYFRLNLVKEQRYQ	112	
DB	59	CRFLTIHRGQVYVYFSKL--KGRGLFWGSGVQGYDGLAARLGYFPSSIVREDQTLK	115	
QY	113	EATKEVPTTIDDFCE 128		
DB	116	PGKVDVKTKRWDFYC 131		
RESULT 6				
MIA_BOVIN				
ID	MIA_BOVIN	STANDARD;	PRT;	130 AA.
AC	Q28Q38;			
DT	01-NOV-1997	(Rel. 35, Created)		
DT	01-NOV-1997	(Rel. 35, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Melanoma derived growth regulatory protein precursor (Melanoma			
DE	inhibitory activity) (Cartilage-derived retinoic acid-sensitive			
DE	protein) (CD-RAP).			
DE	MIA OR CDRAP.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]_SEQUENCE FROM N.A.			
RP	MEDLINE=96216414; PubMed=8621736;			
RX	Dietz U.H., Sandell L.O.;			
RA	"Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and			
RT	during chondrogenesis."			
RL	J. Biol. Chem. 271:3311-3316(1996).			
CC	-!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND			
CC	MAINTENANCE			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.			
CC	-!- INDUCTION: Repressed by retinoic acid.			
CC	-!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.			
CC	-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.			

```
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U51437; AAC48523.1; -.
CC DR HSP; Q16674; 111J.
CC DR InterPro; IPR001452; SH3.
CC DR Pfam; PF00018; SH3; 1.
CC DR SMART; SM00326; SH3; 1.
CC DR PROSITE; PS00002; SH3; 1.
CC KW Growth factor; Signal; SH3 domain.
CC FT SIGNAL 1 22
CC FT CHAIN 23 130
CC FT DOMAIN 42 112
CC FT DISULFID 35 40
CC FT DISULFID 58 129
CC FT CONFLICT 46 47
CC SQ SEQUENCE 130 AA; 14353 MW; 95DI53161C78E02A CRC64;

Query Match 37.9%; Score 256.5; DB 1; Length 130;
Best Local Similarity 43.1%; Pred. No. 1.3e-19;
Matches 56; Conservative 23; Mismatches 36; Indels 15; Gaps 5;

Qy 4 ILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYVTSLSAQEDYNAPDCRFNVKKG 63
Db 11 VLLSAFPGPSA-----GGRPMPLADRMCADECSHPISVAVALQDYVAPDREFLTIHQG 66

Qy 64 QQIVYVSKLVKENGAGE-FWAGSV-----YGDGDEMVGVGYPFRNLVKEQRYVQEAKEV 118
Db 67 QVVYVFSKL---KGRGLFWGSGVQGDYIGDGAARL---GYFPSSIVREDQTLKPAKTDV 120

Qy 119 PTTDIDFFCE 128
Db 121 KTDIWDYFCQ 130

RESULT 7
MIA_RAT ID MIA_RAT STANDARD; PRT; 130 AA.
AC Q62946; P97591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
DE MIA OR CDRAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Mammary gland;
RA Lu J.X.;
RT "Gene expression changes associated with chemically-induced rat
RT mammary carcinogenesis.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 34-124 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=96216414; PubMed=8621736;
RA Dietz U.H., Sandell L.J.;
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
RT during chondrogenesis.";
RL J. Biol. Chem. 271:3311-3316(1996).
CC -1- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
```

```
CC MAINTENANCE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -1- INDUCTION: Repressed by retinoic acid.
CC -1- PM: MAY POSSES TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO THE MIA / OFOR FAMILY.
CC -1- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U51438; AAC52481.1; -.
CC DR EMBL; U67884; AAB40659.1; -.
CC DR HSP; Q16674; 111J.
CC DR InterPro; IPR001452; SH3.
CC DR Pfam; PF00018; SH3; 1.
CC DR SMART; SM00326; SH3; 1.
CC DR PROSITE; PS00002; SH3; FALSE NEG.
CC KW Growth factor; Signal; SH3 domain.
CC FT SIGNAL 1 22
CC FT CHAIN 23 130
CC FT DOMAIN 42 112
CC FT DISULFID 35 40
CC FT DISULFID 58 129
CC FT CONFLICT 46 47
CC SQ SEQUENCE 130 AA; 14536 MW; 5F99149AECF74501 CRC64;

Query Match 37.6%; Score 254; DB 1; Length 130;
Best Local Similarity 40.9%; Pred. No. 2.4e-19;
Matches 52; Conservative 26; Mismatches 39; Indels 10; Gaps 4;

Qy 9 LPGLVAVCAVHGI-----FMDRLASKKLCADDECVYVTSLSAQEDYNAPDCRFNVKKG 63
Db 7 LLGIVILSVFSGLSRADRPMLADRLKCADECSHPISMAVALQDYVAPDREFLTIYRG 66

Qy 64 QQIVYVSKLVKENGAGE-FWAGSVYGDGQDEMVG-VGYFPRNLVKEQRYVQEAKEVPTT 121
Db 67 QVVYVFSKL---KGRGLFWGSGVQGDYIGDLAHLGCFYFPSSIVREDTLKPGKVDKMTD 123

Qy 122 DIDFFCE 128
Db 124 EWDFYFCQ 130

RESULT 8
MIA_MOUSE ID MIA_MOUSE STANDARD; PRT; 130 AA.
AC Q61865; O09086; P97495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
DE MIA OR CDRAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosscherhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettnner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
```



DR PROSITE; PS50002; SH3; 2.  
KW phorbol-ester binding; Zinc: SH2 domain; SH3 domain; Repeat;

OS Mus musculus (Mouse).  
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:

KW Guanine-nucleotide releasing factor; Alternative splicing.  
 FT DOMAIN 1 119 CH.  
 FT DOMAIN 192 371 DH.  
 FT DOMAIN 400 502 EH.  
 FT DOMAIN 514 562 PHORBOL-ESTER AND DAG BINDING.  
 FT DOMAIN 592 660 SH3 1.  
 FT DOMAIN 672 766 SH2.  
 FT DOMAIN 788 847 SH3 2.  
 SQ SEQUENCE 847 AA; 97946 MW; 9AGB63F0D9E60F8F CRC64;

Query Match 13.1%; Score 88.5; DB 1; Length 847;  
 Best Local Similarity 31.3%; Pred. No. 0.24;  
 Matches 21; Conservative 14; Mismatches 21; Indels 11; Gaps 2;

QY 41 ISLSAQEDYNAPDCRFNVKKGQIYVYVSKLVKENGAGFWAGSVYGDQDGMGVGYF 100  
 DB LGIARAYDFCFARDVRELSLLKGMVKIYTKM-----SANGWVRGEVNGR-----VGWVF 838

QY 101 PRNLVKE 107  
 DB 839 PSTYVEE 845

RESULT 10  
 VAV HUMAN STANDARD; PRT; 845 AA.  
 AC P15498; Q15860;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vav proto-oncogene.  
 GN VAV1 OR VAV.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RA Denninger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;  
 RT "Transcriptional regulation of the vav proto-oncogene."  
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 62-845 FROM N.A.  
 RX MEDLINE=90005432; PubMed=2477241;  
 RA Katrav S., Martin-Zanca D., Barbacid M.;  
 RT "vav, a novel human oncogene derived from a locus ubiquitously  
 expressed in hematopoietic cells."  
 RL EMBO J. 8:2283-2290(1989).  
 RN [3]  
 RP SEQUENCE OF 1-61 FROM N.A.  
 RX MEDLINE=91172176; PubMed=2005887;  
 RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;  
 RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-  
 oncogene activates its transforming potential."  
 RL Mol. Cell. Biol. 11:1912-1920(1991).  
 RN [4]  
 RP SEQUENCE OF 299-837 FROM N.A.  
 RA Romero F.;  
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 299-334 FROM N.A.  
 RX MEDLINE=96038895; PubMed=7478592;  
 RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,  
 RA Tortolero M., Fischer S.;  
 RT "The proline-rich region of Vav binds to Grb2 and Grb3-3."  
 RL Oncogene 11:1665-1669(1995).  
 RN [6]  
 RP SIMILARITY TO CDC24 FAMILY.  
 RX MEDLINE=92228488; PubMed=1565462;  
 RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;  
 RT "The hematopoietically expressed vav proto-oncogene shares homology  
 with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene  
 (CDC24) involved in cytoskeletal organization.";

Oncogene 7:611-618(1992).  
 CC -i- FUNCTION: Couples tyrosine kinase signals with the activation of  
 the Rho/Rac GTPases, thus leading to cell differentiation and/or  
 proliferation.  
 CC -i- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2  
 and Grb3.  
 CC -i- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT  
 NOT IN OTHER CELL TYPES.  
 CC -i- PTM: Phosphorylated on tyrosine residues.  
 CC -i- MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew  
 alphabet.  
 CC -i- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
 CC -i- SIMILARITY: Contains 1 DEL-homology (DH) domain.  
 CC -i- SIMILARITY: Contains 1 PH domain.  
 CC -i- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
 binding domain.  
 CC -i- SIMILARITY: Contains 1 SH2 domain.  
 CC -i- SIMILARITY: Contains 2 SH3 domains.  
 CC -i- CAUTION: Ref.2 sequence differs from that shown due to frameshifts  
 in position 322 and 355.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL; AF030227; AAC25011.1; JOINED.  
 CC EMBL; AF030201; AAC25011.1; JOINED.  
 CC EMBL; AF030202; AAC25011.1; JOINED.  
 CC EMBL; AF030203; AAC25011.1; JOINED.  
 CC EMBL; AF030204; AAC25011.1; JOINED.  
 CC EMBL; AF030205; AAC25011.1; JOINED.  
 CC EMBL; AF030206; AAC25011.1; JOINED.  
 CC EMBL; AF030207; AAC25011.1; JOINED.  
 CC EMBL; AF030208; AAC25011.1; JOINED.  
 CC EMBL; AF030209; AAC25011.1; JOINED.  
 CC EMBL; AF030210; AAC25011.1; JOINED.  
 CC EMBL; AF030211; AAC25011.1; JOINED.  
 CC EMBL; AF030212; AAC25011.1; JOINED.  
 CC EMBL; AF030213; AAC25011.1; JOINED.  
 CC EMBL; AF030214; AAC25011.1; JOINED.  
 CC EMBL; AF030215; AAC25011.1; JOINED.  
 CC EMBL; AF030216; AAC25011.1; JOINED.  
 CC EMBL; AF030217; AAC25011.1; JOINED.  
 CC EMBL; AF030218; AAC25011.1; JOINED.  
 CC EMBL; AF030219; AAC25011.1; JOINED.  
 CC EMBL; AF030220; AAC25011.1; JOINED.  
 CC EMBL; AF030221; AAC25011.1; JOINED.  
 CC EMBL; AF030222; AAC25011.1; JOINED.  
 CC EMBL; AF030223; AAC25011.1; JOINED.  
 CC EMBL; AF030224; AAC25011.1; JOINED.  
 CC EMBL; AF030225; AAC25011.1; JOINED.  
 CC EMBL; AF030226; AAC25011.1; JOINED.  
 CC EMBL; X16316; CAA34383.1; ALT\_FRAME.  
 CC EMBL; M59834; AAA63267.1; --  
 CC EMBL; X83931; CAA58783.1; --  
 CC PIR; B39576; TVHUVV.  
 CC HSSP; P29354; IGRI.  
 CC TRANSFAC; T00880; --  
 CC Genew; HGNC:12657; VAV1.  
 CC MIM; 164875; --  
 CC GO; GO:0003700; P:transcription factor activity; TAS.  
 CC GO; GO:0007048; P:oncogenesis; TAS.  
 CC InterPro; IPR001715; Calponin-like.  
 CC InterPro; IPR003247; CH\_type.  
 CC InterPro; IPR002219; DAG\_PE-bind.  
 CC InterPro; IPR001331; GDS\_CDC24.  
 CC InterPro; IPR001849; PH\_--  
 CC InterPro; IPR000219; Rhogef.  
 CC InterPro; IPR000980; SH2.

```

DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS0010; DH_1; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00002; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
FT DOMAIN 1 119
FT DOMAIN 194 373
FT DOMAIN 402 504
FT DOMAIN 516 564
FT DOMAIN 617 660
FT DOMAIN 671 765
FT DOMAIN 782 842
FT DOMAIN 264 264
FT CONFLICT 718 718
FT CONFLICT 718 718
FT CONFLICT 718 718
SQ SEQUENCE 845 AA; 98313 MW; AC3BC9736FD2F138 CRC64;

Query Match 12.8%; Score 86.5; DB 1; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.38;
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;

Qy 44 ASAQEDYNAPDCRFINVKKQIYVYSKLVKENGAGEFWAGSGQDEMVGWGFPPAN 103
Db 787 AKARYDFCARDSELSKEGDII---KILNKKQGGQWWRGEIYGR-----VGMFFAN 835

Qy 104 LVKEQRVYQE 113
Db 836 YVEED--YSE 843

RESULT 11
ID VAV3 HUMAN STANDARD; PRT; 847 AA.
AC Q9UKW4; Q95230; Q9Y5X8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vav-3 protein.
GN VAV3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99455043; PubMed=10523675;
RA Movilla N., Bustelo X.R.;
RT "Biological and regulatory properties of Vav-3, a new member of the
RT Vav family of oncoproteins."

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RL Mol. Cell. Biol. 19:7870-7885(1999).
RN [2].
RP SEQUENCE FROM N.A.
RC TISSUE=Breast, and Colon carcinoma;
RX MEDLINE=98371222; PubMed=9705494;
RA Trenkle T., Welsh J., Jung B., Mathieu-Daude F., McClelland M.;
RT "Non-stoichiometric reduced complexity probes for cDNA arrays.";
Nucleic Acids Res. 26:3883-3891(1998).
RL CC -!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
STATES OF THOSE GTPASES.
CC CC -!- ALTERNATIVE PRODUCTS:
CC CC Event-Alternative splicing; Named isoforms=2;
CC CC Name=Alpha;
CC CC Name=Beta;
CC CC IsoId=Q9UKW4-1; Sequence=Displayed;
CC CC IsoId=Q9UKW4-2; Sequence=VSP_001820;
CC CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC CC -!- SIMILARITY: Contains 1 PH domain.
CC CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
binding domain.
CC CC -!- SIMILARITY: Contains 1 SH2 domain.
CC CC -!- SIMILARITY: Contains 2 SH3 domains.
CC CC -----
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CC CC -----
CC CC EMBL; AF118887; AAD20349.1; -.
CC CC EMBL; AF118886; AAD20348.1; -.
CC CC EMBL; AF067817; AAC79695.1; -.
CC CC HSSP; P29355; 1SEM.
CC CC Genew; HGNC:12659; VAV3.
CC CC MIM; 605541; -.
CC CC GO; GO:0005096; F:GTPase activator activity; TAS.
CC CC GO; GO:0005070; F:SH3/SH2 adaptor protein activity; TAS.
CC CC GO; GO:0007264; P:small GTPase mediated signal transduction; TAS.
CC CC InterPro; IPR001715; Calponin-like.
CC CC InterPro; IPR003247; CH type.
CC CC InterPro; IPR002219; DAG_PE-bind.
CC CC InterPro; IPR001331; GDS_CDC24.
CC CC InterPro; IPR001849; PH.
CC CC InterPro; IPR000219; RhoGEF.
CC CC InterPro; IPR000980; SH2.
CC CC InterPro; IPR001452; SH3.
CC CC InterPro; IPR003096; SM22_calponin.
CC CC Pfam; PF00307; CH; 1.
CC CC Pfam; PF00130; DAG_PE-bind; 1.
CC CC Pfam; PF00169; PH; 1.
CC CC Pfam; PF00621; RhoGEF; 1.
CC CC Pfam; PF00017; SH2; 1.
CC CC Pfam; PF00018; SH3; 1.
CC CC PRINTS; PR00401; SH2DOMAIN.
CC CC PRINTS; PR00452; SH3DOMAIN.
CC CC PRINTS; PR00888; SM22CALPONIN.
CC CC ProDom; PD001527; CH type; 1.
CC CC ProDom; PD000093; SH2; 1.
CC CC ProDom; PD000066; SH3; 1.
CC CC SMART; SM00109; C1; 1.
CC CC SMART; SM00033; CH; 1.
CC CC SMART; SM00233; PH; 1.
CC CC SMART; SM00325; RhoGEF; 1.
CC CC SMART; SM00252; SH2; 1.
CC CC SMART; SM00326; SH3; 2.
CC CC PROSITE; PS00021; CH; 1.
CC CC PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
CC CC PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
CC CC PROSITE; PS0010; DH_1; 1.
CC CC PROSITE; PS00741; DH_1; 1.
CC CC PROSITE; PS00003; PH DOMAIN; 1.
CC CC PROSITE; PS00002; SH2; 1.
CC CC PROSITE; PS00002; SH3; 2.

```



Tue Dec 30 10:20:54 2003

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DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vav proto-oncogene.
OS VAV1 OR VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92228488; PubMed=1565462;
RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the dbi GTP-exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization.";
RL Oncogene 7:611-618(1992).
RN [2]
RP SEQUENCE OF 1-93 FROM N.A.
RA MEDLINE=91172176; PubMed=2005887;
RA Katav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RT oncogene activates its transforming potential.";
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [3]
RP INTERACTION WITH SLA.
RA MEDLINE=20130290; PubMed=10662792;
RA Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
RT "Src-like adaptor protein (SLAP) is a negative regulator of T cell
RT receptor signaling.";
RL J. Exp. Med. 191:463-474(2000).
CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
CC proliferation.
CC -!- SUBUNIT: Interacts with SLA.
CC -!- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but
CC not in other cell types.
CC -!- PM: Phosphorylated on tyrosine residues (By similarity).
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DSL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG
CC binding domain.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X64361; CAA45713.1; -.
CC EMBL; M59633; AAG63402.1; -.
CC PIR; A61187; TVMSV.
CC PDB; 1F5X; 15-SEP-00.
CC PDB; 1GCP; 28-JAN-03.
CC PDB; 1GCO; 28-JAN-03.
CC PDB; 1X1Z; 18-DEC-02.
CC TRANSFAC; T01230; -.
CC MGD; MGI:98923; Vav1.
CC InterPro; IPR001715; Calponin-like.
CC InterPro; IPR003247; CH type.
CC InterPro; IPR002219; DAG PE-bind.
CC InterPro; IPR001331; GDS_CDC24.
CC InterPro; IPR001849; PH_CDC24.
CC InterPro; IPR000219; RhoGEF.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001452; SH3.
CC InterPro; IPR003096; SM22_calponin.
CC Pfam; PF00307; CH; 1.
CC Pfam; PF00130; DAG_PE-bind; 1.
CC Pfam; PF00169; PH; 1.

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Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00101; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
KW proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
KW 3D-structure.
FT DOMAIN 1 119 CH.
FT DOMAIN 194 373 DH.
FT DOMAIN 402 504 PH.
FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 617 660 SH3 1.
FT DOMAIN 671 765 SH2.
FT DOMAIN 782 842 SH3 2.
FT CONFLICT 29 29 Q -> E (IN REF. 2).
SQ SEQUENCE 845 AA; 98136 MW; 3666DCCD1C5229DA CRC64;
Query Match 12.6%; Score 85.5; DB 1; Length 845;
Best Local Similarity 31.4%; Pred. No. 0.49;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;
QY 44 ASAQEDYNAPDREFINVKKGQIIYVYSLKVENAGAFWAGSVVGDQDEWGVGVYPRN 103
DB 787 AKARYDFCARDSELSLKEGDI-----KILNKGQGGWRRGEIYGR-----IGWFFSN 835
QY 104 LVKQRVYOE 113
DB 836 YVEED--YSE 843
RESULT 14
VAV2_MOUSE
ID VAV2_MOUSE STANDARD; PRT; 868 AA.
AC Q60932;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vav-2 protein.
GN VAV2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6;
RX MEDLINE=96313271; PubMed=8710375;
RA Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,
RA Goldman D., Lee I.J.;
RT "Isolation and characterization of murine vav2, a member of the vav
RT family of proto-oncogenes.";
RL Oncogene 13:363-371(1996).
CC -!- FUNCTION: Guanine nucleotide exchange factor for the Rho family
CC of Ras-related GTPases (By similarity).

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DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RHOGEF; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR ProDom; PD001527; CH type; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 2.  
 DR SMART; SM00109; CH; 1.  
 DR SMART; SM00033; CH; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RHOGEF; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50021; CH; 1.  
 DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS50010; DH\_2; 1.  
 DR PROSITE; PS00741; DH\_1; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 DR Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;  
 KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.  
 FT DOMAIN 1 119  
 FT DOMAIN 198 376  
 FT DOMAIN 405 512  
 FT DOMAIN 524 572  
 FT DOMAIN 586 652  
 FT DOMAIN 673 767  
 FT DOMAIN 816 877  
 FT MOD\_RES 142 142  
 FT MOD\_RES 159 159  
 FT MOD\_RES 172 172  
 SQ SEQUENCE 878 AA; 101256 MW; C8PF7681032146B4 CRC64;

Query Match 12.1%; Score 81.5; DB 1; Length 878;  
 Best Local Similarity 26.3%; Pred. No. 1.3;  
 Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;  
 QY 38 VYT---ISLASAQEDYNAPDCRFNVKGGQIYVYKLVKENGAGEFWAGSVYGDGQDEM 94  
 Db 812 VFTPRVIGTAVARYNFAARDMRELSRLREGDVVRIYSRIGGDG---WNKG-----ETN 861  
 QY 95 GVVGYPFRNLVKEQRV 110  
 Db 862 GRIGWFPFTYVEEGI 877

Search completed: December 29, 2003, 16:04:12  
 Job time : 7.01961 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	226.5	33.5	96	11	Q9J109	Q9J109 mesocricetu	
2	215	31.8	268	11	Q8BJE9	Q8BJE9 mus musculus	
3	215	31.8	1239	11	Q8BI84	Q8BI84 mus musculus	
4	185.5	27.4	113	4	Q96PC5	Q96PC5 homo sapien	
5	181	26.8	137	11	Q921X3	Q921X3 mus musculus	
6	176	26.0	119	11	Q91ZV0	Q91ZV0 mus musculus	
7	168.5	24.9	88	13	Q90XFL	Q90XFL tetraodon n	
8	155	22.9	68	11	Q8C999	Q8C999 mus musculus	
9	89	13.2	1257	5	Q9VMA8	Q9VMA8 drosophila	
10	89	13.2	1430	5	Q9VMA7	Q9VMA7 drosophila	
11	88.5	13.1	287	11	Q8R076	Q8R076 mus musculus	
12	88.5	13.1	846	13	Q8UUX6	Q8UUX6 gallus gall	
13	88.5	13.1	1196	4	Q9H0H2	Q9H0H2 homo sapien	
14	88.5	13.1	1196	4	Q9N157	Q9N157 homo sapien	
15	86.5	12.8	719	4	Q96D37	Q96D37 homo sapien	
16	85.5	12.6	166	11	O08526	O08526 mus musculus	

1 T.APKT.CA

1 I.ADRKT.CADQEC SHPI SMA VAL ODYMA PD C R E L T I H R G O V V Y F S K L -- K G R G R L F W G 57



Tue Dec 30 10:20:55 2003

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Davenport L.B., Davies P.,  
RA Cherry J.M., Cawley S., Dahle C., Dahlen C., Dugan-Rocha S., Dunn P.,  
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foslér C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glöckler A., Gong F., Gorrell J.H., Gu Z., Hernandez J.R., Houck J.,  
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,  
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Ibegwam C.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RA "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Celinker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Evans C.A., Gocayne J.D., Holsinger K.E., Rosen B., White O.,  
RA Bantz J., An H., Baldwin D., Bantz J., Beeson K.Y., Busam D.A.,  
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,  
RA Dodson K., Dorset V., Doup L.E., Doyle C., Dresnek D., Farfan D.,  
RA Ferrera S., Frise E., Galle R.F., Garg N.S., George R.A.,  
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,  
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,  
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,  
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Searle F.,  
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,  
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
RA "Sequencing of *Drosophila melanogaster* genome."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Mitra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,  
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
RA Searle S.M.J., Smith E., Shu S., Smutnák F., Whitfield E.,  
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
RA "Annotation of *Drosophila melanogaster* genome."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA FlyBase;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AE003614; AF52413.2; -;  
DR FlyBase; FBgn0051635; CG31635.  
SQ SEQUENCE 1257 AA; 139136 MW; 5843F0540E9A511 CRC64;

Query Match 13.2%; Score 89; DB 5; Length 1257;  
Best Local Similarity 27.4%; Pred. No. 1,2;  
Matches 32; Conservative 18; Mismatches 55; Indels 12; Gaps 3;  
QY 6 LLFLPLVAVCAVHGIFMDRLASKKLCADDECVTISLASAQEDYNAPCRFINVKGGQ 65  
DB 17 LALVLGLLICCLPTLTWATLSDKRLCADPCKEQIISMGIAKITYAIGGGLISFKINSP 76  
QY 66 IYVYSKLKENGAGFEFFAGSVGGQDQEMGVVPPRLNVKEQRV---QEATKEVP 119  
DB 77 IRLVLSKSGSN--MOLW-----GVDINGRGYANKDFIMEKKILVRDKLLYEVP 124  
RESULT 10  
ID Q9VMA7 PRELIMINARY; PRT; 1430 AA.  
AC Q9VMA7;  
DT 01-MAY-2000 (TREMELrel. 13, Created)  
DT 01-MAY-2002 (TREMELrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)  
DE CG11098 protein.  
GN CG11098.  
OS *Drosophila melanogaster* (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Fendell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,  
RA Balaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Brottier P.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Center A., Chandra I.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Davenport L.B., Davies P.,  
RA Cherry J.M., Cawley S., Dahle C., Dahlen C., Dugan-Rocha S., Dunn P.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
RA Foslér C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glöckler A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,  
RA Hostin D., Houston K.A., Howland T.J., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarri C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Ibegwam C.,  
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,  
RA "The genome sequence of *Drosophila melanogaster*."  
RL Science 287:2185-2195(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Adams M.D., Celinker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,  
RA Celinker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

ProDom: PD000066; SH3; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS0001; SH2; 1.  
DR PROSITE; PS0002; SH3; 2.  
KW Hypothetical protein.  
SQ SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;

Query Match 13.1%; Score 88.5; DB 11; Length 287;  
Best Local Similarity 31.3%; Pred.No.0.22; Indels 11; Gaps 2;  
Matches 21; Conservative 14; Mismatches 21; Last annotation update)

QY 41 ISLASAQEDYNAPDCRFINVKQQQIVVYSKLVKENGAGFEWAGSVYGDGQDEMVGYYF 100  
Db 230 LGAIATARYDFCARDRELSLKGMVKIYTKM-----SANGWNRGEVNGR-----VGPF 278  
QY 101 PRLNVKE 107  
Db 279 PSTYVEE 285

RESULT 12  
Q8UUX6 PRELIMINARY; PRT; 846 AA.  
ID Q8UUX6 PRELIMINARY; PRT; 846 AA.  
AC Q8UUX6; 2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE GDP/GTP exchange factor VAV3.  
GN VAV3.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=11805146;  
RA Inabe K., Ishiai M., Scharenberg A.M., Freshney N., Downward J.,  
RA Kurosaki T.;  
RT "Vav3 Modulates B Cell Receptor Responses by Regulating  
RT Phosphoinositide 3-Kinase Activation.";  
J. Exp. Med. 195;189-200(2002). DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
DR EMBL; AY046915; AAL06249.1; -.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR003247; CH type.  
DR InterPro; IPR003219; DAG-PE-bind.  
DR InterPro; IPR001331; GDS\_CDC24.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR000219; RhoGEF.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR003096; SM22\_calponin.  
DR Pfam; PF00307; CH; 1.  
DR Pfam; PF00130; DAG-PE-bind; 1.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhoGEF; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 1.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR PRINTS; PR00888; SM22CALPONIN.  
DR ProDom; PD001527; CH type; 1.  
DR ProDom; PD000093; SH2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00033; CH; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhoGEF; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.

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Query Match      13.1%; Score 88.5; DB 4; Length 1196;
Best Local Similarity 33.3%; Pred. No. 1.3;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

QY      38 VYISLASAQEDYNAPDCRFIVNKKGOQIIVYKLVKENGAGEFWAGSVYGGQDEMGV 97
Db      1050 VDTAPTVALYDYATNARSDELTHRGDIIRVF---FKDN--EDWYVGSIT-KGKGS----- 1098

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Tue Dec 30 10:20:55 2003

OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Straussberg R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.  
DR EMBL; BC013361; AAH13361.1; -.  
DR InterPro; IPR002219; DAG\_PE-bind.  
DR InterPro; IPR001331; GDS\_CDC24.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR000219; RhogEF.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00130; DAG\_PE-bind; 1.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhogEF; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 2.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR ProDom; PD000093; SH2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhogEF; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
DR PROSITE; PS00741; DH\_1; 1.  
DR PROSITE; PS50010; DH\_2; 1.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
DR PROSITE; PS50001; SH2; 1.  
DR PROSITE; PS50002; SH3; 2.  
KW Hypothetical protein; SH3 domain.  
SQ SEQUENCE 719 AA; 83727 MW; A51B757DA543BA6C CRC64;

Query Match 12.8%; Score 86.5; DB 4; Length 719;  
Best Local Similarity 32.9%; Pred. No. 1.1;  
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;  
  
QY 44 ASAQEDYNAPCRFINVKKGQIYVYVKLVKENGAEFWAGSVYGDQDENGWVGYPFRN 103  
Db 661 AKARYDFCARDSELSLKEGDII----KILNKGQGGWWRGEIYGR-----VGVFPAN 709  
QY 104 LVKEQRYQOE 113  
Db 710 YVEED--YSE 717

Search completed: December 29, 2003, 16:06:24  
Job time : 22.7199 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 25.098 Seconds  
(without alignments)  
809.506 Million cell updates/sec

Title: US-10-019-455A-6  
Perfect score: 676  
Sequence: 1 MARILLFLPGLNAVCVHG.....RVQEAKEVPTTIDFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues  
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq 19Jun03.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	676	100.0	128	22	Human growth regul
2	676	100.0	128	22	Human MLP protein
3	676	100.0	128	23	Human angiogenesis
4	676	100.0	128	23	Human PRO9873 prot
5	676	100.0	128	23	Human PRO protein,
6	676	100.0	128	23	Novel human secre
7	602	89.1	128	22	Mouse MLP protein
8	600	88.8	128	22	Rat MLP protein se
9	590	87.3	110	22	Human MLP protein

10	561	83.0	105	22	AA82672	Human growth regul
11	547	80.9	110	22	AA82671	Mouse MLP protein
12	541	80.0	110	22	AA82671	Rat MLP protein se
13	417	61.7	87	22	AA82671	Rat MLP protein se
14	257.5	38.1	131	16	AA82671	Melanoma inhibitor
15	257.5	38.1	131	22	AA82671	Human MIA protein
16	255.5	37.8	137	22	AA82671	Recombinant human
17	215.5	34.2	130	16	AA82671	Melanoma inhibitor
18	226.5	33.5	138	22	AA82671	Human protein sequ
19	225.5	33.4	125	23	AA82671	Human TANGO 130 MI
20	225.5	33.4	410	21	AA82671	Human TANGO 130 pr
21	225.5	33.4	410	21	AA82671	Human TANGO 130 pa
22	225.5	33.4	1907	23	AA82671	Human TANGO 130 po
23	217	32.1	499	22	AA82671	Human PRO polypept
24	217	32.1	499	24	AA82671	Human secreted/pro
25	217	32.1	499	24	AA82671	Human secreted/tra
26	217	32.1	499	24	AA82671	Novel human secret
27	217	32.1	499	24	AA82671	Human secreted/tra
28	217	32.1	499	24	AA82671	Human PRO polypept
29	217	32.1	499	24	AA82671	Human PRO polypept
30	217	32.1	499	24	AA82671	Human secreted/tra
31	217	32.1	499	24	AA82671	Human secreted/tra
32	217	32.1	499	24	AA82671	Human TANGO 130 MI
33	215	31.8	303	22	AA82671	Human PRO polypept
34	215	31.8	303	22	AA82671	Human PRO polypept
35	215	31.8	303	22	AA82671	Human secreted/tra
36	215	31.8	303	23	AA82671	Human angiogenesis
37	215	31.8	303	23	AA82671	Human PRO19670 pro
38	215	31.8	303	23	AA82671	Human secreted pol
39	215	31.8	303	24	AA82671	Human secreted/tra
40	215	31.8	303	24	AA82671	Human PRO19670 pro
41	215	31.8	303	24	AA82671	Human secreted/tra
42	215	31.8	303	24	AA82671	Human PRO polypept
43	215	31.8	303	24	AA82671	Human secreted/tra
44	215	31.8	303	24	AA82671	Novel human secret
45	215	31.8	303	24	AA82671	Human secreted/tra

ALIGNMENTS

RESULT 1  
AA82671  
ID AA82671 standard; Protein; 128 AA.  
AC AA82671;  
XX  
XX 02-OCT-2001 (first entry)  
XX  
XX Human growth regulatory-like polypeptide.  
XX  
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
XX neuroectodermal tumour; glioma; cancer; therapy; diagnosis.  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX Peptide 1..23  
XX Protein /label= Signal\_peptide  
XX /label= Mature\_protein  
XX /note= "separately claimed in Claim 10"  
XX  
XX WO200155332-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-US02455.  
XX  
XX 25-JAN-2000; 2000US-0491404.  
XX 02-MAY-2000; 2000US-0563786.  
XX (HYSE-) HYSEQ INC.  
XX

XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
PI Drmanac RT;  
XX WPI; 2001-483233/52.  
DR N-PSDB; AAH26343.  
XX Isolated human growth regulatory-like polypeptide useful for treating  
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
PT hyperproliferative disorders, coagulation disorders, and nervous system  
PT disorders -  
XX Claim 10; Page 116-117; 119pp; English.  
XX The present sequence is that of a novel human growth regulatory-like  
CC polypeptide (GRLP). The amino acid sequence is predicted from a  
CC novel assembled cDNA (see AAH26343) based on Hyseq clone number  
CC 1637272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
CC belongs to the same protein family as growth regulatory proteins,  
CC growth factors, human melanoma derived growth regulatory protein,  
CC precursor (64% similarity and 45% identity over 111 amino acids)  
CC or melanoma inhibitory activity, cattle cartilage-derived  
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
CC similarity over 126 amino acids) and other retinoic acid-sensitive  
CC proteins. GRLP polypeptides and polynucleotides of the invention  
CC can be used in the prophylaxis, treatment (including gene therapy)  
CC and diagnosis of disorders and diseases caused by, or involving,  
CC cartilage development and maintenance, inhibition of melanoma cell  
CC growth and tumours, including neuroectodermal tumours such as  
CC gliomas. The polypeptides, which include the GRLP mature protein,  
CC may also have nutritional uses, cytokine and cell proliferation  
CC or differentiation activity, stem cell growth factor activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC immunosuppressive or immunostimulant activity, activin/inhibin  
CC activity, chemotactic/chemokinetic activity, haemostatic and  
CC thrombolytic activity, use in cancer diagnosis and therapy,  
CC drug screening, receptor/ligand activity, antiinflammatory  
CC activity, and treatment of leukaemia, nervous system disorders,  
CC arthritis and inflammation.  
XX Sequence 128 AA;  
Query Match 100.0%; Score 676; DB 22; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.9e-80;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFNV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFNV 60  
QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDENGWVGVPFRNLVKQRVYQEATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDENGWVGVPFRNLVKQRVYQEATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128  
RESULT 2  
AAB69123  
ID AAB69123 standard; Protein; 128 AA.  
XX AAB69123;  
XX 23-APR-2001 (first entry)  
XX Human MLP protein sequence SEQ ID NO:6.  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiac; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.

XX Homo sapiens.  
XX WO200102564-A1.  
XX 11-JAN-2001.  
XX 29-JUN-2000; 2000WO-JP04278.  
XX 30-JUN-1999; 99JP-0186718.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX WPI; 2001-159271/16.  
DR N-PSDB; AAF59065.  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX Claim 2; Page 91-92; 111pp; Japanese.  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX Sequence 128 AA;  
Query Match 100.0%; Score 676; DB 22; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.9e-80;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFNV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFNV 60  
QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDENGWVGVPFRNLVKQRVYQEATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDENGWVGVPFRNLVKQRVYQEATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128  
RESULT 3  
AAB95602  
ID AAB95602 standard; Protein; 128 AA.  
XX AAB95602;  
XX 19-JUL-2002 (first entry)  
XX Human angiogenesis related protein PRO9873 SEQ ID NO: 360.  
XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnery;  
KW antiarteriosclerotic.  
XX Homo sapiens.  
XX WO200208284-A2.  
XX



```

PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001US-0796498.
PR 01-MAR-2001; 2001US-0806520.
PR 01-MAR-2001; 2001US-0806520.
PR 09-MAR-2001; 2001US-0806520.
PR 14-MAR-2001; 2001US-0806520.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854208.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001US-0866034.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001US-0870574.
PR 01-JUN-2001; 2001US-0871743.
PR 01-JUN-2001; 2001US-0871743.
PR 01-JUN-2001; 2001US-0871780.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Goddard A, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Goddard A, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
XX N-PSDB; ABL88251.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 11; Fig 360; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABL884817 to
XX ABL88503. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX antiangiogenic, hypotensive, vulnary and antiarteriosclerotic
XX activities, and can be used in gene therapy. The PRO polynucleotides,
XX proteins, agonists and antagonists are useful for treating or diagnosing
XX a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX degeneration, atherosclerosis, hypertension, arterial restenosis,
XX rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX carcinoma) and wound healing. The PRO polynucleotides have applications
XX in molecular biology, including use as hybridisation probes, and in
XX chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX probes used in the exemplification of the present invention.
XX
XX Sequence 128 AA;
XX
XX Query Match 100.0%; Score 676; DB 23; Length 128;
XX Best Local Similarity 100.0%; Pred. No. 7.9e-80;
XX Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Qy 1 MARILLPLGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60
XX Db 1 MARILLPLGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60
XX
XX Qy 61 KKGQIYVYKLVKENGAGFWAGSVGQDQGVGFPRNLVKEQRYVQATKEVPT 120
XX Db 61 KKGQIYVYKLVKENGAGFWAGSVGQDQGVGFPRNLVKEQRYVQATKEVPT 120
XX
XX Qy 121 TDIDFFCE 128
XX Db 121 TDIDFFCE 128
XX
XX RESULT 5
XX AAU83627
XX ID AAU83627 standard; Protein; 128 AA.
XX
XX AC AAU83627;
XX
XX DT 08-MAY-2002 (first entry)
XX
XX Human PRO protein, Seq ID No 72.
XX
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
XX breast cancer; prostate tumour; rectal tumour; liver tumour;
XX pericyte cell proliferation; chondrocyte cell proliferation;
XX tumour necrosis factor-alpha.
XX
XX Homo sapiens.
XX
XX WO200208288-A2.
XX
XX 31-JAN-2002.
XX
XX 29-JUN-2001; 2001WO-US21066.
XX
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220585P.
XX 25-JUL-2000; 2000US-220605P.
XX 25-JUL-2000; 2000US-220607P.
XX 25-JUL-2000; 2000US-220624P.
XX 25-JUL-2000; 2000US-220638P.
XX 25-JUL-2000; 2000US-220664P.
XX 25-JUL-2000; 2000US-220666P.
XX 26-JUL-2000; 2000US-220893P.
XX 28-JUL-2000; 2000WO-US20710.
XX 23-AUG-2000; 2000WO-US23522.
XX 24-AUG-2000; 2000WO-US23328.
XX 15-SEP-2000; 2000US-000000P.
XX 10-NOV-2000; 2000WO-US30873.
XX 28-NOV-2000; 2000US-253646P.
XX 01-DEC-2000; 2000WO-US22678.
XX 20-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 28-FEB-2001; 2001WO-US06520.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001WO-US17092.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2002-172001/22.
XX N-PSDB; ABL83571.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX useful for treating a PRO related disorder and for diagnosing tumours
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX tumour or liver tumour -
XX
XX Claim 11; Figure 72; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX agonists and antagonists are useful for treating a PRO related disorder.
XX The PRO polypeptides are useful for diagnosing tumours, especially lung
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX liver tumour. The PRO polypeptides are useful for stimulating the
XX proliferation of, or gene expression, in pericyte cells, for stimulating
XX the proliferation or differentiation of chondrocyte cells, for
XX stimulating the release of tumour necrosis factor-alpha from human blood,
XX for stimulating or inhibiting the proliferation of normal human dermal
XX fibroblast cells. The PRO polypeptide may also be used as molecular
XX weight markers and for tissue typing. The PRO nucleic acids have
XX applications in molecular biology, including use as hybridisation probes,
XX and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
XX protein sequences of the invention.
XX
XX Sequence 128 AA;
XX
XX Query Match 100.0%; Score 676; DB 23; Length 128;

```



Best Local Similarity 100.0%; Pred. No. 7.9e-80;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDEMVGVPFRNLVKEQRYQVQATKEVPT 120  
DB 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDEMVGVPFRNLVKEQRYQVQATKEVPT 120  
QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128

RESULT 6  
AAU09871  
ID AAU09871 standard; Protein; 128 AA.  
XX AAU09871;  
XX  
XX  
XX  
XX 26-FEB-2002 (first entry)  
XX Novel human secreted protein #12.  
XX  
XX Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine;  
XX antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
XX human; cancer; autoimmune disease; wound healing disorder; infection;  
XX haematopoietic disorder; inflammatory disorder; infertility;  
XX neurological disease; psychiatric disease; cardiovascular disease;  
XX respiratory disease; renal; gastrointestinal.  
XX Homo sapiens.  
XX  
XX WO200179454-A1.  
XX  
XX 25-OCT-2001.  
XX  
XX 11-APR-2001; 2001WO-US11797.  
XX  
XX 13-APR-2000; 2000US-196603P.  
XX 24-APR-2000; 2000US-199417P.  
XX (SMIK ) SMITHKLINE BEECHAM CORP.  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
XX  
XX WPI; 2002-061975/08.  
XX N-PSDB; AAS17583.  
XX  
XX New secreted proteins or polypeptides, useful for treating e.g. cancer,  
XX autoimmune diseases, wound healing disorder, infections, haematopoietic  
XX disorders, inflammatory disorders, infertility, neurological and  
XX psychiatric diseases, cardiovascular diseases, respiratory diseases,  
XX renal diseases, or gastrointestinal diseases. These may also be used to  
XX treat diseases, abnormalities and disorders caused by abnormal  
XX expression, production, function and/or metabolism of the genes, as  
XX vaccines for inducing immunological responses in a mammal, and in  
XX screening methods for detecting the effect of added compounds on the  
XX production of mRNA and polypeptide in cells. The polypeptides can be used  
XX as immunogens to produce antibodies immunospecific for the polypeptides,  
XX and to identify membrane-bound or soluble receptors. The polynucleotides  
XX may be used as diagnostic reagents, in chromosome localisation studies,  
XX and in tissue expression studies. The present sequence represents the

CC amino acid sequence of novel human secreted protein #12.  
XX  
XX  
SQ Sequence 128 AA;  
Query Match 100.0%; Score 676; DB 23; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.9e-80; Indels 0; Gaps 0;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDEMVGVPFRNLVKEQRYQVQATKEVPT 120  
DB 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDGDEMVGVPFRNLVKEQRYQVQATKEVPT 120  
QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128

RESULT 7  
AAB69125  
ID AAB69125 standard; Protein; 128 AA.  
XX AAB69125;  
XX  
XX 23-APR-2001 (first entry)  
XX Mouse MLP protein sequence SEQ ID NO:12.  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX cardiant; gene therapy; secretory cell function regulator; promoter;  
XX inhibitor.  
XX Mus musculus.  
XX  
XX WO200102564-A1.  
XX  
XX 11-JAN-2001.  
XX  
XX 29-JUN-2000; 2000WO-JP04278.  
XX  
XX 30-JUN-1999; 99JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
XX Tanaka H;  
XX  
XX WPI; 2001-159271/16.  
XX N-PSDB; AAF59068.  
XX  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
XX encoded DNA, applicable as drugs, in diagnosis and development of  
XX promoters and inhibitors for preventing or treating e.g. bone and joint  
XX diseases -  
XX  
XX Claim 4; Page 93-94; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
XX activities, and can be used in gene therapy and as secretory cell  
XX function regulators. The MLP proteins and DNAs can be used in drugs, in  
XX the diagnosis and development of promoters and inhibitors for preventing  
XX or treating bone and joint diseases as well as pathologic angiogenesis.  
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
XX in the exemplification of the present invention.  
XX  
XX Sequence 128 AA;  
Query Match 89.1%; Score 602; DB 22; Length 128;

Best Local Similarity 86.7%; Pred. No. 3.6e-70;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60  
DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFIDV 60

QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDQDMGVGVGFPRNLVKQRVYQEAKEVPT 120  
DB 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDQDMGVGVGFPRNLVKQRVYQEAKEIPT 120

QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128

RESULT 8  
AAB69130  
ID AAB69130 standard; Protein; 128 AA.  
XX  
AC AAB69130;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Rat MLP protein sequence SEQ ID NO:47.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX  
OS Rattus sp.  
XX  
PN WO200102564-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 29-JUN-2000; 2000WO-JP04278.  
XX  
PR 30-JUN-1999; 95JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
DR WPI; 2001-159271/16.  
DR N-PSDB; AAF59098.  
XX  
PT Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
PS Claim 6; Page 106; 11lpp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 128 AA;

Query Match 88.8%; Score 600; DB 22; Length 128;  
Best Local Similarity 86.7%; Pred. No. 6.6e-70;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60  
DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFIDV 60

Db 1 MARILLLLGGIVALCAGHGMFMDKLSKKLCADEECYVTTISLARAQEDYNAPDCRFINV 60

QY 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDQDMGVGVGFPRNLVKQRVYQEAKEVPT 120  
DB 61 KKGQIYVYVKLVKENGAGFEWAGSVYGDQDMGVGVGFPRNLVKQRVYQEAKEIPT 120

QY 121 TDIDFFCE 128  
DB 121 TDIDFFCE 128

RESULT 9  
AAB69126  
ID AAB69126 standard; Protein; 110 AA.  
XX  
AC AAB69126;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human MLP protein sequence SEQ ID NO:24.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX  
OS Homo sapiens.  
XX  
PN WO200102564-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 29-JUN-2000; 2000WO-JP04278.  
XX  
PR 30-JUN-1999; 95JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
DR WPI; 2001-159271/16.  
DR N-PSDB; AAF59079.  
XX  
PT Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
PS Claim 1; Page 97-98; 11lpp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 110 AA;

Query Match 87.3%; Score 590; DB 22; Length 110;  
Best Local Similarity 100.0%; Pred. No. 1.1e-68;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 HGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKENG 78  
DB 1 HGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKENG 60

QY 79 GEFWAGSVYGDQDMGVGVGFPRNLVKQRVYQEAKEVPTTIDIDFFCE 128  
DB 61 GEFWAGSVYGDQDMGVGVGFPRNLVKQRVYQEAKEVPTTIDIDFFCE 110



## RESULT 12

AAB69131 ID AAB69131 standard; Protein; 110 AA.  
 AC AAB69131;  
 XX 23-APR-2001 (first entry)  
 DT XX  
 DE Rat MLP protein sequence SEQ ID NO:49.  
 XX  
 XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor.  
 XX  
 OS Rattus sp.  
 XX  
 XX WO200102564-A1.  
 FN  
 PD 11-JAN-2001.  
 XX  
 XX 29-JUN-2000; 2000WO-JP04278.  
 PF  
 XX 30-JUN-1999; 99JP-0186718.  
 PR  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX  
 XX WPI; 2001-159271/16.  
 DR  
 DR N-PSDB; AAF59099.  
 XX  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 XX Claim 5; Page 107; 111pp; Japanese.  
 PS  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 110 AA;  
 Query Match 80.0%; Score 541; DB 22; Length 110;  
 Best Local Similarity 89.1%; Pred. No. 2.7e-62;  
 Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
 Qy 19 HGFMFMDKLKLCADCECVYTIISLAQAQEDYNAPDCRFINVKKGQIYVYVKLVKXNGA 78  
 Db 1 HGFMFMDKLKLCADCECVYTIISLAQAQEDYNAPDCRFINVKKGQIYVYVKLVKXNGA 60  
 Qy 79 GEFWAGSVYGDQDEMGVYGFPRNLVKEQRYVQATKEVPTTIDIDFFCE 128  
 Db 61 GAFWAGSVYGDQDEMGVYGFPRNLVKEQRYVQATKEVPTTIDIDFFCE 110  
 RESULT 13  
 AAB69129 ID AAB69129 standard; Protein; 87 AA.  
 XX  
 AC AAB69129;  
 XX  
 XX 23-APR-2001 (first entry)  
 DT  
 DE Rat MLP protein sequence SEQ ID NO:39.  
 XX

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor.  
 XX  
 OS Rattus sp.  
 XX  
 XX WO200102564-A1.  
 FN  
 PD 11-JAN-2001.  
 XX  
 XX 29-JUN-2000; 2000WO-JP04278.  
 PF  
 XX 30-JUN-1999; 99JP-0186718.  
 PR  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX  
 XX WPI; 2001-159271/16.  
 DR  
 DR Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 XX Example 9; Page 103; 111pp; Japanese.  
 PS  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 87 AA;  
 Query Match 61.7%; Score 417; DB 22; Length 87;  
 Best Local Similarity 88.5%; Pred. No. 3e-46;  
 Matches 77; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
 Qy 24 DRLASKKLCADCECVYTIISLAQAQEDYNAPDCRFINVKKGQIYVYVKLVKXNGAFWA 83  
 Db 1 DKLSSKKLCADCECVYTIISLAQAQEDYNAPDCRFINVKKGQIYVYVKLVKXNGAFWA 60  
 Qy 84 GSVYGDQDEMGVYGFPRNLVKEQRYV 110  
 Db 61 GSVYGDQDEMGVYGFPRNLVKEQRYV 87  
 RESULT 14  
 AAB69811 ID AAB69811 standard; Protein; 131 AA.  
 XX  
 AC AAB69811;  
 XX  
 XX 25-MAR-2003 (updated)  
 DT 26-OCT-1995 (first entry)  
 DE Melanoma inhibiting protein (human).  
 XX  
 XX Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;  
 KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;  
 KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;  
 KW probe; fusion protein.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9503328-A2.

XX PD 02-FEB-1995.  
XX PF 19-JUL-1994; 94WO-EP02369.  
XX PR 20-JUL-1993; 93DE-4324247.  
XX PA (BOEF ) BOHRINGER MANNHEIM GMBH.  
XX PI Bogdahn U, Buettner R, Kaluza B;  
XX WPI; 1995-075191/10.  
XX DR N-PSDB; AAQ84050, AAQ84051.  
XX  
PT New melanoma inhibiting protein and related nucleic acid -  
PT vectors, transformed cells, antibodies etc., useful for treating  
PT tumours and as immunosuppressant e.g. by gene therapy  
XX  
PS Claim 1; Page 54; 85pp; German.  
XX  
CC This protein has melanoma-inhibiting activity and can be used to  
CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell  
CC lung cancer, neuroectodermal tumours) or as an immunosuppressant  
CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of  
CC peripheral blood lymphocytes). Antibodies raised against the  
CC protein can be used to detect cell producing the protein and also  
CC for protein purification. Probes derived from DNA encoding the  
CC protein (AAQ84050, AAQ84051) can be used to detect sequences encoding  
CC the protein or related proteins. The protein may be expressed as  
CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 131 AA;  
Query Match 38.1%; Score 257.5; DB 16; Length 131;  
Best Local Similarity 41.2%; Pred. No. 3.6e-25;  
Matches 56; Conservative 26; Mismatches 41; Indels 13; Gaps 5;  
Qy 1 MARILLFLPGLVAVCA-----VHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPD 54  
Db 1 MARSLVCL--GVIIILSAFSGPGVGRGPMPLADRLKLCADQECSPISMAVALQDYMAPD 58  
Qy 55 CRFINVKKGQIYYVYKLVKENGAGE-FWAGSVYGDGDENGV-VGYFPRNLVKEQRYVQ 112  
Db 59 CRFLTIRHGQVYVYVFSKL---KGRGLFWGSGVQDYYGDLAARLGYFPSSIVREDQTLK 115  
Qy 113 EATKEVPTTIDFFCE 128  
Db 116 PGKVDVKTDKWDFYCQ 131  
RESULT 15  
ID AAG65614  
XX AAG65614 standard; Protein; 131 AA.  
XX AC AAG65614;  
XX  
DT 07-JAN-2002 (first entry)  
XX Human MIA protein sequence.  
XX  
KW MIA; melanoma inhibiting activity protein; antiinflammatory; human;  
KW antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;  
KW immunosuppressive; ophthalmological; dermatological; antidiabetic;  
KW neuroprotective; immune tolerance; T-cell tolerance.  
XX  
OS Homo sapiens.  
XX  
PN WO200170253-A1.  
XX  
PD 27-SEP-2001.  
XX  
PF 15-MAR-2001; 2001WO-EP02991.

XX 23-MAR-2000; 2000EP-0201063.  
XX PA (ALKU ) AKZO NOBEL NV.  
XX PI Nelissen RLH, Verheijden GFM;  
XX DR WPI; 2001-611446/70.  
XX DR N-PSDB; AAH47783.  
XX  
PT Use of melanoma inhibiting activity protein or its derivatives as  
PT immune modulatory agents for the treatment of inflammatory diseases,  
PT specifically rheumatoid arthritis -  
XX  
PS Example 4; Page 34; 41pp; English.  
XX  
CC The invention relates to the use of melanoma inhibiting activity (MIA)  
CC protein and/or its fragments that have anti-inflammatory effects and  
CC induce systemic immune tolerance or specific T-cell tolerance to MIA  
CC antigen, for manufacturing a preparation against inflammatory diseases  
CC and for induction of systemic immune tolerance or specific T-cell  
CC tolerance in patients suffering from or susceptible to inflammatory  
CC diseases. A fragment of MIA is useful as a therapeutic substance and is  
CC useful for manufacture of pharmaceutical preparations against  
CC inflammatory diseases such as an immune-cell mediated cartilage  
CC destruction disease, specifically rheumatoid arthritis, autoimmune  
CC diseases like Graves' disease, juvenile arthritis, primary  
CC glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,  
CC myasthenia gravis, Addison's disease, primary biliary sclerosis,  
CC uveitis, systemic lupus erythematosus, inflammatory bowel disease,  
CC multiple sclerosis or diabetes. The MIA polypeptides have specific  
CC effect on the autoreactive T-cells thus leaving the other components of  
CC the immune system intact as compared to the non-specific suppressive  
CC effect of immunosuppressive drugs. The present sequence represents a  
CC human MIA protein.  
XX  
SQ Sequence 131 AA;  
Query Match 38.1%; Score 257.5; DB 22; Length 131;  
Best Local Similarity 41.2%; Pred. No. 3.6e-25;  
Matches 56; Conservative 26; Mismatches 41; Indels 13; Gaps 5;  
Qy 1 MARILLFLPGLVAVCA-----VHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPD 54  
Db 1 MARSLVCL--GVIIILSAFSGPGVGRGPMPLADRLKLCADQECSPISMAVALQDYMAPD 58  
Qy 55 CRFINVKKGQIYYVYKLVKENGAGE-FWAGSVYGDGDENGV-VGYFPRNLVKEQRYVQ 112  
Db 59 CRFLTIRHGQVYVYVFSKL---KGRGLFWGSGVQDYYGDLAARLGYFPSSIVREDQTLK 115  
Qy 113 EATKEVPTTIDFFCE 128  
Db 116 PGKVDVKTDKWDFYCQ 131

Search completed: December 29, 2003, 16:09:02  
Job time : 27.098 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 ; Search time 17.5686 Seconds  
(without alignments)  
1449.984 Million cell updates/sec

Title: US-10-019-455A-6

Perfect score: 676

Sequence: 1 MARILLFLPGLVAVCAVHG.....RVYQKATKEVPTTDIDFFCE 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues

Total number of hits satisfying chosen parameters: 724715

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
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17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676	100.0	128	12	US-10-216-163-72
2	676	100.0	128	12	US-10-218-765-72
3	676	100.0	128	12	US-10-219-063-72
4	676	100.0	128	12	US-10-219-066-72
5	676	100.0	128	12	US-10-219-067-72
6	676	100.0	128	12	US-10-219-068-72
7	676	100.0	128	12	US-10-219-073-72
8	676	100.0	128	12	US-10-219-074-72
9	676	100.0	128	12	US-10-219-475-72
10	676	100.0	128	12	US-10-219-480-72
11	676	100.0	128	12	US-10-219-483-72
12	676	100.0	128	12	US-10-219-525-72
13	676	100.0	128	12	US-10-219-526-72
14	676	100.0	128	12	US-10-219-530-72
15	676	100.0	128	12	US-10-219-531-72

16	676	100.0	128	12	US-10-219-532-72	Sequence 72, Appl
17	676	100.0	128	12	US-10-219-533-72	Sequence 72, Appl
18	676	100.0	128	12	US-10-223-081-360	Sequence 360, App
19	676	100.0	128	12	US-10-230-437-72	Sequence 72, Appl
20	676	100.0	128	12	US-10-232-228-72	Sequence 72, Appl
21	676	100.0	128	12	US-10-223-082-360	Sequence 360, App
22	676	100.0	128	15	US-10-227-884-72	Sequence 72, Appl
23	676	100.0	128	15	US-10-230-163-72	Sequence 72, Appl
24	676	100.0	128	15	US-10-230-338-72	Sequence 72, Appl
25	676	100.0	128	15	US-10-218-631-72	Sequence 72, Appl
26	676	100.0	128	15	US-10-230-414-72	Sequence 72, Appl
27	676	100.0	128	15	US-10-216-1598-72	Sequence 72, Appl
28	676	100.0	128	15	US-10-218-849-72	Sequence 72, Appl
29	676	100.0	128	15	US-10-227-883-72	Sequence 72, Appl
30	676	100.0	128	15	US-10-219-076-72	Sequence 72, Appl
31	676	100.0	128	15	US-10-230-434-72	Sequence 72, Appl
32	676	100.0	128	15	US-10-219-003-72	Sequence 72, Appl
33	676	100.0	128	15	US-10-219-075-72	Sequence 72, Appl
34	676	100.0	128	15	US-10-219-464-72	Sequence 72, Appl
35	676	100.0	128	15	US-10-219-466-72	Sequence 72, Appl
36	676	100.0	128	15	US-10-219-479-72	Sequence 72, Appl
37	676	100.0	128	15	US-10-219-481-72	Sequence 72, Appl
38	676	100.0	128	15	US-10-230-260-72	Sequence 72, Appl
39	676	100.0	128	15	US-10-232-231-72	Sequence 72, Appl
40	676	100.0	128	15	US-10-232-233-72	Sequence 72, Appl
41	676	100.0	128	15	US-10-216-165-72	Sequence 72, Appl
42	676	100.0	128	15	US-10-218-956-72	Sequence 72, Appl
43	676	100.0	128	15	US-10-219-468-72	Sequence 72, Appl
44	676	100.0	128	15	US-10-219-478-72	Sequence 72, Appl
45	676	100.0	128	15	US-10-219-478-72	Sequence 72, Appl

#### ALIGNMENTS

#### RESULT 1

US-10-216-163-72  
; Sequence 72, Application US/10216163  
; Publication No. US20030149239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530P1C3  
; CURRENT APPLICATION NUMBER: US/10/216,163  
; CURRENT FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASQEDYNAPDCRFNV 60
Db 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASQEDYNAPDCRFNV 60

Qy 61 KKGQIYVSKLVKENGAGFWAGSVYGDQDENGWVGVYFPRNLVKEQRYVQATKEVPT 120
Db 61 KKGQIYVSKLVKENGAGFWAGSVYGDQDENGWVGVYFPRNLVKEQRYVQATKEVPT 120

Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 2
US-10-218-765-72
; Sequence 72, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
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; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/154418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred No. 7,8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60
DB 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINV 60

QY 61 KKGQIYVYVKLVKENGAGFWAGSVYGDQDGMVGVGFPRLVKEQRYQEAATKEVPT 120
DB 61 KKGQIYVYVKLVKENGAGFWAGSVYGDQDGMVGVGFPRLVKEQRYQEAATKEVPT 120

QY 121 TDIDFFCE 128
DB 121 TDIDFFCE 128

RESULT 3
US-10-219-063-72
; Sequence 72, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PLC24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72

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Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

## RESULT 6

US-10-219-068-72  
; Sequence 72, Application US/10219068  
; Publication No. US20030187205A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530PIC31  
; CURRENT APPLICATION NUMBER: US/10/219,068  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-219-068-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

US-10-219-068-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

## RESULT 7

US-10-219-069-72  
; Sequence 72, Application US/10219069  
; Publication No. US20030187206A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530PIC40  
; CURRENT APPLICATION NUMBER: US/10/219,069  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien

US-10-219-069-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

US-10-219-069-72  
Query Match 100.0%; Score 676; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 7.8e-74;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINV 60  
QY 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVAGSVYGDQDMGVGFPRNLVKEQRYVQATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

RESULT 8  
US-10-219-073-72  
; Sequence 72, Application US/10219073  
; Publication No. US20030187207A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.

REMAINING PILOT APPLICATION DATA REMOVED - SEE THE WRAPPER OF FATH.  
NUMBER OF SEQ TO NOS. 246

RESULT 10  
US-10-219-480-72  
; Sequence 72, Application US/10219480  
; Publication No. US20030187209A1  
; GENERAL INFORMATION.

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/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/
/ FILE REFERENCE: P3530PIC38
/ CURRENT APPLICATION NUMBER: US/10/219,480

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; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-480-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60
DB 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60
QY 61 KKGQOIYVYVKLVKENGAGFWAGSVYGDQDMGVYGFPRNLVKEQRYQVQATKEVPT 120
DB 61 KKGQOIYVYVKLVKENGAGFWAGSVYGDQDMGVYGFPRNLVKEQRYQVQATKEVPT 120
QY 121 TDIDFFCE 128
DB 121 TDIDFFCE 128

RESULT 11
US-10-219-483-72
; Sequence 72, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC43
; CURRENT APPLICATION NUMBER: US/10/219,483
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-483-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60
DB 1 MARILLFLGLVAVCAVHGIFMDRLASKKLCADDECVYTIISLASAQEDYNAPDCRFINV 60
QY 61 KKGQOIYVYVKLVKENGAGFWAGSVYGDQDMGVYGFPRNLVKEQRYQVQATKEVPT 120
DB 61 KKGQOIYVYVKLVKENGAGFWAGSVYGDQDMGVYGFPRNLVKEQRYQVQATKEVPT 120
QY 121 TDIDFFCE 128
DB 121 TDIDFFCE 128

RESULT 12
US-10-219-525-72
; Sequence 72, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910

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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-526-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVCYTISLASAQEDYNAPDCRFINV 60
   |||||||
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVCYTISLASAQEDYNAPDCRFINV 60
   |||||||

QY 61 KKGQIYVYKLVKENGAGFWAGSVYGDGDENGWVGYFPRNLVKEQRYQATKEVPT 120
   |||||||
Db 61 KKGQIYVYKLVKENGAGFWAGSVYGDGDENGWVGYFPRNLVKEQRYQATKEVPT 120
   |||||||

QY 121 TDIDFFCE 128
   |||||||
Db 121 TDIDFFCE 128
   |||||||

RESULT 13
US-10-219-526-72
; Sequence 72, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-525-72

Query Match      100.0%; Score 676; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 7.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVCYTISLASAQEDYNAPDCRFINV 60
   |||||||
Db 1 MARILLFLPGLVAVCAVHGIFMDRLASKKLCADDECVCYTISLASAQEDYNAPDCRFINV 60
   |||||||

QY 61 KKGQIYVYKLVKENGAGFWAGSVYGDGDENGWVGYFPRNLVKEQRYQATKEVPT 120
   |||||||
Db 61 KKGQIYVYKLVKENGAGFWAGSVYGDGDENGWVGYFPRNLVKEQRYQATKEVPT 120
   |||||||

QY 121 TDIDFFCE 128
   |||||||
Db 121 TDIDFFCE 128
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RESULT 14
US-10-219-530-72
; Sequence 72, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-530-72
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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	257.5	38.1	131	1	US-08-578-649-5	Sequence 2, Appli
2	231.5	34.2	130	1	US-08-578-649-5	Sequence 5, Appli
3	85.5	12.6	844	1	US-07-646-537B-2	Sequence 2, Appli
4	81.5	12.1	54	3	US-09-346-510B-21	Sequence 21, Appl
5	78.5	11.6	1589	3	US-09-356-952-4	Sequence 4, Appli
6	78	11.5	625	3	US-08-996-139-15	Sequence 15, Appl
7	78	11.5	625	3	US-08-995-659-15	Sequence 15, Appl
8	78	11.5	625	3	US-09-215-649A-15	Sequence 15, Appl
9	78	11.5	625	4	US-09-577-780-15	Sequence 15, Appl
10	78	11.5	625	4	US-09-577-800-15	Sequence 15, Appl
11	78	11.5	625	4	US-09-466-496-15	Sequence 15, Appl
12	78	11.5	625	4	US-09-871-856-15	Sequence 15, Appl
13	78	11.5	625	4	US-09-871-291-15	Sequence 15, Appl
14	76	11.2	526	4	US-09-071-035-84	Sequence 84, Appl
15	76	11.2	546	4	US-09-071-035-82	Sequence 82, Appl
16	75	11.1	462	4	US-08-630-915A-38	Sequence 38, Appl
17	72.5	10.7	48	3	US-09-346-510B-24	Sequence 24, Appl
18	70.5	10.4	663	4	US-09-134-078-61	Sequence 61, Appl
19	70.5	10.4	680	4	US-09-134-078-61	Sequence 25, Appl
20	66.5	9.8	62	4	US-08-630-915A-135	Sequence 135, App
21	66.5	9.8	642	2	US-08-345-511-48	Sequence 48, Appl
22	66.5	9.8	642	2	US-08-600-993A-48	Sequence 48, Appl
23	66.5	9.8	1326	4	US-09-328-353-4886	Sequence 4886, Ap
24	66	9.8	248	4	US-08-630-915A-40	Sequence 40, Appl
25	66	9.8	280	1	US-08-434-255-8	Sequence 8, Appli
26	66	9.8	280	1	US-08-459-967-8	Sequence 8, Appli
27	66	9.8	280	1	US-08-460-327-8	Sequence 8, Appli

Db 1 MARSLVCL--GVILLSAFSGPVRGPGMPKLRKLCADQECSPHISMVAVALQDYWAPD 58  
QY 55 CRRLNVKGGQIYVYVKLVKENGAGE-FWAGSVYGGQDQEMGV-VGYFPRNLVKEQRYQ 112  
Db 59 CRFLTHRGQGVVVFVKL---KRGRLFWGGSVQSDYVYGDIAARLGYFPSSIVREDQTLK 115  
QY 113 EATKEVPTTDDPFCE 128  
Db 116 PGKVDVKTCKWDFYCQ 131

## RESULT 2

US-08-578-649-5  
; Sequence 5, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajolloff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 130 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-578-649-5

Query Match 34.2%; Score 231.5; DB 1; Length 130;  
Best Local Similarity 43.5%; Pred. No. 1.7e-22;  
Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;

QY 23 MDRLSKLCADDECVVTTISLSAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAGE-F 81  
Db 26 MPKLADWKLCADEBSCSPISMVAVALQDYVAPDCRFITRGQVYVFSKL---KGRGLF 82

QY 82 WAGSVYGGQDQEMGV-VGYFPRNLVKEQRYQATKEVPTTDDPFCE 128  
Db 83 WGGSVQGGYGYDLAARLGYFPSSIVREDLNSKPKIDMKTDQWDFYCQ 130

## RESULT 3

US-07-646-537B-2  
; Sequence 2, Application US/07646537B  
; Patent No. 5348864  
; GENERAL INFORMATION:

; APPLICANT: Barbacid, Mariano  
; TITLE OF INVENTION: Vav Proto-Oncogene Protein  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bristol-Myers Squibb Company  
; STREET: P.O. Box 4000  
; CITY: Princeton  
; STATE: New Jersey  
; COUNTRY: U.S.A.  
; ZIP: 08543-4000

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/646,537B  
; FILING DATE:

; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gaul, Timothy J.

; REGISTRATION NUMBER: 33,111  
; REFERENCE/DOCKET NUMBER: DC10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (609) 921-5901

; TELEFAX: (609) 921-4526  
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 844 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein

US-07-646-537B-2

Query Match 12.6%; Score 85.5; DB 1; Length 844;

Best Local Similarity 31.4%; Pred. No. 0.039;  
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 44 ASAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAGEFWAGSVYGGQDQEMGVYFPRN 103  
Db 786 AKARYDFCARDSELSKEGDII---KILNKKGGQGWVRGEIYGR-----IGMFFSN 834

QY 104 LVKEQRYQVE 113  
Db 835 YVEED--YSE 842

## RESULT 4

US-09-346-510B-21  
; Sequence 21, Application US/09346510B  
; Patent No. 6281014

; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.

; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof  
; FILE REFERENCE: D6221CIP

; CURRENT APPLICATION NUMBER: US/09/346,510B  
; CURRENT FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: 08/871,732  
; PRIOR FILING DATE: 1997-06-09

; NUMBER OF SEQ ID NOS: 32  
; SEQ ID NO 21

; LENGTH: 54

; TYPE: PRT  
; ORGANISM: unknown

; FEATURE:

; NAME/KEY: Domain

; OTHER INFORMATION: amino acid sequence of Vav SH3 domain

US-09-346-510B-21

Query Match 12.1%; Score 81.5; DB 3; Length 54;

Best Local Similarity 32.3%; Pred. No. 0.0024;  
Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;





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; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-995-659-15

Query Match 11.5%; Score 78; DB 3; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADDECYVTISLA 44
Db 217 VLLLFISVVAAIIFGVYRKGGKALTANLWNVNDACSSLGKSSGDRGAGSHSAT 276
QY 45 SAQEDYNAPDCRFNVKKGQIYVYKLVKENGAGEFW----AGSVYGDGDGVGVGYF 100
Db 277 SSQDEV---CEGILLMTREE-----KNVPEDGAGVCGPVCAGGPAEVRDSRTF 323
QY 101 PRNLVKEQRYVQEAATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 8
US-09-215-649A-15
; Sequence 15, Application US/09215649A
; Patent No. 6271349
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,649A
; FILING DATE: 17-Dec-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

Query Match 11.5%; Score 78; DB 3; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADDECYVTISLA 44
Db 217 VLLLFISVVAAIIFGVYRKGGKALTANLWNVNDACSSLGKSSGDRGAGSHSAT 276
QY 45 SAQEDYNAPDCRFNVKKGQIYVYKLVKENGAGEFW----AGSVYGDGDGVGVGYF 100
Db 277 SSQDEV---CEGILLMTREE-----KNVPEDGAGVCGPVCAGGPAEVRDSRTF 323
QY 101 PRNLVKEQRYVQEAATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 9
US-09-577-780-15
; Sequence 15, Application US/09577780
; Patent No. 6419929
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/577,780
; FILING DATE: 24-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/995,659
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2852-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
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;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-780-15

Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPGLVAVCAVGHIFMDR-----LASKKLCADECVYTISLA 44
Db 217 VLLLFISVVVAALIFGVYRKGGKALTANLWNVNDACSSLSGNKSSGDRCAAGSHSAT 276
QY 45 SAQEDYNADCRFINVKKGQIYVYKLVKENGAGEFW-----AGSVYGDGQDEMGVVGYP 100
Db 277 SSQGEV-----CEGILLMTREE-----KMPEDGAGVCGPVCAAGGPWAEVRDSRTF 323
QY 101 PRNLVKEQRYQVQATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 10
US-09-577-800-15
; Sequence 15, Application US/09577800
; Patent No. 6479635
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION NUMBER: US/09/577,800
; FILING DATE: 24-MAY-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/996,139
; FILING DATE: 22 DECEMBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-466-496-15

;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-577-800-15

Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPGLVAVCAVGHIFMDR-----LASKKLCADECVYTISLA 44
Db 217 VLLLFISVVVAALIFGVYRKGGKALTANLWNVNDACSSLSGNKSSGDRCAAGSHSAT 276
QY 45 SAQEDYNADCRFINVKKGQIYVYKLVKENGAGEFW-----AGSVYGDGQDEMGVVGYP 100
Db 277 SSQGEV-----CEGILLMTREE-----KMPEDGAGVCGPVCAAGGPWAEVRDSRTF 323
QY 101 PRNLVKEQRYQVQATKEVPTTD 122
Db 324 --TLVSEVETQGLSRKIPTED 343

RESULT 11
US-09-466-496-15
; Sequence 15, Application US/09466496
; Patent No. 6528482
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION NUMBER: US/09/466,496
; FILING DATE: 17-Dec-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-466-496-15
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Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

QY 4 ILLFLPLGLVAVCAVHGIFMDR-----LASKKLCADCECVYTISLA 44
DB 217 VLLLFISVVVVAALIFGVYRKGGKALTANLWNWDACSSLSGNKSSGDRACAGSHSAT 276

QY 45 SAQEDYNAPDCRFINVKKGQOIYVYKLVKENGAGEFW-----AGSVYGDGQDEMVGWGYF 100
DB 277 SSQGEV-----CEGILLMTREE-----KMWPDGAGVCGPVCAGGPPWAEVRDSRTF----- 323

QY 101 PRNLVKEQRVYQEAATKEVPTTD 122
DB 324 --TLVSEVETQGLSRKIPTD 343

RESULT 13
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-871-856-15

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Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

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DB 217 VLLLFISVVVVAALIFGVYRKGGKALTANLWNWDACSSLSGNKSSGDRACAGSHSAT 276

QY 45 SAQEDYNAPDCRFINVKKGQOIYVYKLVKENGAGEFW-----AGSVYGDGQDEMVGWGYF 100
DB 277 SSQGEV-----CEGILLMTREE-----KMWPDGAGVCGPVCAGGPPWAEVRDSRTF----- 323

QY 101 PRNLVKEQRVYQEAATKEVPTTD 122
DB 324 --TLVSEVETQGLSRKIPTD 343

RESULT 13
US-09-871-856-15
; Sequence 15, Application US/09871856
; Patent No. 6537763
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; Galibert, Laurent
; Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/871,856
; FILING DATE: 31-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/996,139
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-09-871-856-15

Query Match      11.5%; Score 78; DB 4; Length 625;
Best Local Similarity 21.1%; Pred. No. 0.24;
Matches 30; Conservative 26; Mismatches 48; Indels 38; Gaps 5;

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DB 217 VLLLFISVVVVAALIFGVYRKGGKALTANLWNWDACSSLSGNKSSGDRACAGSHSAT 276
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
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(without alignments)  
2485.278 Million cell updates/sec

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Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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41: em\_htgo\_other.\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	676	100.0	384	6	BD010802 Novel pol
2	676	100.0	384	6	BD093103 Novel pol
3	676	100.0	521	6	AX358818 Sequence
4	676	100.0	521	6	AX362311 Sequence
5	676	100.0	521	6	AX454774 Sequence
6	676	100.0	521	6	AX491252 Sequence
7	676	100.0	846	9	AF233261 Homo sapi
8	676	100.0	865	9	AF243505 Homo sapi
9	676	100.0	923	6	BD010820 Novel pol
10	676	100.0	923	6	BD093121 Novel pol
11	676	100.0	1422	9	AJ242552 Homo sapi
12	602	89.1	384	6	BD010805 Novel pol
13	602	89.1	384	6	BD093106 Novel pol
14	602	89.1	929	10	AF243504 Mus muscu
15	602	89.1	947	6	BD010821 Novel pol
16	602	89.1	947	6	BD093122 Novel pol
17	602	89.1	958	10	MMU243939 Mus muscu
18	602	89.1	1054	10	AF233333 Mus muscu
19	600	88.8	384	6	BD010835 Novel pol
20	600	88.8	384	6	BD093136 Novel pol
21	590	87.3	330	6	BD010816 Novel pol
22	590	87.3	330	6	BD093117 Novel pol
23	547	80.9	330	6	BD010817 Novel pol
24	547	80.9	330	6	BD093118 Novel pol
25	541	80.0	330	6	BD010836 Novel pol
26	541	80.0	330	6	BD093137 Novel pol
27	480	71.0	484	5	AF233518 Gallus ga
28	472	69.8	307	6	BD010830 Novel pol
29	472	69.8	307	6	BD093131 Novel pol
30	413	61.1	261	6	BD010829 Novel pol
31	413	61.1	261	6	BD093130 Novel pol
32	391	57.8	466	5	AF233519 Rana cate
33	355	52.5	121151	9	HS705D16 Human DNA
34	324.5	48.0	215581	2	AC106161 Rattus no
35	321.5	47.6	144765	2	BX510362 Mus muscu
36	257.5	38.1	396	9	BT007044 Homo sapi
37	257.5	38.1	396	12	BT007775 Synthetic
38	257.5	38.1	459	6	A42942 Sequence 1
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ALIGNMENTS

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LOCUS
DEFINITION    Novel polypeptide and DNA thereof.
ACCESSION    BD010802
VERSION      BD010802.1 GI:18639175
KEYWORDS     JP 2001069994-A/3.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS      Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE        Novel polypeptide and DNA thereof
JOURNAL      Patent: JP 2001069994-A 3 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT      OS Homo sapiens (human)
PN JP 2001069994-A/3
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
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BASE COUNT 99 a _ 70 c 106 g 109 t
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Pred. No.: 9.67e-77 Length: 384
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40
Db 61 ATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 121 ATTTCTCTGGCTAGTCTCAAGAGAAATATTAATGCCCGGACTGTAGATTCAATTAACGTT 180
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db 181 AAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGTGGAGAA 240
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db 241 TTTTGGSGCTGGCAGTGTATTATGGTGTATGGCCAGGACGAGATGGAGTCTGGGTATTTC 300
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Db 361 ACCGATATTGACITCTTCTCGGAG 384
RESULT 2
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DEFINITION    Novel polypeptide and its DNA.
ACCESSION    BD093103
VERSION      BD093103.1 GI:22638691
KEYWORDS     WO 0102564-A/3.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS      Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE        Novel polypeptide and its DNA
JOURNAL      Patent: WO 0102564-A 3 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT      OS Homo sapiens (human)
PN WO 0102564-A/3
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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FH Key source 1. .384 Location/Qualifiers
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FT /mol_type="genomic DNA"
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BASE COUNT 99 a _ 70 c 106 g 109 t
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Alignment Scores:
Pred. No.: 9.67e-77 Length: 384
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
Db 61 ATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 121 ATTTCTCTGGCTAGTCTCAAGAGAAATATTAATGCCCGGACTGTAGATTCAATTAACGTT 180
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
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QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
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QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 301 CCCAGAACTTGGTCAAGAAACAGCGTGTGTACCAAGGAGCTACCAAGGAAGTCCACC 360

QY 121 ThrAspIleAspPheCysGlu 128  
 DB 361 ACGGATATTGACTTCTTCTGGAG 384

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 ACCESSION AX358818  
 VERSION AX358818.1 GI:18675310  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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 JOURNAL Patent: WO 0193983-A 71 13-DEC-2001;  
 Genentech Inc. (US)  
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 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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US-10-019-455A-6 (1-128) x AX358818 (1-521)

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QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
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QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
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QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
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QY 121 ThrAspIleAspPheCysGlu 128  
 DB 398 ACGGATATTGACTTCTTCTGGAG 421

RESULT 5  
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QY 121 ThrAspIleAspPheCysGlu 128  
 DB 398 ACGGATATTGACTTCTTCTGGAG 421

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 DEFINITION Sequence 71 from Patent WO0208288.  
 ACCESSION AX362311  
 VERSION AX362311.1 GI:18694613  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,  
 Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,  
 Watanabe, C.K. and Wood, W.I.  
 TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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 JOURNAL Patent: WO 0208288-A 71 31-JAN-2002;  
 Genentech, Inc. (US)  
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 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
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QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 338 CCCAGGAATTTGGTCAAGGAACAGCGTGTGTACCAAGGAGCTACCAAGGAAGTCCACC 397

QY 121 ThrAspIleAspPheCysGlu 128  
 DB 398 ACGGATATTGACTTCTTCTGGAG 421

RESULT 5  
 LOCUS AX454774 521 bp DNA linear PAT 06-JUL-2002



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DEFINITION Sequence 359 from Patent WO0208284.
ACCESSION AX454774
VERSION AX454774.1 GI:21714011
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Genentech, Inc. (US)
FEATURES
source
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Location/Qualifiers
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BASE COUNT 167 a 86 c 131 g 137 t
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Alignment Scores:
Pred. No.: 1.4e-76 Length: 521
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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QY 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTCTCGCAG 421
RESULT 7
AF233261
LOCUS
DEFINITION Homo sapiens otoraplin (OTOR) mRNA, complete cds.
ACCESSION AF233261
VERSION AF233261.1 GI:8927427
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1 (bases 1 to 846)  
AUTHORS Roberton,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S., Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.  
TITLE A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping  
JOURNAL Genomics 66 (3), 242-248 (2000)  
MEDLINE 20334619  
PUBMED 10873378  
REFERENCE 2 (bases 1 to 846)  
AUTHORS Roberton,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S., Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.  
TITLE Direct Submission  
JOURNAL Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA  
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BASE COUNT 235 a 147 c 205 g 259 t  
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Alignment Scores:  
Pred. No.: 2,53e-76 Length: 846  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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Qy 81 PheTyrAlaGlySerValTyrGlyAspGlyClnAspGluMetGlyValValGlyTyrPhe 100  
Db 285 TTTTGGCTGGCAGTGTATTATGTTGATGGCAGACGAGATGGAGTCGGGTATTATTC 344  
Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
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Qy 121 ThrAspIleAspPhePheCysGlu 128

Db 405 ACGGATATTGACTTCTTCTGCGAG 428  
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AF243505  
LOCUS Homo sapiens fibrocyte-derived protein (FDP) mRNA linear PRI 26-DEC-2000  
DEFINITION AF243505  
ACCESSION AF243505  
VERSION AF243505.1 GI:11991843  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 865)  
AUTHORS Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and Petit,C.  
TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme  
JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)  
MEDLINE 20568254  
PUBMED 10998416  
REFERENCE 2 (bases 1 to 865)  
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France  
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BASE COUNT 258 a 145 c 207 g 255 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 2,6e-76 Length: 865  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-10-019-455A-6 (1-128) x AF243505 (1-865)  
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Db 8 ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 67  
Qy 21 IlePheMetAspArgLeuAlaSerLysLeuLeuCysAlaAspGluCysValTyrThr 40  
Db 68 ATATTATGACCGCTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 127  
Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
Db 128 ATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACGTAGATTCAATTAAGTT 187  
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80

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Db      198 AAAAAAGGCGCAGCATCTATGTGTACTCAAGAGCTGTTAAAAAGAAAAATGGAGCTGGAGAA 247
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Db      248 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 307
Qy      101 ProArgAsnLeuValLysGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db      308 CCCAGGAACCTGGTCAAGAAACAGCGTGTTACCAAGGAAGCTACCAAGGAAGTCCCCACC 367
Qy      121 ThrAspIleAspPheCysGlu 128
Db      368 ACGGATATTGACTTCTCTCGCGAG 391

RESULT 9
LOCUS   BD010820
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010820
VERSION   BD010820.1 GI:18639193
KEYWORDS JP 2001069994-A/21.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 21 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2001069994-A/21
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
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Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-019-455A-6 (1-128) x BD010820 (1-923)

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Qy      21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
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Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db      214 AAAAAAGGCGCAGCATCTATGTGTACTCAAGAGCTGGTAAAAAGAAAAATGGAGCTGGAGAA 273
Qy      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db      274 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTTATTTC 333
Qy      101 ProArgAsnLeuValLysGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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Qy      121 ThrAspIleAspPheCysGlu 128
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RESULT 10
LOCUS   BD093121
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093121
VERSION   BD093121.1 GI:22638709
KEYWORDS WO 0102564-A/21.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 21 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Homo sapiens (human)
PN WO 0102564-A/21
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC
A61K38/17
PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088//(C12P21/
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Alignment Scores:
Pred. No.: 2.82e-76 Length: 923
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Best Local Similarity: 100.00% Mismatches: 0
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DB: 6 Gaps: 0

US-10-019-455A-6 (1-128) x BD093121 (1-923)

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Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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Db 394 ACGGATATTGACTTCTTCTGCGAG 417

RESULT 11
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LOCUS HSA242552
DEFINITION Homo sapiens mRNA for melanoma inhibitory activity like protein
(MIAL gene).
ACCESSION AJ242552
VERSION AJ242552.1 GI:12619172
KEYWORDS melanoma inhibitory activity like protein; Mial gene.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Cararrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Rendtorff,N.D., Frodin,M., Attie-Bitach,T., Vekemans,M. and
Tommerup,N.
TITLE Identification and characterization of an inner ear-expressed human
melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
polymorphism that abolishes translation
JOURNAL Genomics 71 (1), 40-52 (2001)
MEDLINE 21100875
PUBMED 11161796
REFERENCE 2 (bases 1 to 1422)
AUTHORS Rendtorff,N.D.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical
Genetics, Institute of Medical Biochemistry and Genetics,
Blegdamsvej 3, 2200 Copenhagen N, DENMARK
REMARK Revised by author 03-AUG-1999
COMMENT Related sequence: AJ243939 (Mus musculus mRNA)
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BASE COUNT 417 a 220 c 306 g 479 t
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DB: 9 Gaps: 0
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Qy 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40
Db 61 ATATTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATACT 120
Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db 121 ATTTCTCTGGCTAGTGTCAAGAAGATTATTAATCCCGGACTGTAGATTATTAAACGTT 180
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyValaGlyGlu 80
Db 181 AAAAAAGGACAGACTATGTACTCAAAAGCTGTGTAAGAAATATGGAGCTGGAGAA 240
Qy 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db 241 TTTTGGGCTGGCAGTGTATTGTGTATGGTGTATGGCAGACGAGATGGAGTCTGGGTATTTC 300
Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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QY 121 ThrAspIleAspPheCysGlu 128
Db 361 ACCGATATTGACTTCTCTCGGAG 384

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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Mus sp. (mouse)
PN JP 2001069994-A/6
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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Query Match: 89.05% Indels: 0
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Db 61 GTATTATGGATAAATCTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTCTATACT 120
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Db 121 ATTTCTCTGGCAAGACAGAGAAAGATTACAATGCCAGACTGATAGGTTCATCGATGTC 180
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db 181 AAGAAAGGGCAGCATCTATCTTTACCCAGAGCTGGTAACAGAAAACGAGCTGGAG 240
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QY 121 ThrAspIleAspPheCysGlu 128
Db 361 ACCGATATTGACTTCTCTGTGAA 384

RESULT 13
BD093106
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Mus sp. (mouse)
PN WO 0102564-A/6
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PF 30-JUN-1999 JP 99P 186718
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
PI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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Pred. No.: 2,48e-67 Length: 384
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 6 Gaps: 0

US-10-019-455A-6 (1-128) x BD093106 (1-384)

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Db 61 GTATTATGGATAAATCTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTCTATACT 120
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Db      181 AAGAAGGGCGACAGACATCTATGTTTACTCCAAAGCTGGTAACAGAAAACGGAGCTGAGAG 240
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RESULT 14
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LOCUS      929 bp mRNA linear ROD 26-DEC-2000
DEFINITION Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.
ACCESSION AF243504
VERSION AF243504.1 GI:11991841
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 929)
Cohen-Salmon,M., Frensz,D., Liu,W., Verpy,E., Voegelings,S. and
Petit,C.
Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
in vitro effect on the early differentiation of the inner ear
mesenchyme
J. Biol. Chem. 275 (51), 40036-40041 (2000)
JOURNAL MEDLINE
PUBMED 20568254
REFERENCE 2 (bases 1 to 929)
Cohen-Salmon,M., Frensz,D., Verpy,E., Voegelings,S. and Petit,C.
AUTHORS Direct Submission
TITLE Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
JOURNAL du Dr. Roux, Paris 75015, France
FEATURES
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BASE COUNT 260 a 156 c 220 g 293 t
ORIGIN

Alignment Scores:
Pred. No.: 7,29e-67 Length: 929
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 10 Gaps: 0

US-10-019-455A-6 (1-128) x AF243504 (1-929)

```

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Qy      21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40
Db      69 GTATTATGGGATAAACTTCTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTGCTATATA 128
Qy      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db      129 ATTCTCTGGCAAGACACAGAGATTACAAATGCCAGACTGTAGGTTTCATCGATGTC 188
Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
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Qy      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db      309 CCCAGCAACTTGGTGAAGAGCAGCGTGTATACCAAGAGGGCCACCAGAGAGATCCCAACC 368
Qy      121 ThrAspIleAspPheCysGlu 128
Db      369 ACGGATATTGACTTCTCTGTGAA 392

RESULT 15
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LOCUS      947 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010821
VERSION BD010821.1 GI:18639194
KEYWORDS JP 2001069994-A/22.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 947)
Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 22 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Mus sp. (mouse)
PN JP 2001069994-A/22
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
G01N33/53//
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BASE COUNT 279 a 158 c 221 g 289 t
ORIGIN

Alignment Scores:
Pred. No.: 7,47e-67 Length: 947

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Score: 602.00 Matches: 111  
Percent Similarity: 93.75% Conservative: 9  
Best Local Similarity: 86.72% Mismatches: 8  
Query Match: 89.05% Indels: 0  
DB: 6 Gaps: 0

US-10-019-455A-6 (1-128) x BD010821 (1-947)

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          |||||
QY      21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
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          |||||
QY      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
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Db      131 ATTTCTCTGGCAAGGACACAGGAAGATTACAATGCCCAGACTGTAGGTTTCATCGATGTC 190
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QY      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
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QY      81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
          |||||
Db      251 TTTTGGGCTGGCAGTGTATTATGGTGACCCACAGGATGAGATGGGAATTGTAGGTTATTTC 310
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QY     101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
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Db     311 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC 370
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QY     121 ThrAspIleAspPheCysGlu 128
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Db     371 ACGGATATTGACTTCTTCTGTGAA 394
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Search completed: December 29, 2003, 19:57:14  
Job time : 2110.98 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:23:14 ; Search time 1324.28 Seconds  
(without alignments)  
2349.180 Million cell updates/sec

Title: US-10-019-455A-6  
Perfect score: 676  
Sequence: 1 MARILLFLPLGLVAVCAVHG.....RVYQATKEVPTTIDIFFCE 128

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPRO\_pool/US10019455/runat\_29122003\_160347\_254/app\_query.fasta\_1.1770  
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10019455.qcgn 1.1 6063 @runat\_29122003\_160347\_254 -ICPU=3  
-NO MWAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
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-XGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
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2: em\_esthum:\*  
3: em\_estin:\*  
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5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_btc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_est3:\*  
12: gb\_est4:\*  
13: gb\_est5:\*  
14: gb\_estfun:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_pro:\*  
26: em\_gss\_rod:\*  
27: em\_gss\_phg:\*  
28: em\_gss\_vri:\*  
29: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	602	89.1	488	13	BQ564607	BQ564607 gi19h02.y
3	602	89.1	514	13	BQ568498	BQ568498 gi109c02.y
4	602	89.1	534	13	BQ564134	BQ564134 gi11d01.y
5	602	89.1	560	13	BQ569741	BQ569741 gi135f01.y
6	602	89.1	608	13	BQ564944	BQ564944 gi127g09.y
7	602	89.1	630	13	BQ568471	BQ568471 gi108g04.y
8	602	89.1	696	10	BB611549	BB611549 BB611549
9	597	88.3	474	13	BQ565637	BQ565637 gi42g03.y
10	595	88.0	684	13	BQ563768	BQ563768 gi06c09.y
11	572	84.6	409	13	BQ566932	BQ566932 gi173g09.y
12	541	80.0	490	13	BQ565411	BQ565411 gi37b12.y
13	522	77.2	527	10	BE236443	BE236443 144645 MA
14	512	75.7	365	13	BY232622	BY232622 BY232622
15	502	74.3	604	13	BQ567343	BQ567343 gi88d08.y
16	413	61.1	485	13	BQ565179	BQ565179 gi32a07.y
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18	390	57.7	280	13	BQ568785	BQ568785 gi114f04.y
19	377.5	55.8	533	9	AL925854	AL925854 AL925854
20	343	50.7	588	13	BQ566776	BQ566776 gi69b07.y
21	321.5	47.6	677	13	BQ563227	BQ563227 gi01a05.y
22	302.5	44.7	678	10	AK047965	AK047965 Mus muscu
23	285	42.2	349	9	AW023324	AW023324 df53d01.y
24	279	41.3	633	14	CD360404	CD360404 AGENCOURT
25	258.5	38.2	929	13	BU195892	BU195892 AGENCOURT
26	257.5	38.1	480	12	BM715936	BM715936 UI-E-EJ0-
27	257.5	38.1	492	12	EM856478	EM856478 K-EST0140
28	257.5	38.1	507	12	BM674250	BM674250 UI-E-EJ0-
c 29	257.5	38.1	515	13	BQ892734	BQ892734 AGENCOURT
30	257.5	38.1	522	13	BQ681978	BQ681978 AGENCOURT
31	257.5	38.1	522	13	BU157778	BU157778 AGENCOURT
32	257.5	38.1	529	13	BU194561	BU194561 AGENCOURT
33	257.5	38.1	609	12	BM791767	BM791767 K-EST0071
34	257.5	38.1	890	12	EG766328	EG766328 602739014
35	257.5	38.1	1140	12	BG765502	BG765502 602739414
c 36	256.5	37.9	437	9	AV592759	AV592759 AV592759
c 37	256.5	37.9	442	9	AA282143	AA282143 zt02b05.s
c 38	256.5	37.9	517	10	BE665724	BE665724 154861 MA
c 39	255.5	37.8	473	14	CA433401	CA433401 UI-H-COO-
c 40	254	37.6	594	14	CA509768	CA509768 UI-R-F50-
c 41	252.5	37.4	453	9	AA627297	AA627297 nq68g01.s
c 42	252.5	37.2	430	10	BF439750	BF439750 nad13c10.
c 43	251.5	37.1	544	13	BQ208982	BQ208982 UI-R-DY1-
c 44	251	37.1	544	13	BQ208982	BQ208982 UI-R-DY1-
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ALIGNMENTS

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DEFINITION gi143b10.y1 Mouse Organ of Corti cDNA pbluescript Mus musculus cDNA  
clone gi143b10 5', mRNA sequence.  
ACCESSION BQ570035  
VERSION BQ570035.1 GI:21473352  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 398)



# AUTHORS TITLE JOURNAL COMMENT

Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 143 row: b column: 10  
Seq primer: M13RPl reverse primer (ABI).  
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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xli Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 1,100,000 recombinants. Stratagene's EXAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25<sup>th</sup> strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster

## FEATURES source

City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t  
ORIGIN

### Alignment Scores:

Pred. No.: 3-21e-70 Length: 398  
Score: 602.00 Matches: 111  
Percent Similarity: 93.75% Conservative: 9  
Best Local Similarity: 86.72% Mismatches: 8  
Query Match: 89.05% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ570035 (1-398)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
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QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
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Db 313 CCCAGCAACTTGGTAGAGGAGGAGGCTGTATACCAAGAGGCCACCAAGGAGATCCCAACC 372  
QY 121 ThrAspIleAspPhePheCysGlu 128  
Db 373 ACGGATATTGACTTCTTCTGTGAA 396

### RESULT 2

BQ564607

### LOCUS

DEFINITION

g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone g119h02 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ564607 488 bp mRNA linear EST 19-JUN-2002  
g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone g119h02 5', mRNA sequence.

BQ564607

EST BQ564607.1 GI:21467924

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 488)

Kachar,B.

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

Unpublished

Contact: Kachar,B.

National Cell Biology

Structural Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 19 row: h column: 02

Seq primer: M13RPl reverse primer (ABI).



from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN

Alignment Scores:  
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Score: 602.00 Matches: 111  
Percent Similarity: 93.7% Conservative: 9  
Best Local Similarity: 86.7% Mismatches: 8  
Query Match: 89.0% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ568498 (1-514)

QY 1 MetAlaArgIleGluLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 5 ATGGCAAGGATATTGATTTTGGCTTGGGGCCCTTGTGTTTATGTCGGCGCATGGT 64  
QY 21 llePheMetAspArgLeuSerLysLeuCysAlaAspGluCysValThr 40  
DB 65 GTATTATGGATAAACTTCTCTTAAAGATTGTGCGGATGAGGAGTGTCGTATACT 124

QY 41 lleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
DB 125 ATTTCTCTGGCAAGAGCACAGGAAGATTACATGCCCCAGACTGTAGGTTCATCGATGTC 184  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 185 AAGAAGGGCAGCAGATCTATGTTTCTCCAGCTGGTAAACAGAAAACGAGACTGGAGAG 244  
QY 81 PheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 245 TTTTGGGCTGGCAGTGTATGTTGTCGACCAACAGGATGAGATGGGAATTTAGATTATTTC 304  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThriLysGluValProThr 120  
DB 305 CCACCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATCCCAACC 364  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 365 ACGGATATTGACTTCTCTGTGAA 388

RESULT 4  
BQ564134  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BQ564134 534 bp mRNA linear EST 19-JUN-2002  
gilld01.V1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gilld01 5', mRNA sequence.  
BQ564134  
BQ564134.1 GI:21467451  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
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/sex="male and female"  
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organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the micro Fasttrack kit  
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
to manufacturer's instructions. Reverse transcription and  
library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both

from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

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BASE COUNT      155 a      87 c      148 g      144 t
ORIGIN
Alignment Scores:
Pred. No.:      4.9e-70      Length:      534
Score:          602.00      Matches:      111
Percent Similarity: 93.75%      Conservative: 9
Best Local Similarity: 86.72%      Mismatches: 8
Query Match:      89.05%      Indels: 0
DB:              13      Gaps: 0

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US-10-019-455A-6 (1-128) x BQ564134 (1-534)

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Db      63  GTATTATGATAAATCTTCTTCTAGAAAGTTGTGTGCGGATGAGAGTGCTGTACT 122
Qy      41  IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db      123  ATTTCTCTGCAAGAGACACAGGAAGATTACAATGCCCGACACTGTAGTTTCATCGATGTC 182
Qy      61  LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
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Qy      81  PheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
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Qy      101  ProArgAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluValProThr 120
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Qy      121  ThrAspIleAspPhePheCysGlu 128
Db      363  ACGGATATTGACTTCTTCTGTGAA 386

RESULT 5
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LOCUS      BQ569741      560 bp      mRNA      linear      EST 19-JUN-2002
DEFINITION      g1135f01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
Clone g1135f01 5', mRNA sequence.
ACCESSION      BQ569741
VERSION      BQ569741.1 GI:21473058
KEYWORDS      EST.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kachar, B.
1 (bases 1 to 560)
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished
Contact: Kachar, B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 135 row: f column: 01
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
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/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The
organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
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Gigapack III Gold Cloning kit (catalog # 237612), both
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manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adapters in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)

```

columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

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BASE COUNT      160 a      92 c      154 g      153 t
ORIGIN
Alignment Scores:
Pred. No.:      5,25e-70      Length:      560
Score:          602.00      Matches:      111
Percent Similarity: 93.75%      Conservative: 9
Best Local Similarity: 86.72%      Mismatches: 8
Query Match:      89.05%      Indels: c
DB:              13      Gaps: 0

US-10-019-455A-6 (1-128) x BQ569741 (1-560)

QY      1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValHisGly 20
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Db      66 GTATTATTGGATAAACTTCTTCTAAGAAGTTGTGTGGGATGAGGAGTGTCTCTACT 125

QY      41 IleSerLeuAlaSerAlaGlnGluAspTyrrAsnAlaProAspCysArgPheIleAsnVal 60
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QY      61 LysLysGlyGlnGlnIleTyrrValTyrrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
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QY      101 ProArgAsnLeuValLysGlnArgValTyrrGlnGluAlaThrLysGluValProThr 120
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QY      121 ThrAspIleAspPheCysGlu 128
Db      366 ACGGATATTGACTTCTCTGTGAA 389

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## RESULT 6

BQ564944  
LOCUS 608 bp mRNA linear EST 19-JUN-2002  
DEFINITION g127g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone g127g09 5', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
TITLES  
AUTHORS  
JOURNAL  
COMMENT

BQ564944  
BQ564944.1 GI:21468261  
EST.  
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Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar, B.  
1 (bases 1 to 608)  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharb@nidcd.nih.gov  
Plate: 27 row: 9 column: 09  
Seg primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

FEATURES  
source

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/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen,

Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25 $\times$  strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t

ORIGIN

Alignment Scores:  
 Pred. No.: 5,9e-70 Length: 608  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ564944 (1-608)

Qy 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 Db 13 ATGGCAAGGATATTGATCTTTTGGCTGGGGGCTTGTGTTCTATGTGCGGGCATGGT 72  
 Qy 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40  
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 Db 133 ATTTCTCTGGCAAGCAGCAGCAAGATTAACAATGCCAGACTGTAGTTCATCGATGTC 192  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 Db 193 AAGAAAGGGCGACGAGATCTATGTTTACTCCCAAGCTGGTAAACAGAAACGGAGCTGGAGAG 252  
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 Db 253 TTTTGGGCTGCAGTGTATTGTTGACACACAGATGATGATGGATTTAGTTATTTC 312  
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RESULT 7

BQ568471

LOCUS

DEFINITION BQ568471 630 bp mRNA linear EST 19-JUN-2002  
 clone gi108904.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

VERSION BQ568471

KEYWORDS BQ568471.1 GI:21471788

SOURCE EST.

ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Kachar, B.

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished

JOURNAL Contact: Kachar, B.

COMMENT

# Structural Cell Biology

National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 108 row: g column: 04

Seq primer: M13Rpl reverse primer (ABI).

Location/Qualifiers

1. .630

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/note="Organ: Organ of Corti; Vector: pBluescript; The

organ of Corti (OC) was fine dissected from a total of 386

OC as follows: 102 samples from post-natal (P) day 5; 72

from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;

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Gigapack III Gold Cloning kit (catalog # 237612), both

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manufacturer's instructions. Briefly: 1.5 ug mRNA was

reverse transcribed using a hybrid oligo(dT) linker-primer

that contains an Xho I site. First strand synthesis was

primed with the linker- primer and transcribed using

Moloney murine leukemia virus reverse transcriptase

(MMLV-RT) and 5-methyl dCTP. The second strand was

synthesized with DNA polymerase and RNase H. Complementary

DNA was blunt ended with Pfu DNA polymerase, ligated with

EcoR I adapters in the presence of ligase and digested

with Xho I. The cDNA was sequentially size fractionated

over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)

columns to enrich for cDNAs greater than 400bp and 1000 bp

, respectively. The cDNA was then directionally ligated to

the Uni-Zap XR vector, which had been predigested with

EcoR I and Xho I. The phagemid was packaged with Gigapack

III Gold and, upon titration on XLI Blue MRF' cells, the

yield of the phage library was estimated to be 11,100,000

recombinants. Stratagene's ExAssist Interference

resistance helper phage (catalogue # 211203) was adopted

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rescued library, individual cDNA clones were selected and

grown in 96-well, 2 ml growth plate. Plasmid DNA was

purified from 200 ul of saturated culture with the

Concert96(TM) plasmid purification kit (Invitrogen,

Carlsbad, CA) as instructed by the manufacturer. ESTs from

the 5' end of the cDNA clones were generated with the

universal M13 reverse primer (CAGGAACAGTATGACC) and 25 $\times$

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have hits in GenBank, but do not have assigned function;





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Db      144 ATTTCTCTGCAGACAGACAGGAGATTACAAATGCCCCAGACTGTAGTTCATCGATGTC 203
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ACCESSION BQ565637  
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 KEYWORDS EST.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  
 1 (bases 1 to 474)  
 Kachar,B.

REFERENCE EST analysis of gene expression in the mouse Organ of Corti at the  
 onset of hearing  
 Unpublished

JOURNAL Structural Cell Biology  
 COMMENT National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1599

Email: kachar@nidcd.nih.gov  
 Plate: 42 row: 9 column: 03  
 Seq primer: M13RP1 reverse primer (ABI).  
 Location/Qualifiers

FEATURES  
 source  
 1..474  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
 /clone="gi42903"  
 /sex="male and female"  
 /dev\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was

reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on Xli Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 145 a 78 c 131 g 120 t

ORIGIN

Alignment Scores:

Pred. No.: 1.92e-69 Length: 474  
 Score: 597.00 Matches: 110  
 Percent Similarity: 92.97% Conservative: 9  
 Best Local Similarity: 85.94% Mismatches: 9  
 Query Match: 88.31% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ565637 (1-474)

Qy 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 Db 14 ATGCCAAGGATATTGATTTCTTTGGGGCCCTTCTGTTCTATGTCGGCGCATGGT 73  
 Qy 21 IlePheMetAspArgLeuAlaSerLysLeuValCysAlaAspGlyCysValTyrThr 40  
 Db 74 GTATTATGATAAACATTTCTTCTTAATAGTTGTGCGGATGAGGATGTCTACT 133  
 Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 Db 134 ATTTCCTGCAAGACAGACAGAGAGATTACATGCCCACTGTAGTTCATCGATGTC 193  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAenGlyAlaGlyGlu 80  
 Db 194 AAGAAAGGGCAGCAGATCTATGTTTACTTCCAAAGCTGGTAAACAGAAACCGGAGCTGGAGAG 253  
 Qy 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 Db 254 TTTTGGGCTGCAGCTGTTTATGGTGACACACAGATGAGATGGGAATTGTAGGTTATTTTC 313  
 Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluValProThr 120



Db 314 CCAGCAACTTGGTGGAGGACGCTGTATATACCGAGGCGCCACCAAGGAGATCCCAACC 373

QY 121 ThrAspIleAspPheCysGlu 128

Db 374 ACGGATATTGACTTCTCTGTGAA 397

## RESULT 10

BQ563768

## LOCUS

DEFINITION

gi06c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

clone gi06c09 5', mRNA sequence.

## ACCESSION

BQ563768

## VERSION

BQ563768.1

## KEYWORDS

Mus musculus (house mouse)

## ORGANISM

Mus musculus

## REFERENCE

Kachar, B.

## AUTHORS

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

## JOURNAL

Unpublished

## COMMENT

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 06 row: C column: 09

Seq primer: M13Rpi reverse primer (ABI).

Location/Qualifiers

1..684

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="gi06c09"

/sex="male and female"

/dev\_stage="post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to

the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT

ORIGIN

## Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-10-019-455A-6 (1-128) x BQ563768 (1-684)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20

Db 13 ATGCGAGGAGATATTGATCTTTTGTGGGGGCTTGTGGTCTATGTCGGGGCATGCT 72

QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40

Db 73 GTATTATGATGATAAATCTTCTTAAGAGATTGTGGCGATGAGGAGTGTCTATACT 132

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60

Db 133 ATTTCTCTGGCAAGACGACAGGAGATTACATGCCCCAGACTGTAGGTTTCATCGATGTC 192

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80

Db 193 AAGAAAGGGCGACAGATCTATGTTTACTTCCAAAGCTGGTAACAGAAACCGAGCTGGAGAG 252

QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100

Db 253 TTTTGGGCTGGCAGGTTTATGTCACCCAGATGAGATGGGAATTTAGGTTATTATTC 312

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120

Db 313 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATATACGAGGAGGCCACCAAGGAGATCCCAACC 372

QY 121 ThrAspIleAspPheCysGlu 128

Db 373 ACGGATATTGACTTCTCTGTGAA 396

RESULT 11

BQ566932

LOCUS

DEFINITION

gi73909.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi73909 5', mRNA sequence.

ACCESSION

BQ566932

VERSION

BQ566932.1

GI:21470249

KEYWORDS  
SOURCE  
ORGANISM

EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 409)  
Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 73 row: 9 column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

FEATURES  
source

1..409  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
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/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/note="Organ of Corti; Vector: phluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the micro Fasttrack kit  
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
to manufacturer's instructions. Reverse transcription and  
library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both  
from Stratagene (La Jolla, CA, USA), according to  
manufacturer's instructions. Briefly: 1.5 ug mRNA was  
reverse transcribed using a hybrid oligo(dT) linker-primer  
that contains an Xho I site. First strand synthesis was  
primed with the linker- primer and transcribed using  
Moloney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was  
synthesized with DNA polymerase and RNase H. Complementary  
DNA was blunt ended with Pfu DNA polymerase, ligated with  
EcoR I adapters in the presence of ligase and digested  
with Xho I. The cDNA was sequentially size fractionated  
over Pharmacia Size Sep400 (Pharmacia, Uppeala, Sweden)  
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)  
columns to enrich for cDNAs greater than 400bp and 1000 bp  
respectively. The cDNA was then directionally ligated to  
the Uni-ZAP XR vector, which had been predigested with  
EcoR I and Xho I. The phagemid was packaged with Gigapak  
III Gold and, upon titration on XL1 Blue MRP' cells, the  
yield of the phage library was estimated to be 11,100,000  
recombinants. Stratagene's ExAssist interference  
resistance helper phage (catalogue # 211203) was adopted  
to rescue plasmid DNA from the phages. Upon plating of the  
rescued library, individual cDNA clones were selected and  
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purified from 200 ul of saturated culture with the  
Concert96(TM) plasmid purification kit (Invitrogen,  
Carlsbad, CA) as instructed by the manufacturer. ESTs from  
the 5' end of the cDNA clones were generated with the

universal M13 reverse primer (CAGGACAGCTATGACC) and 25x  
strength BigDye terminator sequencing chemistry (Applied  
Biosystems, Foster City, CA). Sequencing reactions were  
performed on MJ Tetrad thermal cyclers (MJ Research,  
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sequencers using POP5 polymer (Applied Biosystems, Foster  
City, CA). The frequency distribution of the library is  
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;  
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of  
genes are present in GenBank and have known function; 23%  
have hits in GenBank, but do not have assigned function;  
12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 102 a 75 c 121 g 111 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3,42e-66 Length: 409  
Score: 572.00 Matches: 108  
Percent Similarity: 91.41% Conservative: 9  
Fast Local Similarity: 84.38% Mismatches: 10  
Query Match: 84.62% Indels: 1  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ566932 (1-409)

Qy 1 MetAlaAaRgLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
Db 27 ATGCCAAGGATATTGATTCCTTTGCTGGGGGCCCTTCGGGTTCTATGTCGGGCATGTT 86  
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Db 87 GTATTATGATAAATCTTCTTAAGAAGTTGTGCTGTGATGAGGAGTGTGCTATAC 146  
Qy 40 rLleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVa 60  
Db 147 TATTTCTCTGCAAGACACAGCAAGATTCAATGCCGCCAGCTGTAGTTCATCGATGT 206  
Qy 60 LlysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyG 80  
Db 207 CAGAAAGGGCAGCAGATCTATGTTTCTCAACTGTGTACAGAAACCGAGCTGGAGA 266  
Qy 80 uPheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPh 100  
Db 267 GTTTTGGCTGGCAGTGTATTATGTCACCCAGGATGAGATGGGAATTGTAGGTTATT 326  
Qy 100 eProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProTh 120  
Db 327 CCCAGCAACTTGTGTGAAGGAGCAGCGTGTATACCAGAGGCCACCAAGGAGATCCCAAC 386  
Qy 120 rThrAspIleAspPhePheCys 127  
Db 387 CACGGCTATTGACTTCTTCGT 408

RESULT 12  
BQ565411

LOCUS BQ565411 490 bp mRNA linear EST 19-JUN-2002  
DEFINITION G337b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus CDNA  
clone g137b12 5', mRNA sequence.  
ACCESSION BQ565411  
VERSION BQ565411.1 GI:21468728  
KEYWORDS EST.

SOURCE  
ORGANISM  
Mus musculus (house mouse)

REFERENCE  
AUTHORS  
TITLE

1 (bases 1 to 490)  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders

JOURNAL  
COMMENT

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kacharb@nid.nih.gov

Plate: 37 row: b column: 12

Seq primer: M13P1 reverse primer (ABI).

Location/Qualifiers

1. 490

FEATURES  
source

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="BALB/c"  
/db\_xref="taxon:10090"  
/clone="gi37b12"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

191 a

BASE COUNT

# ORIGIN

## Alignment Scores:

Pred. No.: 6.18e-62 Length: 490  
Score: 541.00 Matches: 100  
Percent Similarity: 90.32% Conservative: 12  
Best Local Similarity: 80.65% Mismatches: 12  
Query Match: 80.03% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ565411 (1-490)

Qy 5 LeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyIlePheMetAsp 24  
Db 99 TTGATCTTTTGGTGGGGCCCTTGGGGTCTATGTCGGCGCATGGGTATTATGGAT 158  
Qy 25 ArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThrIleSerLeuAla 44  
Db 159 AAATCTTCTTCTAAATAATCTGTGGGATAGGAGTGTCTATCTATTCTCTGGCA 218  
Qy 45 SerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGlyGln 64  
Db 219 AGAGCACAGGAAATACAAATGCCCAACCTGATGTCATCGATGTCAAAAAGGGCAG 278  
Qy 65 GlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAlaGly 84  
Db 279 CAATCTAATGTTTACTCCAGCTGTGTACAAAACGAGCTGGAAAGTTTGGCTGGC 338  
Qy 85 SerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeu 104  
Db 339 AGTGTATTATGGGACCCAGGATGAAATGGAATGTAGGTATTATTCGCCCAACTTG 398  
Qy 105 ValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThrThrAspIleAsp 124  
Db 399 GTGAAGGAGGACGCGTGTATACAGGAGCCCAAGAGGATGCCCAACCGATATTGAC 458  
Qy 125 PhePheCysGlu 128  
Db 459 TCTTCTCGGAA 470

## RESULT 13

BE236443

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BE236443 527 bp mRNA linear EST 25-APR-2001  
14645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.

BE236443

BE236443.1 GI:9021161

EST.

Bos taurus (cow)

Bos taurus

Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

Bovidae; Bovinae; Bos.

1 (bases 1 to 527)

Smith, T.P.L., Grosche, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,

Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C., Bennett

G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G.,

Pertea, G., Holt, I., Karameycheva, S., Liang, F., Quackenbush, J. and

Keefe, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

21180013

11282978

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt\_trimmed with phred

v0.980904.e. Vector identified by cross\_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGAACAACAGTATGACCAT  
 BACKWARD: GTTTCCTCCAGTCACGACG  
 Plate: 54 row: C column: 18  
 Seq primer: ATTAGTGACACATATAG.

# FEATURES

Location/Qualifiers  
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 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
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 /clone\_lib="WARC 4BOV"  
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 Library made from pooled tissue from day 20 and day 40  
 embryos."

BASE COUNT 173 a 94 c 126 g 134 t  
 ORIGIN

Alignment Scores:  
 Pred. No.: 2,38e-59 Length: 527  
 Score: 522.00 Matches: 102  
 Percent Similarity: 83.72% Conservative: 6  
 Best Local Similarity: 79.07% Mismatches: 7  
 Query Match: 77.22% Indels: 14  
 DB: 10 Gaps: 2

US-10-019-455A-6 (1-128) x BE236443 (1-527)

Qy 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 Db 35 ATGCGAAGATTGGTGTACTTTCTCCAGGCTTGTGCCATATGCTGTGCATGGA 94  
 Qy 21 IlePheMetAspArgLeuAlaSerLysLeuLeuCysAlaAspGluCysValTyrThr 40  
 Db 95 ATATTATGACAGACTGTGTTCCAGAAGCTGTGCAGATGAATGTGCTACTACT 154  
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 Db 155 ATTCTCTGCGCAGACTCAAGAGATTACAAATGCTCCGGACTGTAGATTCAATACGTT 214  
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 Qy 81 PheTrpAlaGlySerValTyrGlyAsp---GlyGlnAspGluMetGlyValValGlyTyr 99  
 Db 251 -----GCTATGGCAATCAGTCTCGAGTGAATGGAACCGTGGTAT 295  
 Qy 100 PheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValPro 119  
 Db 296 TTTCACCAACCTGGTCCAGAACCAACATGTGTACCAAGAGCCACCAAGGAAGTTCT 355  
 Qy 120 ThrThrAspLeuAspPhePheCysGlu 128  
 Db 356 ACCACGGATATTGACTTTTTCCTGCGAG 382

# RESULT 14

BY232622 BY232622 365 bp mRNA linear EST 10-DEC-2002  
 LOCUS  
 DEFINITION BY232622 RIKEN full-length enriched, adult inner ear Mus musculus  
 cDNA clone F930026J20 5', mRNA sequence.

ACCESSION BY232622

VERSION BY232622.1 GI:26413732

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 365)

REFERENCE Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamakata, I., Kiyosawa, H.,  
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Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,  
 Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V., Chothia, C., Corbani,  
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 Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M.,  
 King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,  
 P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki,  
 H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G.,  
 Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ring,  
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 B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,  
 M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,  
 R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,  
 Watanabe, Y., Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa,  
 M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, X., Zimmer, A.,  
 Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,  
 M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,  
 Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,  
 K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,  
 E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

JOURNAL 22354683

MEDLINE 12466851

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki  
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 Email: genome-res@gscc.riken.go.jp/  
 URL: http://genome.gsc.riken.go.jp/  
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane,  
 T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,  
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 Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with  
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 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
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 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National  
 Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose  
 assistance we gratefully acknowledge. Please visit our web site  
 (http://genome.gsc.riken.go.jp) for further details.

# FEATURES

source

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 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
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 /dev\_stage="adult"  
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 BASE COUNT 97 a 60 c 110 g 98 t

## ORIGIN

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 Pred. No.: 3,05e-58 Length: 365  
 Score: 512.00 Matches: 97  
 Percent Similarity: 92.11% Conservative: 8  
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 Query Match: 75.74% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BY232622 (1-365)

QY 1 MetAlaArgLeuLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 DB 24 ATGGCAAGGATATGATCTTTTGGCTTGGGGCCCTTGTGTTCTATGTGCGGGCATGTT 83  
 QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspAspGluCysValTyrThr 40  
 DB 84 GTATTATGATTAACCTTCTTCTAAGAAGTTGTGTGCGGATGAGAGTGTCTATACT 143  
 QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 DB 144 ATTCTCTGCAAGAGCACAGGAGATTACAAATGCCACACTGTAGTTTCATCGATGC 203  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 DB 204 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGTAAACAGAAACGGAGCTGGAG 263  
 QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 DB 264 TTTGGGGCTGGCAGTTTATGTTGACCCAGGATGAGATGGGAATTGTAGTTATTTC 323  
 QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAla 114  
 DB 324 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGGCC 365

## RESULT 15

BQ567343 604 bp mRNA linear EST 19-JUN-2002  
 LOCUS gi88d08.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 DEFINITION clone gi88d08 5', mRNA sequence.

ACCESSION BQ567343

VERSION BQ567343.1 GI:21470660

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 604)

AUTHORS Kachar,B.

TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished

COMMENT Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

TEL: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 88 row: d column: 08

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1..604

source

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="gi88d08"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The

BASE COUNT 178 a 108 c 152 g 166 t  
 ORIGIN

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Pred. No.: 1.37e-56 Length: 604  
 Score: 502.00 Matches: 92  
 Percent Similarity: 96.00% Conservative: 4  
 Best Local Similarity: 92.00% Mismatches: 4  
 Query Match: 74.26% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x BQ567343 (1-604)

QY 29 LysLysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAlaSerAlaGlnGlu 48

DB 1 AAGAAGTTGTGTGCGGATGAGAGTGTGTCTATACTATTCTCTGGCAGACGACGAA 60

QY 49 AspTyrAsnAlaProAspCysArgPheIleAsnValLysGlyGlnGlnIleTyrVal 68

organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and the Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

Accession	Protein	Sequence
61	Db	GAITTACAATGCCCCAGACTGTGAGGTTTCATCGATGTCAAGAAAGGGCACGACATCTATGTT 120
69	Qy	TyrSerIysLeuValLysGluAsnGlyAlaGlyGluPheTrpAlaGlySerValTyrGly 88
121	Db	TACTCCAAGCTGGTAAACAGAAAACGGAGCTCGAGAGTGTTCGGCTGGCAGTGTTCATGCT 180
89	Qy	AspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeuValLysGluGln 108
181	Db	GACCACCAGGATGAGATGGGAATTGTAGTGTTATTTCCCCACGCAACTGGTGAAGAGGACG 240
109	Qy	ArgValTyrGlnGluAlaThrLysGluValProThrThrAspIleAspPheCysGlu 128
241	Db	CGTGTATACAGAGGCCACCAAGAGATGCCACACCGGATATTGACTTCTTCGTGAA 300

Search completed: December 29, 2003, 22:00:44  
Job time : 1330.28 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 154.353 Seconds  
(without alignments)  
2238.558 Million cell updates/sec

Title: US-10-019-455a-6

Perfect score: 676

Sequence: 1 MARILLFLPLGLVAVCAVHG.....RVYQATKEVPTTIDIDFCE 128

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Zgapop 6.0 , Zgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-O=/cgn2\_1/USPTO spool/US10019455/runat\_29122003.160347\_230/app\_query.fasta\_1.1770  
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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	676	100.0	384	22	AAF59065	Human MLP nucleoti
2	676	100.0	387	24	AAH17583	DNA encoding novel
3	676	100.0	426	22	AAH26341	Human growth regul
4	676	100.0	521	24	ABL95740	Human angiogenesis
5	676	100.0	521	24	ABL88251	Human PRO9873 CDNA
6	676	100.0	521	24	ABK33571	cDNA encoding huma
7	676	100.0	891	22	AAH98228	Human EST-derived
8	676	100.0	891	22	AAH26342	Human growth regul
9	676	100.0	923	22	AAF59083	Human MLP nucleoti
10	676	100.0	1201	22	AAH26343	Human growth regul
11	602	89.1	384	22	AAF59068	Mouse MLP nucleoti
12	602	89.1	947	22	AAF59084	Mouse MLP nucleoti
13	600	88.8	384	22	AAF59098	Rat MLP nucleotide
14	590	87.3	330	22	AAF59079	Human MLP nucleoti
15	547	80.9	330	22	AAF59080	Mouse MLP nucleoti
16	541	80.0	330	22	AAF59099	Rat MLP nucleotide
17	472	69.8	307	22	AAF59093	Rat MLP nucleotide
18	413	61.1	261	22	AAF59092	Rat MLP nucleotide
19	257.5	38.1	459	16	AAQ84050	Sequence encoding
20	257.5	38.1	459	22	AAI70083	Melanoma inhibitor
21	257.5	38.1	459	22	AAI18732	Human antisense ol
22	256.5	37.9	442	24	ABL63602	Breast cancer rela
23	256.5	37.9	442	24	ABL64012	Breast cancer rela
24	255.5	37.8	433	22	AAH47783	Recombinant human
25	255.5	37.8	555	23	ABV59229	Human prostate exp
26	253.5	37.5	330	16	AAQ84061	Sequence encoding
27	232.5	34.4	581	16	AAQ84052	Sequence encoding
28	226.5	33.5	417	22	AAH99775	Human protein enco
29	225.5	33.4	884	22	AAH22459	Human cDNA encodin
30	225.5	33.4	1230	24	ABQ79850	Human TANGO 130 pa
31	225.5	33.4	1263	21	AAZ51245	Human TANGO 130 CD
32	225.5	33.4	1363	24	ABQ79849	Human TANGO 130 po
33	225.5	33.4	4409	23	ABV21035	Human prostate exp
34	225.5	33.4	4409	23	ABV23751	Human prostate exp
35	225.5	33.4	4409	23	ABV26878	Human prostate exp
36	225.5	33.4	4409	23	ABV29625	Human prostate exp
37	225.5	33.4	5724	24	ABQ79852	Human TANGO 130 po
38	225.5	33.4	8121	24	ABQ79851	Human TANGO 130 po
39	217	32.1	2037	22	AAH46220	Human DNA encoding
40	217	32.1	2037	25	ACA57978	Human PRO20088 cDN
41	217	32.1	2037	25	ABX98448	Human cDNA encodin
42	217	32.1	2037	25	ABX98950	Novel human secret
43	217	32.1	2037	25	ACA05995	Human secreted/tra
44	217	32.1	2037	25	ABX98039	Human PRO polynucl
45	217	32.1	2037	25	ABX78823	Human PRO polynucl

# ALIGNMENTS

RESULT 1

AAF59065  
ID AAF59065 standard; DNA; 384 BP.  
AC AAF59065;  
XX  
XX  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human MLP nucleotide sequence SEQ ID NO:4.

XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
OS Homo sapiens.  
XX

```

PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JF04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
DR P-PSDB; AAB69123.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
XX Example 1; Page 91; 111pp; Japanese.
XX
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;

Alignment Scores:
Pred. No.: 7.79e-87 Length: 384
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAF59065 (1-384)

Qy 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
Db 1 ATGGCAGAAATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 60

Qy 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValThr 40
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Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysAArgPheIleAsnVal 60
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Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db 181 AAAAAGGCGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAAATGGAGCTGGAGAA 240

Qy 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db 241 TTTTGGCTGGCAGTGTATGGTATGGCCAGGACGAGATGGAGTGTGGGTATTTC 300

Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db 301 CCCAGAACTTGTTCAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTCCACC 360

Qy 121 ThrAspIleAspPheCysGlu 128
Db 361 ACGGATATTGACTTCTTCGCG 384

RESULT 2

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AAS17583  
 ID AAS17583 standard; cDNA; 387 BP.  
 XX  
 AC AAS17583;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel secreted protein #12.  
 XX  
 KW Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine;  
 KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
 KW human; cancer; autoimmune disease; wound healing disorder; infection;  
 KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..387  
 FT /\*tag= a  
 FT /product= "Human secreted protein"  
 XX  
 PN WO200179454-A1.  
 XX  
 PD 25-OCT-2001.  
 XX  
 PF 11-APR-2001; 2001WO-US11797.  
 XX  
 PR 13-APR-2000; 2000US-196603P.  
 PR 24-APR-2000; 2000US-199417P.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 XX  
 WPI; 2002-061975/08.  
 DR P-PSDB; AAU09871.  
 XX  
 PT New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, cancer -  
 XX  
 Claim 2; Page 44; 92pp; English.  
 XX  
 The invention relates to an isolated novel secreted polypeptide (I) and  
 polynucleotide (II). (I) and (II) are useful for treating cancer,  
 autoimmune diseases, wound healing disorder, infections, haematopoietic  
 disorders, inflammatory disorders, infertility, neurological and  
 psychiatric diseases, cardiovascular diseases, respiratory diseases,  
 renal diseases, or gastrointestinal diseases. These may also be used to  
 treat diseases, abnormalities and disorders caused by abnormal  
 expression, production, function and/or metabolism of the genes, as  
 vaccines for inducing immunological response in a mammal, and in  
 screening methods for detecting the effect of added compounds on the  
 production of mRNA and polypeptide in cells. The polypeptides can be used  
 as immunogens to produce antibodies immunospecific for the polypeptides,  
 and to identify membrane-bound or soluble receptors. The polynucleotides  
 may be used as diagnostic reagents, in chromosome localisation studies,  
 and in tissue expression studies. The present sequence represents the  
 CC coding sequence of novel human secreted protein #12.  
 XX  
 SQ Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;

Alignment Scores:  
 Pred. No.: 7.87e-87 Length: 387  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0



```

US-10-019-455A-6 (1-128) x AAS17593 (1-387)
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 1 ATGGCAAGAATAATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA 60
QY 21 IlePheMetAspArgLeuAlaSerLysLeuValCysAlaAspAspGluCysValTyrThr 40
DB 61 ATATTATATGGACCGCTAGCTTCCCAAGAAAGCTGTGTCAGATGATGAGTGTGTCTATCT 120
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 121 ATTCTCTGGCTAGTGTCTCAAGAGATTTAATGCCCCGAGCTGTAGATTCATTACGTT 180
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 181 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTAAAGAAATAATGGAGCTGGAGAA 240
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 241 TTTTGGCTGGCAGTGTATTATGTGTATGGCCAGGACGAGATGGAGTCGGTGGTTATTTC 300
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 301 CCCAGGAACCTTGTCAAGGACACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACC 360
QY 121 ThrAspIleAspPheCysGlu 128
DB 361 ACGGATATTGACTTCTTCGCGAG 384

RESULT 3
AAH26341
ID AAH26341 standard; cDNA; 426 BP.
AC AAH26341;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide clone 16372272.
XX
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200155332-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02455.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 02-MAY-2000; 2000US-0563786.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX
DR WPI; 2001-483233/52.
XX
PT Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
PT hyperproliferative disorders, coagulation disorders, and nervous system
PT disorders -
XX
PE Example 1; Page 114; 119pp; English.
XX
PS The present sequence is that of Hyseq clone identification number
CC 16372272, which was obtained from a human thymus cDNA library
CC using standard PCR with primers specific for vector sequences
CC flanking the inserts, sequencing by hybridisation sequence

```

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CC signature analysis, and Sanger sequencing techniques. This
CC expressed sequence tag was used in the assembly of a full-length
CC cDNA sequence (see AAH26343) encoding a novel human growth
CC regulatory-like polypeptide (GRLP, see AAB82671). The GRLP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived and 64%
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRLP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.
XX
SQ Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

Alignment Scores:
Pred. No.: 9,05e-87 Length: 426
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAH26341 (1-426)
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 19 ATGGCAAGAATAATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA 78
QY 21 IlePheMetAspArgLeuAlaSerLysLeuValCysAlaAspAspGluCysValTyrThr 40
DB 79 ATATTATATGGACCGCTAGCTTCCCAAGAAAGCTGTGTCAGATGATGAGTGTGTCTATCT 138
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 139 ATTCTCTGGCTAGTGTCTCAAGAGATTTAATGCCCCGAGCTGTAGATTCATTACGTT 198
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 199 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTAAAGAAATAATGGAGCTGGAGAA 258
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 259 TTTTGGCTGGCAGTGTATTATGTGTATGGCCAGGACGAGATGGAGTCGGTGGTTATTTC 318
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 319 CCCAGGAACCTTGTCAAGGACACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACC 378
QY 121 ThrAspIleAspPheCysGlu 128
DB 379 ACGGATATTGACTTCTTCGCGAG 402

RESULT 4
ABL95740
ID ABL95740 standard; cDNA; 521 BP.
XX
AC ABL95740;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.
XX
KW Human angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;

```

KW antiarteriosclerotic; gene; ss.  
XX  
OS Homo sapiens.  
XX WO200208284-A2.  
XX 31-JAN-2002.  
XX 09-JUL-2001; 2001WO-US21735.  
XX 20-JUL-2000; 2000US-219558P.  
XX 25-JUL-2000; 2000US-220624P.  
XX 25-JUL-2000; 2000US-220664P.  
XX 28-JUL-2000; 2000WO-US20710.  
XX 02-AUG-2000; 2000US-222695P.  
XX 17-AUG-2000; 2000US-0643657.  
XX 23-AUG-2000; 2000WO-US23522.  
XX 24-AUG-2000; 2000WO-US23328.  
XX 07-SEP-2000; 2000US-230978P.  
XX 15-SEP-2000; 2000US-000000P.  
XX 18-SEP-2000; 2000US-0664610.  
XX 18-SEP-2000; 2000US-0665350.  
XX 24-OCT-2000; 2000US-242922P.  
XX 08-NOV-2000; 2000US-0709238.  
XX 08-NOV-2000; 2000WO-US30952.  
XX 10-NOV-2000; 2000WO-US30873.  
XX 01-DEC-2000; 2000WO-US32678.  
XX 20-DEC-2000; 2000US-0747259.  
XX 20-DEC-2000; 2000WO-US34956.  
XX 22-JAN-2001; 2001US-0767609.  
XX 28-FEB-2001; 2001US-0796498.  
XX 28-FEB-2001; 2001WO-US06520.  
XX 01-MAR-2001; 2001WO-US06666.  
XX 09-MAR-2001; 2001US-0802706.  
XX 14-MAR-2001; 2001US-0808689.  
XX 22-MAR-2001; 2001US-0816744.  
XX 05-APR-2001; 2001US-0828366.  
XX 10-MAY-2001; 2001US-0854208.  
XX 10-MAY-2001; 2001US-0854280.  
XX 25-MAY-2001; 2001US-0866028.  
XX 25-MAY-2001; 2001US-0866034.  
XX 25-MAY-2001; 2001WO-US17092.  
XX 30-MAY-2001; 2001US-0870574.  
XX 30-MAY-2001; 2001WO-US17443.  
XX 01-JUN-2001; 2001WO-US17800.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 28-JUN-2001; 2001WO-US00000.  
XX (GETH ) GENENTECH INC.  
PA (BAKE/) BAKER K P.  
PA (FERR/) FERRARA N.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (MARS/) MARSTERS S A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (STEP/) STEPHAN J F.  
PA (WATA/) WATANABE C K.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
XX WPI; 2002-171999/22.  
XX P-PSDB; ABB95602.  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
XX infarction), endothelial or angiogenic disorders in a mammal -  
XX Claim 1; Fig 359; 567pp; English.  
XX  
CC The present invention provides the protein and coding sequences of human  
CC PRO proteins. These are useful for treating or diagnosing a  
CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
CC hypertrophy, trauma, cancer, age-related macular degeneration,  
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
CC angiogenesis (such as breast carcinoma and liver carcinoma), wound  
CC healing. The present sequence is a coding sequence of the invention.  
XX  
SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
  
Alignment Scores:  
Pred. No.: 1-21e-86 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 24  
DB: Gaps: 0  
  
US-10-019-455A-6 (1-128) x ABL95740 (1-521)  
Qy 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
Db 38 ATGGCAAGAAATATTGTTACTTTTCCTCCGGGCTTTGGCTGTATGCTGTCATGGA 97  
Qy 21 IlePheMetAspArgIleuAlaSerLysLysLeuCysAlaAspAspGluCysValThr 40  
Db 98 ATATTATGACCCCTAGCTTCCAGAGATTTCCAGAGCTCTGTGCAGATGATGATGCTTACT 157  
Qy 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
Db 158 ATTTCTCTGGCTAGTCTCAAGAGATTATATAATGCCCGGACTCTAGATTCAATTAACGTT 217  
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyValGlyGlu 80  
Db 218 AAAAAGGCGCAGACATCTATGTACTCAAGCTGGTAAAGAAATGGAAGCTGGAGAA 277  
Qy 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
Db 278 TTTTGGGCTGCAGTGTTATGTTGATGCCAGACGAGATGGAGTCTGGGTATTATTC 337  
Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
Db 338 CCCAGGAACCTTGTCAAGGAACACAGCTGTGTACCAGGAAGCTACCAAGGAAGTCCACC 397  
Qy 121 ThrAspIleAspPhePheCysGlu 128  
Db 398 ACGGATATTGACTTCTTCTCGGAG 421  
  
RESULT 5  
ABL88251  
ID ABL88251 standard; cDNA; 521 BP.  
XX  
AC ABL88251;  
XX  
DT 16-MAY-2002 (first entry)  
XX  
DE Human PRO9873 cDNA sequence SEQ ID NO:359.  
XX  
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
KW age-related macular degeneration; arterial restenosis; angina;  
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
KW wound healing; chromosome mapping; gene mapping; gene; ss.  
XX

OS Homo sapiens.  
PN WO200200690-A2.  
XX 03-JAN-2002.  
XX 20-JUN-2001; 2001WO-US19692.  
XX 23-JUN-2000; 2000US-213637P.  
PR 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 02-AUG-2000; 2000US-222695P.  
PR 17-AUG-2000; 2000US-0643657.  
PR 23-AUG-2000; 2000WO-US23322.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 07-SEP-2000; 2000US-230978P.  
PR 18-SEP-2000; 2000US-0664610.  
PR 08-SEP-2000; 2000US-0665350.  
PR 24-OCT-2000; 2000US-242922P.  
PR 08-NOV-2000; 2000US-0709238.  
PR 08-NOV-2000; 2000WO-US30952.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-DEC-2000; 2000WO-US34956.  
PR 22-JAN-2001; 2001US-0767609.  
PR 28-FEB-2001; 2001US-0796498.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 01-MAR-2001; 2001WO-US06666.  
PR 09-MAR-2001; 2001US-0802706.  
PR 14-MAR-2001; 2001US-0808689.  
PR 22-MAR-2001; 2001US-0816744.  
PR 05-APR-2001; 2001US-0828366.  
PR 10-MAY-2001; 2001US-0854208.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001US-0866028.  
PR 25-MAY-2001; 2001US-0866034.  
PR 25-MAY-2001; 2001WO-US17092.  
PR 30-MAY-2001; 2001US-0870574.  
PR 30-MAY-2001; 2001WO-US17443.  
PR 01-JUN-2001; 2001WO-US17800.  
PA (GETH ) GENENTECH INC.  
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
PI Godowski PJ, Gurney AL, Hillan KU, Marsters SA, Pan J, Paoni NF;  
PI Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;  
XX WPI; 2002-090516/12.  
DR P-PSDB; ABB84996.  
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
PT infarction), endothelial or angiogenic disorders in a mammal -  
XX Claim 2; Fig 359; 565pp; English.  
PS  
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.

XX SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
Alignment Scores:  
Pred. No.: 1,21e-86 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 24 Gaps: 0  
US-10-019-455A-6 (1-128) x ABL88251 (1-521)  
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAATATTGTACTTTCTCCCGGGTCTTTGGCTGTATGTCTGTGCATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTTACT 157  
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTGCTCAAGAAGATTATAATGCCCGGACTGTAGATTCATTACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 218 AAAAAAGGCGCAGATCTATGTACTCAAGAGCTGTGTAAGAAATAATGGAGCTGGAGAA 277  
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTATTATGTATGCCAGGACGATGGAGTCGTGGTATTATTC 337  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAAGCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCCACC 397  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 398 ACGGATATTGACTTCTCTCGAG 421  
RESULT 6  
ABK33571  
ID ABK33571 standard; cDNA; 521 BP.  
XX AC ABK33571;  
XX DT 08-MAY-2002 (first entry)  
XX DE cDNA encoding human PRO protein, Seq ID No 71.  
XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX OS Homo sapiens.  
XX PN WO200208288-A2.  
XX 31-JAN-2002.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.

```
PR 28-JUL-2000; 2000WO-US20710.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 15-SEP-2000; 2000US-000000P.
PR 10-NOV-2000; 2000WO-US30873.
PR 28-NOV-2000; 2000US-233646P.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 28-DEC-2000; 2000WO-US34956.
PR 20-FEB-2001; 2001WO-US06520.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001WO-US17092.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski FJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2002-172001/22.
DR P-PSDB; AAU83627.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT tumour or liver tumour -
XX
XX Claim 2; Figure 71; 359pp; English.
XX
XX The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human
CC PRO protein coding sequences of the invention.
XX
XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 1.21e-86 Length: 521
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 24 Gaps: 0
US-10-019-455A-6 (1-128) x ABK33571 (1-521)
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 38 ATGCCAAGAAATATTGTTACTTTTCTCCCGGGTCTTGCGGTGATGCTGCTGCATGGA 97
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
DB 98 ATATTATGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGCTACT 157
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATACGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA 277
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QY 81 PheTIPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB 278 TTTTGGGCTGGCAGTGTATTATGTTATGTCGATGCCAGAGAGATGGAGTCGTCGGTATTTC 337
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB 338 CCACAGGAACCTTGGTCAAGGACAGCGTGTGTACCAAGAGCTACCAAGGAAGTTCACACC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTCGGAG 421
RESULT 7
AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX
XX AAH98228;
XX
XX 12-OCT-2001 (first entry)
XX
XX Human EST-derived coding sequence SEQ ID NO: 85.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder;
XX biodiversity; gene therapy; nutrition; ss.
XX
XX Homo sapiens.
XX
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02687.
XX
XX 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
XX 03-AUG-2000; 2000US-0631451.
XX 15-SEP-2000; 2000US-0663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
XX WPI; 2001-476164/51.
XX P-PSDB; AAM23569.
XX
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX
XX Claim 1; Page 236; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.
XX
XX Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 2.64e-86 Length: 891
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0
US-10-019-455A-6 (1-128) x AAH98228 (1-891)
```

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 19 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGTATGCTGTGCATGA 78  
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40  
DB 79 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138  
QY 41 IleSerLeuAlaSerAlaGlnGlnArgValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 60  
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCGAGCTGATGATTCATTAAACGTT 198  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 199 AAAAAAGGCGACAGATCTATGTGTCTCAAGAGCTGTGTTAAAGAAATGAGCTGGAGAA 258  
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 259 TTTTGGGCTGGCAGTGTATTATGCTGATGCCAGGACGAGATGGAGTCTGGGTATTATTC 318  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 319 CCCAGGAATCTGGTCAAGCAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCACCACC 378  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 379 ACGGATATTGACTTCTTCTGCGAG 402  
RESULT 8  
AAH26342  
ID AAH26342 standard; cDNA; 891 BP.  
XX AC AAH26342;  
XX DT 02-OCT-2001 (first entry)  
XX DE Human growth regulatory-like polypeptide partial cDNA clone.  
XX KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
XX KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
XX ss.  
XX OS Homo sapiens.  
XX FN WO200155332-A2.  
XX PD 02-AUG-2001.  
XX PF 25-JAN-2001; 2001WO-US02455.  
XX PR 25-JAN-2000; 2000US-0491404.  
XX PR 02-MAY-2000; 2000US-0563786.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Mize NK, Boyle BJ, Ford JF, Arterburn MC, Tang YT, Liu C;  
PI Drmanac RT;  
XX WPI; 2001-483233/52.  
PT Isolated human growth regulatory-like polypeptide useful for treating  
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
PT hyperproliferative disorders, coagulation disorders, and nervous system  
PT disorders -  
PS Claim 1; Page 115; 119pp; English.  
CC The present sequence is that of a novel nucleic acid that was  
CC assembled from human thymus cDNA library-derived Hyseq clone  
CC identification number 16372272 (see AAH26341). A recursive  
CC algorithm was used to extend the clone by pulling additional  
CC sequences from different databases. A full-length sequence (see

CC AAH26343) encoding novel human growth regulatory-like polypeptide  
CC (GRP, see AAH26341) was subsequently obtained. Human GRP  
CC belongs to the same protein family as growth regulatory proteins,  
CC growth factors, human melanoma derived growth regulatory protein  
CC precursor (64% similarity and 45% identity over 111 amino acids)  
CC or melanoma inhibitory activity, cattle cartilage-derived  
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
CC similarity over 126 amino acids) and other retinoic acid-sensitive  
CC proteins. GRP polypeptides and polynucleotides of the invention  
CC can be used in the prophylaxis, treatment (including gene therapy)  
CC and diagnosis of disorders and diseases caused by, or involving,  
CC cartilage development and maintenance, inhibition of melanoma cell  
CC growth and tumours, including neuroectodermal tumours such as  
CC gliomas. The polynucleotides can also be used to design probes  
CC and primers, for chromosome and gene mapping, in the recombinant  
CC production of protein, in the generation of antisense, ribozyme and  
CC peptide-nucleic acid molecules, and to produce transgenic animals.  
XX SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;  
Alignment Scores:  
Pred. No.: 2,648-86 Length: 891  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0  
US-10-019-455A-6 (1-128) x AAH26342 (1-891)  
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 19 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGTATGCTGTGCATGA 78  
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40  
DB 79 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 138  
QY 41 IleSerLeuAlaSerAlaGlnGlnArgValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 60  
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCGAGCTGATGATTCATTAAACGTT 198  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 199 AAAAAAGGCGACAGATCTATGTGTCTCAAGAGCTGTGTTAAAGAAATGAGCTGGAGAA 258  
QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 259 TTTTGGGCTGGCAGTGTATTATGCTGATGCCAGGACGAGATGGAGTCTGGGTATTATTC 318  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 319 CCCAGGAATCTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCACCACC 378  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 379 ACGGATATTGACTTCTTCTGCGAG 402  
RESULT 9  
AAF59083  
ID AAF59083 standard; DNA; 923 BP.  
XX AC AAF59083;  
XX DT 23-APR-2001 (first entry)  
XX DE Human MLP nucleotide sequence SEQ ID NO:29.  
XX KW MLP; MTA; melanoma inhibitory activity; cancer; bone disease;  
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;  
XX KW inhibitor; ds.  
XX

OS Homo sapiens.  
 PN WO200102564-A1.  
 XX 11-JAN-2001.  
 XX 29-JUN-2000; 2000WO-JP04278.  
 XX 30-JUN-1999; 99JP-0186718.  
 PR (TAKA ) TAKEDA CHEM IND LTD.  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX Example 1; Page 99-100; 111pp; Japanese.  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 XX Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;  
 SQ

Alignment Scores:  
 Pred. No.: 2,77e-86 Length: 923  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAF59083 (1-923)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 DB 34 ATGGCAAGAAATATTGTACTTTCTCCCGGCTTGTGGCTGTATGTGTGCAATGGA 93  
 QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
 DB 94 ATATTATGACCGCTAGCTCCAGAAAGATTAAATGCCCGAGCTGTAGATTCATTACGTT 153  
 QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 DB 154 ATTCTCTGGCTAGTGTCTCAAGAGATTAAATGCCCGAGCTGTAGATTCATTACGTT 213  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 DB 214 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 273  
 QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 DB 274 TTTTGGCTGGAGTGTATTTATGTTATGGATGGCAGGACGAGATGGAGTCGGTATTTTC 333  
 QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 DB 334 CCCAGGAACCTGGTCAAGAACACAGCGTGTGTACCAAGGAAGTACCAAGGAAGTCCACC 393  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 394 ACGGATATTGACTTCTTCTCGGAG 417

RESULT 10  
 AAH26343  
 ID AAH26343 standard; cDNA; 1201 BP.  
 XX  
 AC AAH26343;  
 XX 02-OCT-2001 (first entry)  
 DT Human growth regulatory-like polypeptide cDNA.  
 DE Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.  
 XX Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 33..419 /\*tag= a  
 FT sig\_peptide 33..101 /\*tag= b  
 FT mat\_peptide 102..416 /\*tag= c  
 FT  
 XX WO200155332-A2.  
 PN 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-US02455.  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 02-MAY-2000; 2000US-0563786.  
 XX (HYSE-) HYSEQ INC.  
 XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;  
 XX WPI; 2001-483233/52.  
 DR P-PSDB; AAB82671.  
 XX Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -  
 XX Claim 1; Page 115-116; 119pp; English.  
 XX The present sequence is that of a novel nucleic acid encoding  
 CC human growth regulatory-like polypeptide (GRLP, see AAB82671).  
 CC The sequence was assembled using human thymus cDNA library-derived  
 CC Hyseq clone identification number 16372272 (see AAH26341) as seed,  
 CC using software programs to pull additional sequences from Hyseq's  
 CC proprietary database containing expressed sequence tag sequences,  
 CC and by gel sequencing using primers to extend both 5' and 3' ends.  
 CC The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 CC similarity over 136 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRLP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.  
 CC They may also have cytokine and cell proliferation or  
 CC differentiation activity, stem cell growth factor activity.

CC haematopoiesis regulating activity, tissue growth activity,  
 CC immunosuppressive or immunostimulant activity, activin/inhibin  
 CC activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, use in cancer diagnosis and therapy,  
 CC drug screening, receptor/ligand activity, antiinflammatory  
 CC activity, and treatment of leukaemia, nervous system disorders,  
 CC arthritis and inflammation.

XX  
 SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;

Alignment Scores:  
 Pred. No.: 4,06e-86 Length: 1201  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAH26343 (1-1201)

QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 Db 33 ATGGCAAGAAATATGTACTTTCTCCCGGGCTTTGTGGCTGTATGTGTCATGGA 92  
 QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
 Db 93 ATATTATGGACCGTCTAGCTTCCCAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 152  
 QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 Db 153 ATTTCCTCGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 212  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 Db 213 AAAAAGGCGCAGCAGATCTATGTGACTCAAGCTGTAAAGAAATGGAGCTGGAGAA 272  
 QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 Db 273 TTTTGGCTGGCAGTGTATATGCTGATGCCAGGACAGATGGAGTGTGGTTATTTTC 332  
 QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 Db 333 CCCAGAACTTGGTCAAGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACC 392  
 QY 121 ThrAspIleAspPheCysGlu 128  
 Db 393 ACGGATATTGACTTCTTCTGCGAG 416

RESULT 11

AAF59068  
 ID AAF59068 standard; DNA; 384 BP.

XX  
 AC AAF59068;

XX  
 DT 23-APR-2001 (first entry)

XX  
 DE Mouse MLP nucleotide sequence SEQ ID NO:10.

XX  
 KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.

XX  
 OS Mus musculus.

XX  
 PN WO200102564-A1.

XX  
 PD 11-JAN-2001.

XX  
 PF 29-JUN-2000; 2000WO-JP04278.

XX  
 PR 30-JUN-1999; 99JP-0186718.

XX

PA (TAKE ) TAKEDA CHEM IND LTD.

XX  
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;

XX  
 DR WPI; 2001-159271/16.

DR  
 P-PSDB; AAB69125.

XX

PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases

XX

PS Claim 11; Page 93; 111pp; Japanese.

XX

CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.

SQ Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;

Alignment Scores:

Pred. No.: 2,79e-76 Length: 384  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAF59068 (1-384)

QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
 Db 1 ATGGCAAGAAATATGATCTTTTGTGTTGGGGCTTTGTGGTCTATGTCCGGCATGGT 60

QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
 Db 61 GTATTATGGATAAACTTCTTCTTAAGAAGTTGTGTCCGATGAGAGTGTGTCTATACT 120

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 Db 121 ATTTCCTCGCAAGAGCAGCAGGAAGATTACAATGCCAGACTGTAGTTCATCGATGTC 180

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 Db 181 AAGAAAGGCGCAGCAGATCTATGTTTACTCCAGCTGGTAACAGAAACCGAGCTGGAGAG 240

QY 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 Db 241 TTTTGGCTGGCAGTGTATGTCACCCAGGATGAGATGGGAATTTAGTTATTTC 300

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 Db 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACCCAGGAGGCCACCAAGGAGATCCCAACC 360

QY 121 ThrAspIleAspPheCysGlu 128

Db 361 ACGGATATTGACTTCTTCTGTGAA 384

RESULT 12

AAF59084

ID AAF59084 standard; DNA; 947 BP.

XX  
 AC AAF59084;

XX  
 DT 23-APR-2001 (first entry)

XX  
 DE Mouse MLP nucleotide sequence SEQ ID NO:30.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
XX Mus musculus.  
XX WO200102564-A1.  
XX  
XX 11-JAN-2001.  
XX  
XX 29-JUN-2000; 2000WO-JP04278.  
XX  
XX 30-JUN-1999; 99JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
XX WPI; 2001-159271/16.  
XX  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
XX Example 2; Page 100-101; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;  
SQ

Alignment Scores:  
Pred. No.: Length: 947  
Score: 602.00 Matches: 111  
Percent Similarity: 93.75% Conservative: 9  
Best Local Similarity: 86.72% Mismatches: 8  
Query Match: 89.05% Indels: 0  
DB: 22 Gaps: 0

US-10-019-455A-6 (1-126) x AAF59084 (1-947)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 11 ATGGCAAGGATATGATCTTTTGTCTAGAGAGTGTGTGGGCGCTTGTGTCTCGCGCATGTT 70  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
DB 71 GTATTATGGATAACTTCTTCTAGAGAGTGTGTGGGCGCTTGTGTCTCGCGCATGTT 130  
QY 41 IleSerLeuAlaSerLagInGluAspTyrAsnAlaProAspCysArgPheLeuAsnVal 60  
DB 131 ATTTCTCTGCAAGAGACACAGGAAGATTACAATGCCACAGCTAGGTTCATCGATGTC 190  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 191 AGAAAGGGCAGCAGATCTATGTTTACTCCAGCTGGTAAACAGAAACCGAGCTGGAGAG 250  
QY 81 PheTIPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 251 TTTTGGCTGGCAGTGTATTATGTTGACCCAGAGATGAGATGGGAATTGTAGTTATTTC 310  
QY 101 ProArgAsnLeuValLysGluGlnA-gValTyrGlnGluAlaThrLysGluValProThr 120  
DB 111

DB 311 CCAGCAACTTGGTGAAGGACGCGTGTATACCAGGAGGCCACCAAGAGATCCCAACC 370  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 371 ACGGATATTGACTTCTTCTGTCAA 394  
RESULT 13  
AAF59098  
ID AAF59098 standard; DNA; 384 BP.  
XX  
XX AAF59098;  
XX  
XX 23-APR-2001 (first entry)  
XX  
XX Rat MLP nucleotide sequence SEQ ID NO:46.  
XX  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
XX Rattus sp.  
XX  
XX WO200102564-A1.  
XX  
XX 11-JAN-2001.  
XX  
XX 29-JUN-2000; 2000WO-JP04278.  
XX  
XX 30-JUN-1999; 99JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
XX WPI; 2001-159271/16.  
XX  
XX P-PSDB; AAB69130.  
XX  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
XX Claim 13; Page 105-106; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;  
SQ

Alignment Scores:  
Pred. No.: Length: 384  
Score: 600.00 Matches: 111  
Percent Similarity: 93.75% Conservative: 9  
Best Local Similarity: 86.72% Mismatches: 8  
Query Match: 88.76% Indels: 0  
DB: 22 Gaps: 0

US-10-019-455A-6 (1-128) x AAF59098 (1-384)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 1 ATGGCAAGGATATGATCTTTTGTCTAGAGAGTGTGTGGGCGCTTGTGTCTCGCGCATGTC 60  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
DB 111



Db 61 ATGTTATGATATAAATCTTCTTAAGAAGTTGTGTGAGATGAGGAGTGTGTCTATACC 120  
 Qy 41 ILleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
 Db 121 ATTTCTCTGGCAGAGACAGAGAGACTACAATGCCCGGAGCTGTAGGTTTCATCAATGTC 180  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
 Db 181 AAGAAAGGGCAGCAGATCTATGTTTATTCGAAGCTGGTAAACAGAAATGGAGCTGGGGCA 240  
 Qy 81 PheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
 Db 241 TTCTGGCTGCAGTGTATGTTGACCAACAGATGAGATGGGAATGTGGTTATTTTC 300  
 Qy 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
 Db 301 CCCAGCAACTTGGTTAGAGAGCAACGAGTGTACCAAGGAGGCCACCAAGAGGATTTCCAACC 360  
 Qy 121 ThrAspIleAspPheCysGlu 128  
 Db 361 ACGGATATTGACTTCTTCTGTGAA 384  
 RESULT 14  
 AAF59079  
 ID AAF59079 standard; DNA; 330 BP.  
 XX  
 AC AAF59079;  
 XX  
 DT 23-APR-2001 (first entry)  
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 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
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 OS Homo sapiens.  
 XX  
 PN WO200102564-A1.  
 XX  
 PD 11-JAN-2001.  
 XX  
 PF 29-JUN-2000; 2000WO-JP04278.  
 XX  
 PR 30-JUN-1999; 99JP-0186718.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX  
 DR WPI; 2001-159271/16.  
 XX  
 DR P-PSDB; AAB69126.  
 XX  
 PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 PS Claim 8; Page 97; 11pp; Japanese.  
 XX  
 CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
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 SQ Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;

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 Qy 39 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 58  
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 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
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 PI Tanaka H;  
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 PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 PS Claim 10; Page 98; 11pp; Japanese.

Tue Dec 30 10:20:54 2003

XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
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Job time : 157.353 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 19:57:30 ; Search time 287.193 Seconds  
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Delop 6.0 , Delext 7.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	676	100.0	521	13	US-10-219-063-71	Sequence 71, Appl
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11	676	100.0	521	13	US-10-219-480-71	Sequence 71, Appl
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18	676	100.0	521	13	US-10-219-533-71	Sequence 71, Appl
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20	676	100.0	521	13	US-10-230-437-71	Sequence 71, Appl
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ALIGNMENTS

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; Publication No. US20030124573A1  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjastad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1e1 Growth  
; FILE REFERENCE: HYS-7C1P  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8

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; SEQ ID NO 1
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (426)..(426)
; OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1
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Pred. No.: 9,95e-94 Length: 426
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 15 Gaps: 0
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; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530FIC3
; CURRENT APPLICATION NUMBER: US/10/216,163
; CURRENT FILING DATE: 2002-08-09
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; PRIOR FILING DATE: 2002-04-09
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n = A, T, G, or C
US-10-216-038-1
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Pred. No.: 9,95e-94 Length: 426
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Percent Similarity: 100.00% Conservative: 0
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QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB 19 ATGCCAAGATATGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 78
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RESULT 2
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; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530FIC3
; CURRENT APPLICATION NUMBER: US/10/216,163
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Score: 676.00 Matches: 128
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC19  
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CURRENT FILING DATE: 2002-08-12  
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PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
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PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086392  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089538  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089905  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/090472  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090691  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/090695  
PRIOR FILING DATE: 1998-06-25  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/095302  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095318  
PRIOR FILING DATE: 1998-08-04  
PRIOR APPLICATION NUMBER: 60/095916  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: 60/096146  
PRIOR FILING DATE: 1998-08-11  
PRIOR APPLICATION NUMBER: 60/096791  
PRIOR FILING DATE: 1998-08-17  
PRIOR APPLICATION NUMBER: 60/097986  
PRIOR FILING DATE: 1998-08-26  
PRIOR APPLICATION NUMBER: 60/098544  
PRIOR FILING DATE: 1998-08-31  
PRIOR APPLICATION NUMBER: 60/099596  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099598  
PRIOR FILING DATE: 1998-09-09  
PRIOR APPLICATION NUMBER: 60/099803  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099811  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099812  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/099816  
PRIOR FILING DATE: 1998-09-10  
PRIOR APPLICATION NUMBER: 60/100038  
PRIOR FILING DATE: 1998-09-11  
PRIOR APPLICATION NUMBER: 60/100385  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100848  
PRIOR FILING DATE: 1998-09-18  
PRIOR APPLICATION NUMBER: 60/100919  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: 60/101477  
PRIOR FILING DATE: 1998-09-23  
PRIOR APPLICATION NUMBER: 60/101738  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101741  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101786  
PRIOR FILING DATE: 1998-09-25  
PRIOR APPLICATION NUMBER: 60/101916  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/101922  
PRIOR FILING DATE: 1998-09-24  
PRIOR APPLICATION NUMBER: 60/106178  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: 60/106248  
PRIOR FILING DATE: 1998-10-29  
PRIOR APPLICATION NUMBER: 60/106464  
PRIOR FILING DATE: 1998-10-30  
PRIOR APPLICATION NUMBER: 60/106905  
PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775

Qy	81	PheTpnlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValGlyTyrPhe	100
Db	278	TTTTGGGCTGGCAGTGTATGTTATGGTATGGCCAGACCGAGATGGAGTCGTGGTTATTC	337
Qy	101	ProArgAsnLeuValLysGluInArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	338	CCCAGGAACTTGGTCAAGGAACAGCGTGTGTATCCAGGAAGCTACCAAGGAAGTTCCACC	397
Qy	121	ThrAspIleAspPheCysGlu	128
Db	398	ACGGATATGACTTCTTCTCGGAG	421
RESULT 4			
US-10-219-063-71			
; Sequence 71, Application US/10219063			
; Publication No. US20030187202A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Gerritsen, Mary			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Grimaldi, J. Christopher			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Smith, Victoria			
; APPLICANT: Stephan, Jean-Philippe F.			
; APPLICANT: Watanabe, Colin L.			
; APPLICANT: Wood, William I.			
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
; FILE REFERENCE: P3530PIC24			
; CURRENT APPLICATION NUMBER: US/10/219,063			
; PRIOR FILING DATE: 2002-08-13			
; PRIOR APPLICATION NUMBER: 10/119,480			
; PRIOR FILING DATE: 2002-04-09			
; PRIOR APPLICATION NUMBER: 60/059113			
; PRIOR FILING DATE: 1997-09-17			
; PRIOR APPLICATION NUMBER: 60/062287			
; PRIOR FILING DATE: 1997-10-17			
; PRIOR APPLICATION NUMBER: 60/063549			
; PRIOR FILING DATE: 1997-10-28			
; PRIOR APPLICATION NUMBER: 60/064103			
; PRIOR FILING DATE: 1997-10-31			
; PRIOR APPLICATION NUMBER: 60/069873			
; PRIOR FILING DATE: 1997-12-17			
; PRIOR APPLICATION NUMBER: 60/078910			
; PRIOR FILING DATE: 1998-03-20			
; PRIOR APPLICATION NUMBER: 60/079294			
; PRIOR FILING DATE: 1998-03-25			
; PRIOR APPLICATION NUMBER: 60/079656			
; PRIOR FILING DATE: 1998-03-26			
; PRIOR APPLICATION NUMBER: 60/079728			
; PRIOR FILING DATE: 1998-03-27			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 246			
; SEQ ID NO 71			
; LENGTH: 521			
; TYPE: DNA			
; ORGANISM: Homo Sapien			
US-10-219-063-71			
Alignment Scores:			
Pred. No.:	1,34e-93	Length:	521
Score:	676.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	13	Gaps:	0
US-10-019-455A-6 (1-128) x US-10-219-765-71 (1-521)			
Qy	1	MetAlaArgIleLeuLeuPheLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGATATGTACTTTCTCCGGGCTTGTGCTGTATGCTGTGCTATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr	40
Db	98	ATATTATGGACCGCTCTAGCTTCCAAAGCTCTGTCAGATGATGAGTGTGCTATACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCCTCTGGCTAGTCTCAGAAGATTATATGCCCGGACTGTAGATTCAATTAAGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAGGCAGCAGATCTATGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
US-10-019-455A-6 (1-128) x US-10-219-063-71 (1-521)			
Qy	1	MetAlaArgIleLeuLeuPheLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGATATGTACTTTCTCCGGGCTTGTGCTGTATGCTGTGCTATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr	40
Db	98	ATATTATGGACCGCTCTAGCTTCCAAAGCTCTGTCAGATGATGAGTGTGCTATACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCCTCTGGCTAGTCTCAGAAGATTATATGCCCGGACTGTAGATTCAATTAAGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAGGCAGCAGATCTATGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA	277

Db	38	ATGCCAAGAAATATTGTGTACTTTTCTCCCGGCTCTTGTGGCTGTATGTGTCTGTGCATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerIlyslsYlsLeuCysAlaAspAspGluCysValTyrThr	40
Db	98	ATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTCTATACT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCCTCGCTAGTGTCTCAAGAGATTATATGATCCCGGACTGTAGATTTCATTAAACGTT	217
Qy	61	LysIlyslsGlyGlnGlnIleTyrValTyrSerIlyslsLeuValIlyslsGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAAGGGCAGCAGACTATGTGTACTCAAGAGCTGGTAAAAAGAAATCGAGCTGGAGAA	277
Qy	81	PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	278	TTTTTGGCTGCGAGTGTATTATGGTATGCCAGGACGAGATGGAGTCGTGGGTATTTC	337
Qy	101	ProArgAsnLeuValIlyslsGluGlnArgValTyrGlnGlnAlaThrIlyslsGluValProThr	120
Db	338	CCCAGGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGGAAGCTACCAAGGAAGTTCCACC	397
Qy	121	ThrAspIleAspPheCysGlu	128
Db	398	ACGGATATTGACTTCTTCTCGCAG	421

RESULT 5

US-10-219-066-71

; Sequence 71, Application US/10219066

; Publication No. US20030187203A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3530P1C27

; CURRENT APPLICATION NUMBER: US/10/219,066

; CURRENT FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 71

; LENGTH: 521

; TYPE: DNA

; ORGANISM: Homo Sapien

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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Alignment Scores:
Pred. No.:      1,34e-93      Length:      521
Score:          676.00      Matches:     128
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              13          Gaps:         0

US-10-019-455A-6 (1-128) x US-10-219-067-71 (1-521)
QY      1 MetAlaArgIleuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB      38 ATGGCAAGAATATTGTACTTTTCCCTCCGGGCTTTGTGGCTGTATGTGTGCATGGA 97
QY      21 IlePheMetAspArgIleuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
DB      98 ATATTATTGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTACT 157
QY      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB      158 ATTCTCTGGCTAGTCTCAAGAAGATTATATATGCCCGGACTGTAGATTCAATTAAGTT 217
QY      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB      218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 277
QY      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB      278 TTTTGGGCTGGCAGTGTATTATGTGTATGGCCAGACAGATGGAGTCTGGGGTTATTTC 337
QY      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB      338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTTCCACC 397
QY      121 ThrAspIleAspPheCysGlu 128
DB      398 ACGGATATTGACTTCTTCTCGCAG 421

RESULT 7
US-10-219-068-71
; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ACIDS AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530F1C31
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; CURRENT APPLICATION NUMBER: US/10/219, 068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119, 480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-068-71

Alignment Scores:
Pred. No.:      1,34e-93      Length:      521
Score:          676.00      Matches:     128
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              13          Gaps:         0

US-10-019-455A-6 (1-128) x US-10-219-068-71 (1-521)
QY      1 MetAlaArgIleuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
DB      38 ATGGCAAGAATATTGTACTTTTCCCTCCGGGCTTTGTGGCTGTATGTGTGCATGGA 97
QY      21 IlePheMetAspArgIleuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40
DB      98 ATATTATTGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTACT 157
QY      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
DB      158 ATTCTCTGGCTAGTCTCAAGAAGATTATATATGCCCGGACTGTAGATTCAATTAAGTT 217
QY      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
DB      218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 277
QY      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
DB      278 TTTTGGGCTGGCAGTGTATTATGTGTATGGCCAGACAGATGGAGTCTGGGGTTATTTC 337
QY      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
DB      338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTTCCACC 397
QY      121 ThrAspIleAspPheCysGlu 128
DB      398 ACGGATATTGACTTCTTCTCGCAG 421

RESULT 8
US-10-219-069-71
; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
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Tue Dec 30 10:20:54 2003

APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC40  
CURRENT APPLICATION NUMBER: US/10/219,069  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-069-71

Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-069-71 (1-521)  
QY 1 MetalAargileLeuLeuLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGCGAAGATATGTTACTTCCCTCCCGGGCTTGTGCTGTATGCTGTGCTATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGCTGTACTACT 157  
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATATGCCCGGAGCTGTAGATTCAATACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAenGlyAlaGlyGlu 80  
DB 218 AAAAAAGGGCAGCAGACTATGTTACTCAAGCTGTATAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTirAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTATTATGTTGATGGCAGCAGATGGAGTGGTGGGTATTTC 337

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTTACCAGAGAGTTTCCACC 397  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 398 ACCGATATGACTTCTTCTGCGAG 421  
RESULT 9  
US-10-219-073-71  
Sequence 71, Application US/10219073  
Publication No. US20030187207A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC52  
CURRENT APPLICATION NUMBER: US/10/219,073  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-073-71

Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-073-71 (1-521)  
QY 1 MetalAargileLeuLeuLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGCGAAGATATGTTACTTCCCTCCCGGGCTTGTGCTGTATGCTGTGCTATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysValTyrThr 40

```

Db      98 ATATTTATGACCGCTTACCTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
Qy      41 ILeSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db      158 ATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db      218 AAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTATAAAGAAAATGGAGCTGGAGAA 277
Qy      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db      278 TTTTGGCTGGCAGTGTATTATGCTGATGCCAGGACGAGATGGGAGTCTGGGTTATTTC 337
Qy      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db      338 CCCAGGAACCTGTGTCAAGGAACAGCGTGTGTACCAAGGAAGTACCAGGAAGTCCCCACC 397
Qy      121 ThrAspIleAspPheCysGlu 128
Db      398 ACGGATATTGACTTCTTCTCGGAG 421

```

## RESULT 10

```

US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1997-10-31
; PRIOR FILING DATE: 1997-12-17
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-475-71

```

Alignment Scores:

```

Pred. No.: 1.34e-93 Length: 521
Score: 676.00 Matches: 128
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-475-71 (1-521)

Qy      1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20
Db      38 ATGCCAAGAATATTGTACTTTTCTCCCGGGCTTGTGGCTGTATGCTGTGCTGCATGGA 97
Qy      21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40
Db      98 ATATTTATGGACCGCTCTAGCTTCCAGAGACTCTGTGCAGATGATGAGTGTGCTACT 157
Qy      41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60
Db      158 ATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80
Db      218 AAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTATAAAGAAAATGGAGCTGGAGAA 277
Qy      81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100
Db      278 TTTTGGCTGGCAGTGTATTATGCTGATGCCAGGACGAGATGGGAGTCTGGGTTATTTC 337
Qy      101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
Db      338 CCCAGGAACCTGTGTCAAGGAACAGCGTGTGTACCAAGGAAGTACCAGGAAGTCCCCACC 397
Qy      121 ThrAspIleAspPheCysGlu 128
Db      398 ACGGATATTGACTTCTTCTCGGAG 421

```

## RESULT 11

```

US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

```

; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-480-71

Alignment Scores:  
 Pred. No.: 1,34e-93 Length: 521  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-480-71 (1-521)

Qy	1	MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerIlySlysLeuCysAlaAspAspGluCysValThr	40
Db	98	ATAATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATCT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
Qy	81	PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	278	TTTTGGGCTGGCAGTGTTTATGTTGATGCCAGGACGAGATGGGAGTGGTGGTTATTTC	337
Qy	101	ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	338	CCCAGGAACCTTGGTCAAGAAACAGCGTGTGTACCCAGGAAGCTTACCAAGAAAGTCCCACC	397
Qy	121	ThrAspIleAspPheCysGlu	128
Db	398	ACGGATATTGACTTCTTCTGCGAG	421

RESULT 12

US-10-219-483-71  
 ; Sequence 71, Application US/10219483  
 ; Publication No. US20030187210A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PIC43  
 ; CURRENT APPLICATION NUMBER: US/10/219,483  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-483-71

Alignment Scores:  
 Pred. No.: 1,34e-93 Length: 521  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-483-71 (1-521)

Qy	1	MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly	20
Db	38	ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA	97
Qy	21	IlePheMetAspArgLeuAlaSerIlySlysLeuCysAlaAspAspGluCysValThr	40
Db	98	ATAATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATCT	157
Qy	41	IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal	60
Db	158	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT	217
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu	80
Db	218	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	277
Qy	81	PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe	100
Db	278	TTTTGGGCTGGCAGTGTTTATGTTGATGCCAGGACGAGATGGGAGTGGTGGTTATTTC	337
Qy	101	ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr	120
Db	338	CCCAGGAACCTTGGTCAAGAAACAGCGTGTGTACCCAGGAAGCTTACCAAGAAAGTCCCACC	397
Qy	121	ThrAspIleAspPheCysGlu	128
Db	398	ACGGATATTGACTTCTTCTGCGAG	421

RESULT 13

US-10-219-525-71  
 ; Sequence 71, Application US/10219525  
 ; Publication No. US20030187211A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC29  
CURRENT APPLICATION NUMBER: US/10/219,525  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 245  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-525-71

Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-525-71 (1-521)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAATATTGTTACTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 97

QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTATGGACCGTCTAGCTCCAGAGATTAATATGCGCGGAGCTGTAGATTCAATTAACGTT 157

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnVal 60  
DB 158 ATTCTCTGGCTAGTGTCTCAAGAGATTAATATGCGCGGAGCTGTAGATTCAATTAACGTT 217

QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyCly 80  
DB 218 AAAAAGGGCAGCATCTATGTGACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277

QY 81 PheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTATTGCTGATGCGCAGGACGAGATGGGAGTCTGGTGTATTTC 337

QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120

DB 338 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 397

QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 398 ACGGATATTGACTTCTCTCTCGGAG 421

RESULT 14  
US-10-219-526-71  
Sequence 71, Application US/10219526  
Publication No. US20030187212A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC41  
CURRENT APPLICATION NUMBER: US/10/219,526  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-526-71

Alignment Scores:  
Pred. No.: 1,34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-6 (1-128) x US-10-219-526-71 (1-521)

QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAATATTGTTACTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 97

QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThr 40  
DB 98 ATATTATGGACCGTCTAGCTCCAGAGATTAATATGCGCGGAGCTGTAGATTCAATTAACGTT 157

QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProaspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTATTATGTGTATGGCCAGACGAGATGGAGTCGTGGGTATTTC 337  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAACCTTGTCAAGGACAGCGTGTACCAAGAACTACCAAGGAAGTTCCACC 397  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 15  
US-10-219-530-71  
; Sequence 71, Application US/10219530  
; Publication No. US20030187213A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C54  
; CURRENT APPLICATION NUMBER: US/10/219,530  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-530-71

Alignment Scores:  
Pred. No.: 1.34e-93 Length: 521  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0  
US-10-019-455A-6 (1-128) x US-10-219-530-71 (1-521)  
QY 1 MetAlaArgIleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGly 20  
DB 38 ATGGCAAGAAATATTGTACTTTTCTCCCGGCTTTGTGGCTGTATGTGTGTCATGGA 97  
QY 21 IlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysValTyrThr 40  
DB 98 ATATTTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTACT 157  
QY 41 IleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProaspCysArgPheIleAsnVal 60  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
DB 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277  
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGTGTATTATGTGTATGGCCAGACGAGATGGAGTCGTGGGTATTTC 337  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
DB 338 CCCAGGAACCTTGTGTCAAGGAACAGCGTGTGTACCAAGAACTACCAAGGAAGTTCCACC 397  
QY 121 ThrAspIleAspPhePheCysGlu 128  
DB 398 ACGGATATTGACTTCTTCTCGGAG 421

Search completed: December 30, 2003, 02:01:00  
Job time : 289.193 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:24:24 ; Search time 40.6947 Seconds  
(without alignments)  
1388.315 Million cell updates/sec

Title: US-10-019-455A-6  
Perfect score: 676  
Sequence: 1 MARILLFLPGLVAVCAVHG.....RVQBATKEVFTTIDPFCE 128

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastap -SUPFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR\_SCORE=ptc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEA=SIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10019455 @CGN 1.1 142 @runat 29122003 160348 277 -NCPUS=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	257.5	38.1	459	1	US-08-578-649-1
2	253.5	37.5	330	1	US-08-578-649-18
3	232.5	34.4	581	1	US-08-578-649-4
4	210.5	31.1	305	1	US-08-578-649-8
5	190	28.1	596	1	US-08-578-649-24
6	164.5	24.3	3565	1	US-08-578-649-3
7	86.5	12.8	2757	1	US-08-306-691B-48
8	86.5	12.8	2757	5	PCR-US93-06251-79
9	86.5	12.8	4762	4	US-09-300-958A-30
10	85.5	12.6	2793	1	US-07-646-537B-1
11	79	11.7	467	4	US-09-300-958A-28
12	78.5	11.6	5398	3	US-09-356-952-11

13	78	11.5	1878	3	US-08-996-139-14	Sequence 14, Appl
14	78	11.5	1878	3	US-08-995-659-14	Sequence 14, Appl
15	78	11.5	1878	3	US-09-215-649A-14	Sequence 14, Appl
16	78	11.5	1878	4	US-09-577-780-14	Sequence 14, Appl
17	78	11.5	1878	4	US-09-577-800-14	Sequence 14, Appl
18	78	11.5	1878	4	US-09-466-496-14	Sequence 14, Appl
19	78	11.5	1878	4	US-09-871-856-14	Sequence 14, Appl
20	78	11.5	1878	4	US-09-871-231-14	Sequence 14, Appl
21	76	11.2	1579	4	US-09-071-035-83	Sequence 83, Appl
22	76	11.2	1680	4	US-09-071-035-81	Sequence 81, Appl
23	71.5	10.6	1664976	4	US-08-916-421B-1	Sequence 1, Appl
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25	70.5	10.4	2043	4	US-09-134-078-11	Sequence 11, Appl
26	70.5	10.4	1684976	4	US-08-916-421B-1	Sequence 1, Appl
27	68	10.1	2873	4	US-08-630-915A-193	Sequence 193, App
28	68	10.1	11864	4	US-08-961-527-61	Sequence 61, Appl
29	67	9.9	4403765	3	US-09-103-840A-2	Sequence 2, Appl
30	67	9.9	4411529	3	US-09-103-840A-1	Sequence 1, Appl
31	66.5	9.8	1457	3	US-09-444-053-3	Sequence 3, Appl
32	66.5	9.8	2595	4	US-09-619-353-13	Sequence 13, Appl
33	66.5	9.8	3981	4	US-09-328-352-760	Sequence 760, App
34	66.5	9.8	8651	4	US-08-961-527-181	Sequence 181, App
35	66	9.8	747	4	US-08-630-915A-39	Sequence 39, Appl
36	66	9.8	840	1	US-08-434-255-7	Sequence 7, Appl
37	66	9.8	840	1	US-08-459-967-7	Sequence 7, Appl
38	66	9.8	840	1	US-08-460-327-7	Sequence 7, Appl
39	66	9.8	840	1	US-08-459-871-7	Sequence 7, Appl
40	66	9.8	840	3	US-09-024-532-1	Sequence 1, Appl
41	66	9.8	840	4	US-09-104-623A-1	Sequence 1, Appl
42	66	9.8	840	4	US-09-019-532-1	Sequence 1, Appl
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44	66	9.8	1110	1	US-08-434-255-5	Sequence 5, Appl
45	66	9.8	1110	1	US-08-459-967-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-578-649-1  
; Sequence 1, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Bultner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajolloff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..432
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 112..432
; US-08-578-649-1
;
; Alignment Scores:
; Pred. No.: 2,06e-28 Length: 459
; Score: 257.50 Matches: 56
; Percent Similarity: 60.29% Conservative: 26
; Best Local Similarity: 41.18% Mismatches: 41
; Query Match: 38.09% Indels: 13
; DB: 1 Gaps: 5
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; DB 40 ATGGCCCGGTCCCTGGTGGCCTT-----GGTGCATCATCTGTGCTGCTCTCTCC 93
;
; QY 18 -----ValHisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAsp 34
; DB 94 GCACCTGGTGTACGGGGTGTCTCTATGCCCAAGCTGGTCACCGGAAGCTGTGTGGGAC 153
;
; QY 35 AspGluCysValTyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAsp 54
; DB 154 CAGGAGTCAGCACCCCTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCGGAC 213
;
; QY 55 CysArgPheIleAsnValLysLysGlyGlnIleTyrValTyrSerLysLeuValLys 74
; DB 214 TGCCGATTCTGTACCATTCACCGGGCCCAAGTGTGTGTCTCTCCAGCTG----- 267
;
; QY 75 GluAsnGlyAlaGlyGlu-----PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGlu 93
; DB 268 ---AAGGGCCGTGGCGGCTCTTCTGGGAGGCGAGGCTTCAGGAGATTACTATGGAGAT 324
;
; QY 94 MetGlyVal---ValGlyTyrPhePheProArgAsnLeuValLysGluGlnArgValTyrGln 112
; DB 325 CTGGCTGCTGGCTGGGCTATTTCCTCCAGTAGCATGTCCGAGAGACACGACCTGAA 384
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; QY 113 GluAlaThrLysGluValProThrThrAspIleAspPheCysGlu 128
; DB 385 CCTGGCAATCGCATGTGAAGACAGACAAATGGGATTTCCTACTGCCAG 432
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; RESULT 2
; US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloiff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 7..327
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 4..6
; OTHER INFORMATION: /function= "Startcodon Met"
; US-08-578-649-18
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; Alignment Scores:
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; Query Match: 37.50% Indels: 5
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; QY 23 MetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThrIleSer 42
; DB 13 ATGCCAAATTTAGCAGATCGTAAATTATGTGCAGATCAGGAGTGCAGCCCTATCTCC 72
;
; QY 43 LeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLys 62
; DB 73 ATGGCTGTGGCCCTTCAGGACTACATGGCCCCCGACTGGCGATTCCTGACCATTCACCG 132
;
; QY 63 GlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu---Phe 81
; DB 133 GGCCAAAGTGTGTATGTCTTCTCCAAAGCTG-----AAGGGCCGTGGCGGCTCTTC 183
;
; QY 82 TrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyVal---ValGlyTyrPhe 100
; DB 184 TGGGAGGCGAGCGCTTCAGGAGATTACTATGGAGATTCTGCTGCTCGCTGGGCTATTTC 243
;
; QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120
; DB 244 CCAGTAGCATGTTCGAGAGAGACGACCCCTGAAACCTGGCCAAAGTCGATGTGAAGACA 303
;
; QY 121 ThrAspIleAspPheCysGlu 128
; DB 304 GACAAATGGGATTTCCTACTGCCAG 327
;
; RESULT 3
; US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366
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**Tue Dec 30 10:20:54 2003**

GENERAL INFORMATION:  
APPLICANT: Ulrich Bogdan  
APPLICANT: Reinhard Buttner  
APPLICANT: Brigitte Kaluza  
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,649  
FILING DATE: 29-Jul-1994

CLASSIFICATION: 433  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 24 247.2

ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Tiajolofo  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200

```

/ TELEFAX: (212) 838-3884
/
/ INFORMATION FOR SEQ ID NO: 4:
/
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 581 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/   MOLECULE TYPE: cDNA
/   FEATURE:
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; LOCATION: 110..499
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 110..178
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; NAME/KEY: mat_peptide
; LOCATION: 179..499
US-08-578-649-4

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Pred. No.:	1,298-24	581
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Best Local Similarity:	37.78%	Mismatches: 41
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Query Match:		Gaps: 5
DR:	1	

US-10-019-455A-6 (1-128) x US-08-578-649-4 (1-581)

Qy 5 LeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyIlePhe----- 22  
::: ::::: ||| ::::: ::::: ||| ::::: ::::: ||| ::::: ::::: ||| ::::: ::::: |||

Dt 107 AACATGGAGTGCACCCAGTCCTCATGGCAATC---GTGCCCTGCTGCTGCTTTTTCAGGG 163

**Qy**    23 -----MetAspArgLeuAlaSerLysLysCysAlaAspAsp    35  
               |||::||| |  
**Df**    164 GMAAGACGCGGGTCTGTTCATCATCAACTCCATGCACGCGCGAAGCAG    223  
               |||::||| |

Qy 36 GluCysValTyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCys 55  
||||| :: ||||| :: ||| ||| :: ||||| ||||| ||||| |||||  
Db 224 GAATGCAGGCATCCTATCTCCATGGTGTGCCCTCCAGGACTACGTGGCCCTGATTGC 283

56 Arp phe Ile Asn Val Lys Gly Gln Gln Ile Tyr Val Tyr Ser Lys Leu Val Lys Glu 75

Db	::: ::: :::       :::       :::       :::	284	CGCTCTGTGATATATATAGGGGCCAAGTGGTGATGCTTCTTCCAAGTTG-----	334
Qy	76	AsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMet	94	
Db	335	AAGGCCGTGGCGCCCTTCTCGGGAGGCAGTGTTCAGGAGGTTTACTATCGAGACCTG	394	
Qy	95	GlyVal---ValGlyTyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGlu	113	
Db	395	GCACCCCGCTGGGCTATTTCCCGTAGCAATGTCCGGAGGACCTGAATCGAAACCT	454	
Qy	114	AlaThrLysGluValProThrThrAspIleAspPhePheCysGlu	128	
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## RESULT 4

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US-08-578-649-8
; Sequence 8, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

```

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,649
FILING DATE: 29-July-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: DE P 43 24 247.2  
FILING DATE: 20-July-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Tiajolloff  
REGISTRATION NUMBER: 31.575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 8:

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, INFORMATION FOR SEQ ID NO: 8:
,
, SEQUENCE CHARACTERISTICS:
, LENGTH: 305 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: single
, TOPOLOGY: linear
, MOLECULE TYPE: CDNA
, FEATURE.
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; NAME/KEY: misc RNA
; LOCATION: join(1..29, 277..305)
; OTHER INFORMATION: /function= "Primer"
US-08-578-649-8

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Best Local Similarity:	44.44%
Query Match:	31.14%
DB:	1
Length:	305
Matches:	44
Conservative:	17
Mismatches:	33
Indels:	5
Gaps:	3

US-10-019-455A-6 (1-128) x US-08-578-649-8 (1-305)



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QY 70 SerLysLeuValLysGluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGly 88
Db 127 TCCAAGCTG-----AAGGGCGGTGGGGGCTCTCTCGGAGGAGCAGCGTTCAGGGA 177
QY 89 AspGlyGln---AspGluMetGlyValValGlyTyrPheProArgAsnLeuValLysGlu 107
Db 178 GATTACTATGAGATCTGGTCTCGCTCGCTGGCTATTTCCCAAGTAGCATGTCCGAGAG 237
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RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloif
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: exon

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; LOCATION: 40..166
; FEATURE: exon
; NAME/KEY: 214..347
; LOCATION: 214..347
; FEATURE: exon
; NAME/KEY: 393..503
; LOCATION: 393..503
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; LOCATION: 549..569
; NAME/KEY: -
; LOCATION: one-of(194, 369, 527)
; OTHER INFORMATION: /note="N in positions 194, 369
; OTHER INFORMATION: and 527 denotes an indefinite number and sequence
; OTHER INFORMATION: of nucleotides "
US-08-578-649-24
Alignment Scores:
Pred. No.: 2,1e-18 Length: 596
Score: 190.00 Matches: 57
Percent Similarity: 45.36% Conservative: 26
Best Local Similarity: 31.15% Mismatches: 39
Query Match: 28.11% Indels: 62
DB: 1 Gaps: 9
US-10-019-455A-6 (1-128) x US-08-578-649-24 (1-596)
QY 1 MetAlaArgIleLeuLeuPheLeuProGlyLeuValAlaValCysAla----- 17
Db 40 ATGCCCCGGTCCCTGTGTGCCTT-----GGTGCAATCATCTTGTGTCTCCTTCTCC 93
QY 18 -----ValHisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAsp 34
Db 94 GGAACCTGGTGTGAGGGGTGCTCTATGTCACCAAGTGGCTGACCGAAGCTGTGTGGGAC 153
QY 35 AspGluCysValTyr----- 39
Db 154 CAGGAGTGCAGCCG-TAAGAAATGGGAGGGTGAAGTGGGNCCTTCTTATTCTTCCCTA 212
QY 40 ---ThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 58
Db 213 GACCCATATCTCCATGGCTGTGGCCCTTCAAGGACTACATGCCCCCGGACTGCGGATTCCTG 272
QY 59 AsnValLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 78
Db 273 ACCATTCAACGGGGCCCAAGTGTGTATGTCTTCTCAAGCTG-----AAGGGCGGT 323
QY 79 GlyGlu---PheTrpAlaGlySer----- 85
Db 324 GGGCGGCTCTTCTGGGAGGAGCGGTGGTCTTGGAGAGTGAANAGCTTTTAACCTCT 383
QY 86 -----ValTyrGlyAspGlyGlnAspGluMetGlyVal---ValGlyTyrPhePro 101
Db 384 CTTCCCGGAGTTTCAGGGAGATTACTATGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 443
QY 102 ArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThrThr 121
Db 444 AGTAGCATTTGTCGAGAGGAGCAGACCCCTGAACACCTGGCAAAAGTCGATGTG---AAGACA 500
QY 122 AspIle----- 125
Db 501 GACGTGGAGTGTATGGGGGCTGGCANTTTCCCTTTCTCTTTTTCAGAAATGGGATTTTC 560
QY 126 PheCysGlu 128
Db 561 TACTGCCAG 569
RESULT 6
US-08-578-649-3
; Sequence 3, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:

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Qy 1 MetAlaArgTleLeuLeuPheLeuProGlyLeuValAlaValCysAla----- 17

DB:	1	Gaps:	3
US-10-019-455A-6 (1-128) x US-08-306-691B-48 (1-2757)			
QY	44	AlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGly	63
DB	2325	GCCAAAGCCCGCTATGACTTCTGCGCCGCTGAGCTGCTCAAGGAGGT	2384
QY	64	GlnGlnIleTyrValTyrSerLysLeuValLysGlnAsnGlyAlaGlyGluPheTrpAla	83
DB	2385	GACATCATC-----AAGATCCTTAAACAAGAAAGGACAGCAAGGCTGGTGGCGA	2432
QY	84	GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn	103
DB	2433	GGGAGATCATATGCGCG-----AAGATCCTTAAACAAGAAAGGACAGCAAGGCTGGTGGCGA	2471
QY	104	LeuValLysGlnGlnArgValTyrGlnGlu	113
DB	2472	TACGTGGAGGAAGAT-----TATTCTGAA	2495
RESULT 8			
PCT-US93-06251-79			
Sequence 79, Application PC/TUS9306251			
GENERAL INFORMATION:			
APPLICANT: Wickstrom, Eric and Rife, Jason P.			
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing Stereospecific Alkylphosphonates and Arylphosphonates			
NUMBER OF SEQUENCES: 93			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER			
STREET: 400 Garden City Plaza			
CITY: Garden City			
STATE: NY			
COUNTRY: USA			
ZIP: 11530			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent In Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: PCT/US93/06251			
FILING DATE: 19930630			
CLASSIFICATION:			
ATTORNEY/AGENT INFORMATION:			
NAME: DiGiglio, Frank S.			
REGISTRATION NUMBER: 31,346			
REFERENCE/DOCKET NUMBER: 8586			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: 516-742-4343			
TELEFAX: 516-742-4366			
TELEX: 230 901 SANS UR			
INFORMATION FOR SEQ ID NO: 79:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 2757 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: double			
TOPOLOGY: linear			
MOLECULE TYPE: DNA (genomic)			
PCT-US93-06251-79			
Alignment Scores:			
Pred. No.:	0.0249	Length:	2757
Score:	86.50	Matches:	23
Percent Similarity:	51.43%	Conservative:	13
Best Local Similarity:	32.86%	Mismatches:	21
Query Match:	12.80%	Indels:	13
DB:	5	Gaps:	3
US-10-019-455A-6 (1-128) x PCT-US93-06251-79 (1-2757)			
QY	44	AlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysGly	63

;/ TITLE OF INVENTION: Vav Proto-Oncogene Protein  
;/ NUMBER OF SEQUENCES: 14  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Bristol-Myers Squibb Company  
;/ STREET: P.O. Box 4000  
;/ CITY: Princeton  
;/ STATE: New Jersey  
;/ COUNTRY: U.S.A.  
;/ ZIP: 08543-4000  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/07/646,537B  
;/ FILING DATE:  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Gaul, Timothy J.  
;/ REGISTRATION NUMBER: 33,111  
;/ REFERENCE/DOCKET NUMBER: DC10  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (609) 921-5901  
;/ TELEFAX: (609) 921-4526  
;/ INFORMATION FOR SEQ ID NO: 1:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 2793 base pairs  
;/ TYPE: nucleic acid  
;/ STRANDEDNESS: double  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: cDNA  
;/ HYPOTHETICAL: NO  
;/ FEATURE:  
;/ NAME/KEY: CDS  
;/ LOCATION: 14..2545  
;/ US-07-646-537B-1

Alignment Scores:  
Pred. No.: 0.0355 Length: 2793  
Score: 85.50 Matches: 22  
Percent Similarity: 51.43% Conservative: 14  
Best Local Similarity: 31.43% Mismatches: 21  
Query Match: 12.65% Indels: 13  
DB: 1 Gaps: 3

US-10-019-455A-6 (1-128) x US-07-646-537B-1 (1-2793)  
QY 44 AlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysLysGly 63  
Db 2369 GCCAAGCCCGTACGACCTCTGTGCGCGGACAGGTGCGAACTGTCCTTAAGAGGGT 2428  
QY 64 GlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAla 83  
Db 2429 GATATCATC-----AAGATCCTCAATAAGAGGACAGCAAGCGTGGTGGCGT 2476  
QY 84 GlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsn 103  
Db 2477 GCGGACATTCACGCCGG-----ATCGGCTGGTTCCTCTTAAC 2515  
QY 104 LeuValLysGluGlnArgValTyrGlnGlu 113  
Db 2516 TATGTGGAGGAGAC-----TATTCGGA 2539

RESULT 11  
US-09-300-958A-28  
; Sequence 28, Application US/09300958A  
; Patent No. 6495319  
; GENERAL INFORMATION:  
; APPLICANT: McClelland, Michael  
; APPLICANT: Welsh, John  
; APPLICANT: Trenkle, Thomas  
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of

;/ TITLE OF INVENTION: Using Same  
;/ FILE REFERENCE: P-PH 3457  
;/ CURRENT APPLICATION NUMBER: US/09/300,958A  
;/ CURRENT FILING DATE: 1999-04-27  
;/ PRIOR APPLICATION NUMBER: 60/083,331  
;/ PRIOR FILING DATE: 1998-04-27  
;/ PRIOR APPLICATION NUMBER: 60/098,070  
;/ PRIOR FILING DATE: 1998-08-27  
;/ PRIOR APPLICATION NUMBER: 60/118,624  
;/ PRIOR FILING DATE: 1999-02-04  
;/ NUMBER OF SEQ ID NOS: 85  
;/ SOFTWARE: PatentIn Ver. 2.0  
;/ SEQ ID NO 28  
;/ LENGTH: 467  
;/ TYPE: DNA  
;/ ORGANISM: Homo sapiens  
;/ FEATURE:  
;/ NAME/KEY: unsure  
;/ LOCATION: (428)  
;/ NAME/KEY: unsure  
;/ LOCATION: (462)  
;/ US-09-300-958A-28

Alignment Scores:  
Pred. No.: 0.0225 Length: 467  
Score: 79.00 Matches: 23  
Percent Similarity: 50.00% Conservative: 16  
Best Local Similarity: 29.49% Mismatches: 27  
Query Match: 11.69% Indels: 12  
DB: 4 Gaps: 3

US-10-019-455A-6 (1-128) x US-09-300-958A-28 (1-467)  
QY 46 AlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValLysLysGlyGlnGln 65  
Db 152 GCTCGGTATGACTCTCTGCAAGAGATATGAGAGAGTTCCTCTGTGTAAGAGGATGTG 211  
QY 66 IleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrpAlaGlySer 85  
Db 212 GTGAAGATTTCACAAAGATG-----AGTGCAATGGCTGGTGGAGAGAGAA 259  
QY 86 ValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPheProArgAsnLeuVal 105  
Db 260 GTAATGGCAGG-----GTGGGCTGGTTCATCCACATATGTG 298  
QY 106 LysGluGlnArgValTyrGlnGluAlaThrLysGluValProThrThrAspIle 123  
Db 299 ---GGAAGGAGGATGAATAAATCAATCCCGTGTTCACCCCTGCACCAAAATT 349

RESULT 12  
US-09-356-952-11  
; Sequence 11, Application US/09356952  
; Patent No. 6117663  
; GENERAL INFORMATION:  
; APPLICANT: Boriack-Sjodin, Ann  
; APPLICANT: Margarit, S. M.  
; APPLICANT: Bor-Sogii, Dafna  
; APPLICANT: Cole, Philip  
; APPLICANT: Kuriyan, John  
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE  
; FILE REFERENCE: 600-1-228N  
; CURRENT APPLICATION NUMBER: US/09/356,952  
; CURRENT FILING DATE: 1999-07-19  
; EARLIER APPLICATION NUMBER: 60/093,631  
; EARLIER FILING DATE: 1998-07-21  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 5398  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
; US-09-356-952-11

Alignment Scores: 0.984 Length: 5398  
Pred. No.: 78.50 Matches: 23  
Score: 49.44% Conservative: 21  
Percent Similarity: 25.84% Mismatches: 34  
Best Local Similarity: 11.61% Indels: 11  
Query Match: 3 Gaps: 4  
DB: 4

US-10-019-455A-6 (1-128) x US-09-356-952-11 (1-5398)

QY 26 LeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThrLeuAlaSer 45  
Db 445 CTTCTCTCTCCCTCGACAGTGGTTGACCCAGCATTCGTCCAATTGGAATAGTAGTC 504  
QY 46 AlaGlnGluAspTyrAsnAlaPro-----AspCysArgPheLeuAsnVal 60  
Db 505 GCTGCTTATGACITTAATTATCCCATTAATAAAAGACAGTTCCTTCGCCAACTTTGTCTGTGA 564  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGlu 80  
Db 565 CACAAGGGGAACCAATTATATATCTTAACAAA-----AACTCATCTGGG--- 609  
QY 81 PheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
Db 610 TGGTGGGATGGATTAGTTATTGACGACAGTAATGGGAAAGTTTAC---AGAGGCTGTGTTT 666  
QY 101 ProArgAsnLeuValLysGluGlnArg 109  
Db 667 CCTCAAAACTTCGGTAGACCTTTAAGA 693

RESULT 13  
US-08-996-139-14  
; Sequence 14, Application US/08996139  
; Patent No. 6017729  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent  
; APPLICANT: Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Power Macintosh  
; OPERATING SYSTEM: Apple Operating System 7.5.5  
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/996,139  
; FILING DATE: 22 DECEMBER 1997  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 60/064,671  
; FILING DATE: 14 OCTOBER 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/813,509  
; FILING DATE: 07 MARCH 1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: USSN 08/772,330  
; FILING DATE: 23 DECEMBER 1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perkins, Patricia Anne  
; REGISTRATION NUMBER: 34,693  
; REFERENCE/DOCKET NUMBER: 2851-A  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1878 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Murine  
; IMMEDIATE SOURCE:  
; LIBRARY: Murine Fetal Liver Epithelium  
; CLONE: MURANK  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1875  
US-08-996-139-14

Alignment Scores: 0.245 Length: 1878  
Pred. No.: 78.00 Matches: 30  
Score: 39.44% Conservative: 26  
Percent Similarity: 21.13% Mismatches: 48  
Best Local Similarity: 11.54% Indels: 38  
Query Match: 3 Gaps: 5  
DB: 5

US-10-019-455A-6 (1-128) x US-08-996-139-14 (1-1878)

QY 4 IleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyIlePheMet 23  
Db 649 GTTCTGCTCTCTCTCATCTCTGTGTAGTAGTGCTGCCATCATCTTCGGGGTTACTAC 708  
QY 24 AspArg----- 25  
Db 709 AGGAAGGAGGAGGAAAGCGCTCACAGCTAAATTTGTGGAATTTGGGTCAATGATGCTTGCAGT 768  
QY 26 ---LeuAlaSerLysLysLeuCysAlaAspGluCysValTyrThrLeuAla 44  
Db 769 AGTCTAAGTGGAAATAAGGAGTCTCTCAGGGGACCGTTGTGTCTGTTCCCATCTCGCAACC 828  
QY 45 SerAlaGlnGluAspTyrAsnAlaProAspCysArgPheLeuAsnValLysGlyGln 64  
Db 829 TCCAGTCAGCAAGAAGTG-----TGTCGAAGGTATCTTACTAATGACTCGGGAG 876  
QY 65 GlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAlaGlyGluPheTrp----- 82  
Db 877 GAG-----AAGATGTTCCAGAAAGCGTGTCTGGAGTCTGTGGGCGCTGTG 921  
QY 83 -----AlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
Db 922 TGTGCGGAGGTGGGCGCTTGGGAGAGTCAAGATTTAGGACGTTCC----- 969  
QY 101 ProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
Db 970 -----ACACTGGTCAGCGAGGTTGAGACGCAAGGAGACCTCTCGAGGAAGATTTCCCA 1023  
QY 121 ThrAsp 122  
Db 1024 GAGGAT 1029

RESULT 14  
US-08-995-659-14  
; Sequence 14, Application US/08995659  
; Patent No. 6242213  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; APPLICANT: Galibert, Laurent  
; APPLICANT: Maraskovsky, Eugene  
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department

Tue Dec 30 10:20:54 2003

STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/995,659  
FILING DATE: 22 DECEMBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/064,671  
FILING DATE: 14 OCTOBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2852-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Murine  
IMMEDIATE SOURCE:  
LIBRARY: Murine Fetal Liver Epithelium  
CLONE: muRANK  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1875  
US-08-995-659-14

Alignment Scores:  
Pred. No.: 0.245 Length: 1878  
Score: 78.00 Matches: 30  
Percent Similarity: 39.44% Conservative: 26  
Best Local Similarity: 21.13% Mismatches: 48  
Query Match: 11.54% Indels: 38  
DB: 3 Gaps: 5

US-10-019-455A-6 (1-128) x US-08-995-659-14 (1-1878)

QY 4 IleLeuLeuLeuPheLeuProGlyLeuValAlaValCysAlaValHisGlyIlePheMet 23  
Db 649 GTTCTGCTCTCTTCATCTCTGTGGTAGTAGTGGCTGCCATCATCTTCGGCGTTTACTAC 708  
QY 24 AspArg----- 25  
Db 709 AGGAGGGGGAAGCGCTGACAGCTAATTTGTGGAATTGGTCAATGATGCTTGCAGT 768  
QY 26 ---LeuAlaSerIlyLysLeuCysAlaAspGluCysValTyrThrIleSerLeuAla 44  
Db 769 AGCTAAGTGAATAAGGAGTCTCTCAGGGGACCGTTGTCTGTTGCCACTCGCAACC 828

QY 45 SerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAsnValIysLysGlyGln 64  
Db 829 TCCAGTCAGCAAGAGTG-----TGTGAAGGTAICTTACTATGATCGGAG 876  
QY 65 GlnIleTyrValTyrSerIlyLeuValIysGluAsnGlyAlaGlyGluPheTrp----- 82  
Db 877 GAG-----AAGATGGTTCAGAGAAGCGGTCTGTGGAGTCTGTGGGCTGTG 921  
QY 83 -----AlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGlyTyrPhe 100  
Db 922 TGTGGCGCAGGTGGCCCTGGCGCAGAGTCAGAGATTCTAGGACGTTTC----- 969  
QY 101 ProArgAsnLeuValIysGlnGlnArgValTyrGlnGluAlaThrLysGluValProThr 120  
Db 970 -----ACACTGGTCAGCGAGTTGAGCGGAGGAGGACCTCTCGAGGAAGATCCCA 1023  
QY 121 ThrAsp 122  
Db 1024 GAGGAT 1029  
RESULT 15  
US-09-215-649A-14  
; Sequence 14, Application US/09215649A  
; Patent No. 6271349  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Dirk M.  
; Galibert, Laurent  
; Maraskovsky, Eugene  
; TITLE OF INVENTION: Receptor Activator of NF-kappaB  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Immunex Corporation, Law Department  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: WA  
; COUNTRY: USA  
; ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/215,649A  
FILING DATE: 17-Dec-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/996,139  
FILING DATE: <Unknown>  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2851-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1878 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Murine  
IMMEDIATE SOURCE:



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:08:26 ; Search time 1216 Seconds  
(without alignments)  
12918.830 Million cell updates/sec

Title: US-10-019-455A-4  
Perfect score: 384  
Sequence: 1 atggcaagaatattgttact.....atattgactttcttgcgag 384

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba.\*
- 2: gb\_htg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vi.\*
- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
- 18: em\_in.\*
- 19: em\_mu.\*
- 20: em\_om.\*
- 21: em\_or.\*
- 22: em\_ov.\*
- 23: em\_pat.\*
- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rtd.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_hgo\_hum.\*
- 40: em\_hgo\_mus.\*
- 41: em\_hgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	384	100.0	384	6	BD010802	BD010802 Novel pol
2	384	100.0	384	6	BD093103	BD093103 Novel pol
3	384	100.0	521	6	AX358818	AX358818 Sequence
4	384	100.0	521	6	AX362311	AX362311 Sequence
5	384	100.0	521	6	AX454774	AX454774 Sequence
6	384	100.0	521	6	AX491252	AX491252 Sequence
7	384	100.0	846	9	AF233261	AF233261 Homo sapi
8	384	100.0	865	9	AF243505	AF243505 Homo sapi
9	384	100.0	923	6	BD010820	BD010820 Novel pol
10	384	100.0	923	6	BD093121	BD093121 Novel pol
11	384	100.0	1422	9	HS242552	AJ242552 Homo sapi
12	330	85.9	330	6	BD010816	BD010816 Novel pol
13	330	85.9	330	6	BD093117	BD093117 Novel pol
14	287	74.7	384	6	BD010805	BD010805 Novel pol
15	287	74.7	384	6	BD093106	BD093106 Novel pol
16	287	74.7	929	10	AF243504	AF243504 Mus muscu
17	287	74.7	947	6	BD010821	BD010821 Novel pol
18	287	74.7	947	6	BD093122	BD093122 Novel pol
19	287	74.7	958	10	MMU243939	AJ243939 Mus muscu
20	287	74.7	1054	10	AF233333	AF233333 Mus muscu
21	285.4	74.3	384	6	BD010835	BD010835 Novel pol
22	285.4	74.3	384	6	BD093136	BD093136 Novel pol
23	252.2	65.7	330	6	BD010817	BD010817 Novel pol
24	252.2	65.7	330	6	BD093118	BD093118 Novel pol
25	249	64.8	330	6	BD010836	BD010836 Novel pol
26	249	64.8	330	6	BD093137	BD093137 Novel pol
27	217.4	56.6	307	6	BD010830	BD010830 Novel pol
28	217.4	56.6	307	6	BD093131	BD093131 Novel pol
29	193.8	50.5	261	6	BD010829	BD010829 Novel pol
30	193.8	50.5	261	6	BD093130	BD093130 Novel pol
31	190.2	49.5	484	5	AF233518	AF233518 Gallus ga
32	142	37.0	232	9	HS252325	AJ252325 Homo sapi
33	142	37.0	121151	9	HS705D16	AL034428 Human DNA
34	134	34.9	466	5	AF233519	AF233519 Rana cate
35	116.4	30.3	358	9	HS252324	AJ252324 Homo sapi
36	114.8	23.9	144765	2	EX510362	BS10362 Mus muscu
37	112.4	29.3	215581	2	AC106161	AC106161 Rattus no
38	109	28.4	259	9	HS252326	AJ252326 Homo sapi
39	67.2	17.5	545	10	RNU67884	U67884 Rattus norv
40	64.8	16.9	396	9	BT007044	BT007044 Homo sapi
41	64.8	16.9	396	12	BT007775	BT007775 Synthetic
42	64.8	16.9	433	6	AX253435	AX253435 Sequence
43	64.8	16.9	459	6	A42942	A42942 Sequence 1
44	64.8	16.9	459	6	AX016785	AX016785 Sequence
45	64.8	16.9	459	6	AX252508	AX252508 Sequence

ALIGNMENTS

RESULT 1	BD010802	384 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	BD010802	Novel polypeptide and DNA thereof.			
DEFINITION	BD010802	Novel polypeptide and DNA thereof.			
ACCESSION	BD010802				
VERSION	BD010802.1	GI:18639175			
KEYWORDS	JP 2001069994-A/3.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 384)				
AUTHORS	Ito, Y., Nishi, K., Ogi, K., Ogi, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.				
TITLE	Novel polypeptide and DNA thereof				



JOURNAL	Patent: JP 2001069994-A 3 21-MAR-2001; TAKEDA CHEMICAL INDUSTRIES LTD	TITLE	Yoshimura, K. and Tanaka, H. Novel polypeptide and its DNA
COMMENT	OS Homo sapiens (human) PN JP 2001069994-A/3 PD 21-MAR-2001 PF 29-JUN-2000 JP 2000195911 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P19/02, PC A61P19/08, PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53// PC C12P21/08, C12N15/00, A61K37/02, C12N5/00 CC FH Key Location/Qualifiers FT source 1..384 FT /organism='Homo sapiens (human)'. FT Location/Qualifiers	COMMENT	OS Homo sapiens (human) PN WO 0102564-A/3 PD 11-JAN-2001 PF 29-JUN-2000 WO 2000JP004278 PR 30-JUN-1999 JP 99P 186718 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17, PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088/(C12P21/02, C12R1.19) CC FH Key Location/Qualifiers
FEATURES	Source 1..384 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	FEATURES	source 1..384 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
BASE COUNT	99 a 106 g 109 t	BASE COUNT	99 a 106 g 109 t
ORIGIN	Query Match 100.0%; Score 384; DB 6; Length 384; Best Local Similarity 100.0%; Pred. No. 3.3e-107; Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ORIGIN	Query Match 100.0%; Score 384; DB 6; Length 384; Best Local Similarity 100.0%; Pred. No. 3.3e-107; Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1	ATGCGAAGAAATATGTTACTTTTCTCCCGGGTCTTGCGCTGTATGTTGCTGTCATGGA 60	Qy 1	ATGCGAAGAAATATGTTACTTTTCTCCCGGGTCTTGCGCTGTATGTTGCTGTCATGGA 60
Db 1	ATGCGAAGAAATATGTTACTTTTCTCCCGGGTCTTGCGCTGTATGTTGCTGTCATGGA 60	Db 1	ATGCGAAGAAATATGTTACTTTTCTCCCGGGTCTTGCGCTGTATGTTGCTGTCATGGA 60
Qy 61	ATATTATGACCGTCTAGCTTCCAAGAGCTCTGTCAGATGATGATGTTGTTACT 120	Qy 61	ATATTATGACCGTCTAGCTTCCAAGAGCTCTGTCAGATGATGATGTTGTTACT 120
Db 61	ATATTATGACCGTCTAGCTTCCAAGAGCTCTGTCAGATGATGATGTTGTTACT 120	Db 61	ATATTATGACCGTCTAGCTTCCAAGAGCTCTGTCAGATGATGATGTTGTTACT 120
Qy 121	ATTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 180	Qy 121	ATTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 180
Db 121	ATTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 180	Db 121	ATTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 180
Qy 181	AAAAAGGGCAGCAGATCTATGTTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 240	Qy 181	AAAAAGGGCAGCAGATCTATGTTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 240
Db 181	AAAAAGGGCAGCAGATCTATGTTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 240	Db 181	AAAAAGGGCAGCAGATCTATGTTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 240
Qy 241	TTTGGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGTATTTC 300	Qy 241	TTTGGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGTATTTC 300
Db 241	TTTGGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGTATTTC 300	Db 241	TTTGGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGTATTTC 300
Qy 301	CCAGGAACCTTGGTCAAGGAACACGCTGTGTACCAAGAACTACCAAGGAAGTTCCCA 360	Qy 301	CCAGGAACCTTGGTCAAGGAACACGCTGTGTACCAAGAACTACCAAGGAAGTTCCCA 360
Db 301	CCAGGAACCTTGGTCAAGGAACACGCTGTGTACCAAGAACTACCAAGGAAGTTCCCA 360	Db 301	CCAGGAACCTTGGTCAAGGAACACGCTGTGTACCAAGAACTACCAAGGAAGTTCCCA 360
Qy 361	ACGATATTGACTTCTTCTCGGAG 384	Qy 361	ACGATATTGACTTCTTCTCGGAG 384
Db 361	ACGATATTGACTTCTTCTCGGAG 384	Db 361	ACGATATTGACTTCTTCTCGGAG 384
RESULT 2	BD093103	RESULT 3	AX358818
LOCUS	BD093103	LOCUS	AX358818
DEFINITION	Novel polypeptide and its DNA.	DEFINITION	Sequence 71 from Patent WO0193983.
ACCESSION	BD093103	ACCESSION	AX358818
VERSION	BD093103.1 GI:22638691	VERSION	AX358818.1 GI:18675310
KEYWORDS	WO 0102564-A/3.	KEYWORDS	
SOURCE	Homo sapiens (human)	SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens	ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 384)	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,	AUTHORS	

REFERENCE 1  
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0193983-A 71 13-DEC-2001;  
Genentech Inc. (US)  
FEATURES Location/Qualifiers  
source 1. .521  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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BASE COUNT 167 a 86 c 131 g 137 t  
ORIGIN  
Query Match 100.0%; Score 384; DB 6; Length 521;  
Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGCGGTGATGTGCTGTGCATGGA 60  
DB 38 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGCGGTGATGTGCTGTGCATGGA 97  
QY 61 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGATGATGAGTGCTCTACT 120  
DB 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGATGATGAGTGCTCTACT 157  
QY 121 ATTTCTCTGGCTAGTGCTCAAGAAGATTATATGCCCGGACTGTAGATTCAATTAACGTT 180  
DB 158 ATTTCTCTGGCTAGTGCTCAAGAAGATTATATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 181 AAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGTGTAAGAAAAATGGAGCTGGAGAA 240  
DB 218 AAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGTGTAAGAAAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTTTATGTTGTCATGCCAGACAGATGGAGTGGTGGTTATTTC 300  
DB 278 TTTTGGGCTGGCAGTGTTTATGTTGTCATGCCAGACAGATGGAGTGGTGGTTATTTC 337  
QY 301 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGGAAGTCCCACC 360  
DB 338 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGGAAGTCCCACC 397  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
DB 398 ACGGATATTGACTTCTTCTGCGAG 421  
RESULT 4  
AX362311  
LOCUS AX362311 521 bp DNA linear PAT 15-FEB-2002  
DEFINITION Sequence 71 from Patent WO208288.  
ACCESSION AX362311  
VERSION AX362311.1 GI:18694613  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,  
Watanabe,C.K. and Wood,W.I.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
JOURNAL Patent: WO 0208288-A 71 31-JAN-2002;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
source 1. .521  
/organism="Homo sapiens"  
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BASE COUNT 167 a 86 c 131 g 137 t  
ORIGIN  
Query Match 100.0%; Score 384; DB 6; Length 521;  
Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGCGGTGATGTGCTGTGCATGGA 60  
DB 38 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGCGGTGATGTGCTGTGCATGGA 97  
QY 61 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGATGATGAGTGCTCTACT 120  
DB 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGATGATGAGTGCTCTACT 157  
QY 121 ATTTCTCTGGCTAGTGCTCAAGAAGATTATATGCCCGGACTGTAGATTCAATTAACGTT 180  
DB 158 ATTTCTCTGGCTAGTGCTCAAGAAGATTATATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 181 AAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGTGTAAGAAAAATGGAGCTGGAGAA 240  
DB 218 AAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGTGTAAGAAAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTTTATGTTGTCATGCCAGACAGATGGAGTGGTGGTTATTTC 300  
DB 278 TTTTGGGCTGGCAGTGTTTATGTTGTCATGCCAGACAGATGGAGTGGTGGTTATTTC 337  
QY 301 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGGAAGTCCCACC 360  
DB 338 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGGAAGTCCCACC 397  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
DB 398 ACGGATATTGACTTCTTCTGCGAG 421  
RESULT 5  
AX454774  
LOCUS AX454774 521 bp DNA linear PAT 06-JUL-2002  
DEFINITION Sequence 359 from Patent WO208284.  
ACCESSION AX454774  
VERSION AX454774.1 GI:21714011  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,  
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,  
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.  
and Ye,W.  
TITLE Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
JOURNAL Patent: WO 0208284-A 359 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone  
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ;  
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;  
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)  
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;  
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William  
I. (US)  
FEATURES Location/Qualifiers  
source 1. .521  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
BASE COUNT 167 a 86 c 131 g 137 t  
ORIGIN  
Query Match 100.0%; Score 384; DB 6; Length 521;  
Best Local Similarity 100.0%; Pred. No. 3.4e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCAAGATATTTCTTCTTCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA	60
Db	38	ATGGCAAGAATATTTCTTCTTCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA	97
QY	61	ATATTATGGACCGTCTAGCTTCAAGAAGCTCTGTGCAGATGATGATGCTTACT	120
Db	98	ATATTATGGACCGTCTAGCTTCAAGAAGCTCTGTGCAGATGATGATGCTTACT	157
QY	121	ATTCTCTGGCTAGTGTCTCAAGAAGTATATATGCCCCGACTGTAGATTCAATTAACGTT	180
Db	158	ATTCTCTGGCTAGTGTCTCAAGAAGTATATATGCCCCGACTGTAGATTCAATTAACGTT	217
QY	181	AAAAAGGCGCAGACATCTATGTGTACTCAAGCTGTGTAAAGAAATCGAGCTGGAGAA	240
Db	218	AAAAAGGCGCAGACATCTATGTGTACTCAAGCTGTGTAAAGAAATCGAGCTGGAGAA	277
QY	241	TTTTGGGCTGGCAGTGTATGTGTATGTCAGGACGAGATGGAGTCTGGGTATTTC	300
Db	278	TTTTGGGCTGGCAGTGTATGTGTATGTCAGGACGAGATGGAGTCTGGGTATTTC	337
QY	301	CCAGAACTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACACC	360
Db	338	CCAGAACTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTCCACACC	397
QY	361	ACGATATTGACTTCTTCTGCGAG	384
Db	398	ACGATATTGACTTCTTCTGCGAG	421
RESULT 6			
AX491252		521 bp	DNA linear PAT 16-AUG-2002
LOCUS		Sequence 359 from Patent WO0200690.	
DEFINITION		AX491252	
ACCESSION		AX491252	
VERSION		AX491252.1	GI:22323963
KEYWORDS			
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE			
AUTHORS		Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.	
TITLE		Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis	
JOURNAL		Patent: WO 020690-A 359 03-JAN-2002;	
FEATURES		Genentech, Inc. (US)	
source		Location/Qualifiers	
		1..521	
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		/db_xref="taxon:9606"	
BASE COUNT		167 a 86 c 131 g 137 t	
ORIGIN			
Query Match		100.0%; Score 384; DB 6; Length 521;	
Best Local Similarity		100.0%; Pred. No. 3.4e-107;	
Matches 384; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	ATGCAAGATATTTCTTCTTCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA	60
Db	38	ATGGCAAGAATATTTCTTCTTCTCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA	97
QY	61	ATATTATGGACCGTCTAGCTTCAAGAAGTATATATGCCCCGACTGTAGATTCAATTAACGTT	120
Db	98	ATATTATGGACCGTCTAGCTTCAAGAAGTATATATGCCCCGACTGTAGATTCAATTAACGTT	157
QY	121	ATTCTCTGGCTAGTGTCTCAAGAAGTATATATGCCCCGACTGTAGATTCAATTAACGTT	180
Db	158	ATTCTCTGGCTAGTGTCTCAAGAAGTATATATGCCCCGACTGTAGATTCAATTAACGTT	217

Db	45	ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA	104	Query Match	100.0%;	Score 384;	DB 9;	Length 865;
		Best Local Similarity	100.0%;	Pred. No. 3.6e-107;				
		Matches 384;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA	60					
Db	8	ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA	67					
Qy	61	ATATTTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGCTGTATTA	120					
Db	68	ATATTTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGCTGTATTA	127					
Qy	121	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCA	180					
Db	128	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCA	187					
Qy	181	AAAAAGGGCAGCAGATCTATGTGTA	240					
Db	188	AAAAAGGGCAGCAGATCTATGTGTA	247					
Qy	241	TTTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGAGTGTGG	300					
Db	248	TTTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGAGTGTGG	307					
Qy	301	CCCAGGAACCTTGGTCAAGGAACAGCGTGTACCAAGGAAGCTACCAAGGA	360					
Db	308	CCCAGGAACCTTGGTCAAGGAACAGCGTGTACCAAGGAAGCTACCAAGGA	367					
Qy	361	ACGGATATTGACTTCTTCTGCGAG	384					
Db	368	ACGGATATTGACTTCTTCTGCGAG	391					
RESULT 9	BD010820	923 bp	DNA	linear	PAT 31-JAN-2002			
LOCUS	BD010820	923 bp	DNA	linear	PAT 31-JAN-2002			
DEFINITION	Novel polypeptide and DNA thereof.							
ACCESSION	BD010820							
VERSION	BD010820.1	GI:18639193						
KEYWORDS	JP 2001069994-A/21.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 923) Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.							
AUTHORS	Novel polypeptide and DNA thereof Patent: JP 2001069994-A 21 21-MAR-2001; TAKEDA CHEMICAL INDUSTRIES LTD							
TITLE	OS Homo sapiens (human)							
JOURNAL	PN JP 2001069994-A/21							
MEDLINE	PD 21-MAR-2001							
PUBMED	PF 29-JUN-2000 JP 2000195911							
REFERENCE	PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,							
AUTHORS	PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA							
TITLE	PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,							
JOURNAL	PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//							
FEATURES	PC C12P21/08, C12N15/00, A61K37/02, C12N5/00							
source	Key	Location/Qualifiers						
	PH source	1. .923						
	FT /organism='Homo sapiens (human)'							
	FEATURES	Location/Qualifiers						
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		/organism="Homo sapiens"						
		/mol type="genomic DNA"						
		/db xref="taxon:9606"						
BASE COUNT	303 a	147 c	213 g	260 t				

Db	45	ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA	104	Query Match	100.0%;	Score 384;	DB 9;	Length 865;
		Best Local Similarity	100.0%;	Pred. No. 3.6e-107;				
		Matches 384;	Conservative	0;	Mismatches	0;	Indels	0;
Qy	1	ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA	60					
Db	8	ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTCATGGA	67					
Qy	61	ATATTTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGCTGTATTA	120					
Db	105	ATATTTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGCTGTATTA	164					
Qy	121	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCA	180					
Db	165	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCA	224					
Qy	181	AAAAAGGGCAGCAGATCTATGTGTA	240					
Db	225	AAAAAGGGCAGCAGATCTATGTGTA	284					
Qy	241	TTTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGAGTGTGG	300					
Db	285	TTTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGAGTGTGG	344					
Qy	301	CCCAGGAACCTTGGTCAAGGAACAGCGTGTACCAAGGAAGCTACCAAGGA	360					
Db	345	CCCAGGAACCTTGGTCAAGGAACAGCGTGTACCAAGGAAGCTACCAAGGA	404					
Qy	361	ACGGATATTGACTTCTTCTGCGAG	384					
Db	405	ACGGATATTGACTTCTTCTGCGAG	428					
RESULT 8	AF243505	865 bp	mRNA	linear	PRI 26-DEC-2000			
LOCUS	AF243505	865 bp	mRNA	linear	PRI 26-DEC-2000			
DEFINITION	Homo sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.							
ACCESSION	AF243505							
VERSION	AF243505.1	GI:11991843						
KEYWORDS								
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 865) Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and Petit,C.							
AUTHORS	Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme J. Biol. Chem. 275 (51), 40036-40041 (2000)							
TITLE	20568254							
JOURNAL	10998416							
MEDLINE	2 (bases 1 to 865)							
PUBMED	Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.							
REFERENCE	Direct Submission							
AUTHORS	Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France							
TITLE	Location/Qualifiers							
JOURNAL	1. .865							
FEATURES	/organism="Homo sapiens"							
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	/map="20p11"							
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	NLVKEQVVQEAETKEVPTTDDIFPCE"							
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ORIGIN								

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Query Match	100.0%;	Score 384;	DB 6;	Length 923;		
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Matches 384;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	ATGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGCTGTGCATGGA	60			
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QY	121	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAATTAACGTT	180			
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QY	181	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	240			
Db	214	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	273			
QY	241	TTTTGGCTGGCAGTGTTTATGGTGTATGCCAGGACGAGATGGAGTCGTGGTTATTTC	300			
Db	274	TTTTGGCTGGCAGTGTTTATGGTGTATGCCAGGACGAGATGGAGTCGTGGTTATTTC	333			
QY	301	CCAGGAACCTTGGTCAAGGAAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTCCCACC	360			
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QY	361	ACGGATATTGACTTCTTCTGCGAG	384			
Db	394	ACGGATATTGACTTCTTCTGCGAG	417			
RESULT 10	BD093121	Novel polypeptide and its DNA.	923 bp	DNA	linear	PAT 27-AUG-2002
LOCUS	BD093121	Novel polypeptide and its DNA.				
ACCESSION	BD093121	Novel polypeptide and its DNA.				
VERSION	BD093121.1	GI:22638709				
KEYWORDS	WO 0102564-A/21.					
SOURCE	WO 0102564-A/21.					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 923)				
AUTHORS	Yoshimura, K. and Tanaka, H.					
TITLE	Novel polypeptide and its DNA					
JOURNAL	Patent: WO 0102564-A 21 11-JAN-2001;					
COMMENT	TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA					
OS	Homo sapiens (human)					
PN	WO 0102564-A/21					
PD	11-JAN-2001					
PF	29-JUN-2000	WO 2000JP004278				
PR	30-JUN-1999	JP 99P 186718				
PI	YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,					
PI	YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA					
PC	C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/19, A61K45/00, PC A61K38/17,					
PC	A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/02, C12R1:19)					
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QY	181	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	240			
Db	214	AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA	273			
QY	241	TTTTGGCTGGCAGTGTTTATGGTGTATGCCAGGACGAGATGGAGTCGTGGTTATTTC	300			
Db	274	TTTTGGCTGGCAGTGTTTATGGTGTATGCCAGGACGAGATGGAGTCGTGGTTATTTC	333			
QY	301	CCAGGAACCTTGGTCAAGGAAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTCCCACC	360			
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QY	361	ACGGATATTGACTTCTTCTGCGAG	384			
Db	394	ACGGATATTGACTTCTTCTGCGAG	417			
RESULT 11	HSA242552	Homo sapiens mRNA for melanoma inhibitory activity like protein (MIAL gene).	1422 bp	mRNA	linear	PRI 29-JAN-2001
LOCUS	HSA242552	Homo sapiens mRNA for melanoma inhibitory activity like protein (MIAL gene).				
DE'NITION	DE'NITION					
ACCESSION	AJ242552					
VERSION	AJ242552.1	GI:12619172				
KEYWORDS	melanoma inhibitory activity like protein; Mial gene.					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 1422)				
AUTHORS	Rendtorff, N.D., Prodin, M., Attie-Bitach, T., Vekemans, M. and Tommerup, N.					
TITLE	Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation					
JOURNAL	Genomics 71 (1), 40-52 (2001)					
MEDLINE	21100875					
PUBMED	11161796					
REFERENCE	2	(bases 1 to 1422)				
AUTHORS	Rendtorff, N.D.					
TITLE	Direct Submission					
JOURNAL	Submitted (21-MAY-1999)					
REMARK	Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK					
COMMENT	Revised by author 03-AUG-1999					
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BASE COUNT  
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Query Match 100.0%; Score 384; DB 9; Length 1422;  
Best Local Similarity 100.0%; Pred. No. 3.9e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAAATATTGTTACTTTTCTCCCGGCTGTGGCTGTATGCTGTGATGGA 60  
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QY 181 AAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGAGAA 240  
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QY 241 TTTTGGGCTGGAGCTGTTTATGTGTATGGCAGGACGAGATGGAGTGGTATTTC 300  
DB 241 TTTTGGGCTGGAGCTGTTTATGTGTATGGCAGGACGAGATGGAGTGGTATTTC 300  
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DB 301 CCAGGAACCTTGTGTCAAGGAAACAGCGTGTGTACCAAGGAAGTTCCACC 360  
QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
DB 361 ACGGATATTGACTTCTTCTCGGAG 384  
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LOCUS Novel polypeptide and DNA thereof.  
DEFINITION BD010816  
ACCESSION BD010816.1 GI:18639189  
VERSION JP 2001069994-A/17.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (Bases 1 to 330)  
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
Yoshimura, K. and Tanaka, H.  
TITLE Novel polypeptide and DNA thereof  
JOURNAL Patent: JP 2001069994-A 17 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/17  
PD 21-MAR-2001  
PF 29-JUN-2000 JP 2000195911  
PR PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI  
SHINICHI MOGI,  
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC  
A61P19/08,  
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC  
G01N33/53//  
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00  
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FH Key Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1.5e-90;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 61 TATATCTTCTCGCTAGTCTCAAGAGATTATATGCCCCCGAGCTAGATTCAATT 120  
QY 175 AACGTTAAAGGCGACGAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 234  
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QY 295 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCAAGAACTACCAAGGAAGTT 354  
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|||||

RESULT 14

BD010805

LOCUS

DEFINITION

Novel polypeptide and DNA thereof.

ACCESSION

BD010805

VERSION

BD010805.1 GI:18639178

KEYWORDS

JP 2001069994-A/6.

SOURCE

Mus sp.

ORGANISM

Mus sp.

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Ito Y., Nishi K., Ogi K., Okubo S., Mogi S., Noguchi Y.,

1 (bases 1 to 384)

Yoshimura K. and Tanaka H.

TITLE

Novel polypeptide and DNA thereof

JOURNAL

Patent: JP 2001069994-A 6 21-MAR-2001;

TAKEEDA CHEMICAL INDUSTRIES LTD

COMMENT

OS Mus sp. (mouse)

PN JP 2001069994-A/6

PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911

PR

PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI

SHINICHI MOGI,

PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC

A61P19/08, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC

G01N33/53//

PC C12P21/08, C12N15/00, A61K37/02, C12N5/00

CC

Key Location/Qualifiers

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FT /organism='Mus sp. (mouse)'

FT Location/Qualifiers

1..384

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BASE COUNT 98 a 68 c 111 g 107 t

ORIGIN

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Best Local Similarity 84.3%; Pred. No. 2.8e-77;

Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGAAATTGTTACTTTTCCTCCGGGCTTGTGGCTGTATGCTGTGTCATGGA 60

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QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCTATTAACGTT 180

Db 121 ATTTCTCTGGCAAGAGCAGCAGAGATTACAATGCCCGGACTGTAGGTTTCATCGATGTC 180

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QY 241 TTTTGGGCTGGCAGTGTTTATGTGTCATGCCAGGACGAGATGGGAGTCTGGGTTTATTC 300

Db 241 TTTTGGGCTGGCAGTGTTTATGTGTCATGCCAGGACGAGATGGGAGTCTGGGTTTATTC 300

QY 301 CCCAGGAACTTGGTCAAGGAAACAGCGTGTGTATCCAGGAAGTATCAAGGAAGTCCCACC 360

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[illegible]



GenCore version 5.1.6  
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Run on: December 30, 2003, 01:02:37 ; Search time 1278.03 Seconds  
(without alignments)  
7302.593 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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9: gb\_est1:\*  
10: gb\_est2:\*  
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16: em\_estom:\*  
17: em\_gss\_hum:\*  
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29: gb\_gss2:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES				
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3	287	74.7	514 13	BQ568498
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5	287	74.7	560	13	BQ569741
6	287	74.7	608	13	BQ564944
7	287	74.7	630	13	BQ568471
8	287	74.7	696	10	BB611549
9	285.4	74.3	474	13	BQ565637
10	285.4	74.3	684	13	BQ563768
11	271.8	70.8	409	13	BQ566932
12	260.4	67.8	490	13	BQ565411
13	253	65.9	365	13	BY232622
14	236.6	61.6	604	13	BQ567343
15	234.8	61.1	527	10	BE236443
16	198.6	51.7	795	13	BU748241
17	192.8	50.2	280	13	BQ568785
18	192.4	50.1	485	13	BQ565179
19	164.6	42.9	588	13	BQ566776
20	157.4	41.0	349	9	AW023324
21	131.6	34.3	338	9	AW021345
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26	114.8	29.9	677	13	BQ563227
27	114.8	29.9	3240	11	AK047965
28	110	28.6	678	10	BB647928
29	109	28.4	593	9	AL717905
30	109	28.4	615	9	AL717964
31	108.4	28.2	170	13	BQ563268
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33	101.4	26.4	633	14	CD360404
34	99	25.8	178	13	BQ567219
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36	83.6	21.8	646	13	BQ563767
37	82	21.4	576	12	BI492218
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ALIGNMENTS

RESULT 1  
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LOCUS gi143b10.yl Mouse Organ of Corti cdna pBluescript Mus musculus cdna  
DEFINITION clone gi143b10 5', mRNA sequence.  
ACCESSION BQ570035  
VERSION BQ570035.1 GI:21473352  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 398)  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 143 row: b column: 10  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers

source

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 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the Micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTGAACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t  
 ORIGIN

Query Match  
 Best Local Similarity 74.7%; Score 287; DB 13; Length 398;  
 Matches 323; Conservative 84.3%; Pred. No. 1.6e-75;  
 Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCATGGA 60

Db 13 ATGGCAAGATATTGTTACTTTTCTGGGGCCCTTGTGGTTCTATGTGCCGGCATGGT 72  
 QY 61 ATATTTATGGACCGCTCTAGCTTCAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
 Db 73 GTATTTATGGATAAACTTTCTTCTTAAGAAAGTTGTGTGGGATGAGGAGTGTCTTACT 132  
 QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAAGATTATTAATGCTCCCGGACTGTAGATTCAATTAAGCTT 180  
 Db 133 ATTTCTCTGGCAAGACACACAGAAATTACAATGCCACAGACTGTAGTTTCATCGATGTC 192  
 QY 181 AAAAAAGGCGACGACATCTATGTGTACTCAAGCTGTGTAAAGAAAATCGAGCTGGAGAA 240  
 Db 193 AAAAAAGGCGACGACATCTATGTGTACTCAAGCTGTGTAAAGAAAATCGAGCTGGAGAG 252  
 QY 241 TTTTGGGCTGGCAGTGTTTATGTGTATGGCCAGACGAGATGGGAGTCTGTCGGTTATTTC 300  
 Db 253 TTTTGGGCTGGCAGTGTTTATGTGTATGGCCAGACGAGATGGGAGTCTGTCGGTTATTTC 312  
 QY 301 CCCAGAACTTGGTCAAGAAACAGCGTGTGTACCAAGGAGTACCAAGAAAGTCCCAACC 360  
 Db 313 CCCAGAACTTGGTCAAGGAGCAGCGTGTATACCAAGGAGGCCCAAGAGATCCCAACC 372  
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 Db 373 ACGGATATTGACTTCTCTCTGGA 395

# RESULT 2 BQ564607 LOCUS

DEFINITION  
 clone g119h02.5', mRNA sequence.

ACCESSION  
 BQ564607

VERSION  
 BQ564607.1 GI:21467924

KEYWORDS  
 EST.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus

REFERENCE  
 1 (bases 1 to 488)

AUTHORS  
 Kachar,B.

TITLE  
 EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL  
 Unpublished

COMMENT  
 Contact: Kachar,B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kacharb@nidcd.nih.gov

Seq primer: M13RPI reverse primer (ABI).  
 Location/Qualifiers

1. 488

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="g119h02"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory

BQ564607 488 bp mRNA linear EST 19-JUN-2002  
 g119h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus CDNA  
 clone g119h02.5', mRNA sequence.

ACCESSION  
 BQ564607

VERSION  
 BQ564607.1 GI:21467924

KEYWORDS  
 EST.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus

REFERENCE  
 1 (bases 1 to 488)

AUTHORS  
 Kachar,B.

TITLE  
 EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL  
 Unpublished

COMMENT  
 Contact: Kachar,B.  
 Structural Cell Biology  
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 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
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 Email: kacharb@nidcd.nih.gov

Seq primer: M13RPI reverse primer (ABI).  
 Location/Qualifiers

1. 488

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="g119h02"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory

Tue Dec 30 10:20:46 2003

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BASE COUNT 143 a 83 c 135 g 127 t

ORIGIN

Query Match 74.7%; Score 287; DB 13; Length 488;  
Best Local Similarity 84.3%; Pred. No. 1.7e-75;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATGTTACTTTTCTCCCGGGCTTTGTGGCTGTATGCTGTGCATGGA 60  
DB |||||||  
QY 7 ATGGCAAGATATGTTACTTTTGTGGGGCTTTGTGGTCTATGTTGCGCGGCAATG 66  
DB |||||||

QY 61 ATATTCTGGACCGTCTAGCTTCCCAAGAGCTCTGTGCGAGATGATGAGTGTGCTACT 120  
DB |||||||

QY 67 GTATTATGATATAAATCTTCTCTAAGAGTGTGTGCGGATGAGAGTGTGCTACT 126  
DB |||||||

QY 121 ATTTCTTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTGATTCATTAACGTT 180  
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QY 127 ATTTCTTGGCAAGACACAGGAAGATTACAATGCCCGGACTGTAGTTTCATCGATGC 186  
DB |||||||

QY 181 AAAAAAGGCGAGAGCTATGTGTACTTAAAGCTGTTAAAGAAATGGAGCTGAGAA 240  
DB |||||||

QY 187 AAGAAAGGCGAGAGCTATGTATTACTTCAAGCTGTGTAAACAGAAACGAGCTGAGAG 246  
DB |||||||

QY 241 TTTTGGCTGGCAGTGTATTATGTTGATGGCCAGACGAGATGGAGTGTGGGTATTTC 300  
DB |||||||

QY 247 TTTTGGCTGGCAGTGTATTATGTTGATGACCACAGATGAGATGGGAATTGTAGTTATTTC 306  
DB |||||||

QY 301 CCAGGACTTGGTCAAGGACAGCGTGTACCAGGAAGCTACCAAGGAAGTTCCCAACC 360  
DB |||||||

QY 307 CCAGCAACTTGGTGAAGGAGCGGTGTATACGAGGCGCCCAAGGAGATCCCAACC 366  
DB |||||||

QY 361 ACGGATATTGACTTCTTCTCGGA 383  
DB |||||||

QY 367 ACGGATATTGACTTCTTCTCGGA 389  
DB |||||||

RESULT 3  
B0568498 514 bp mRNA linear EST 19-JUN-2002  
LOCUS g1109c02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
DEFINITION clone g1109c02 5', mRNA sequence.  
ACCESSION B0568498  
VERSION B0568498.1 GI:21471815  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 514)  
AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 109 Row: C Column: 02  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1..514  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="BALB/c"  
/db\_xref="taxon:10090"  
/clone="g1109c02"  
/sex="male and female"  
/dev\_stage="post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated

over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with GigaPak EcoR I and Xho I. The phagemid was packaged with GigaPak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT	147 a	85 c	143 g	139 t
ORIGIN	Query Match 74.7%; Score 287; DB 13; Length 514; Best Local Similarity 84.3%; Pred. No. 1.8e-75; Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;			
QY	1	ATGCCAAGATATGTTACTTTTCTCCCGGCTCTGCTGCTATGCTGTGCTATGGA	60	
Db	5	ATGCCAAGGATATGTTACTTTTCTGTTGGGGCTCTGCTGCTATGCTGTGCTATG	64	
QY	61	ATATTATGACCGCTAGCTTCCAGAGCTCTGTCAGATGATGATGCTGTCTATACT	120	
Db	65	GTATTATGATGAACCTTTCTTAAAGAGTTGTTGCGGATGAGGAGTGTCTATACT	124	
QY	121	ATTCTCTGCTAGTGTCTCAAGAGATTATATGCCCCCGGACTGTAGATTCATTAACT	180	
Db	125	ATTCTCTGCGAAGACACAGGAAGATTACAATGCCCGGACTGTAGTTTCATCGATGC	184	
QY	181	AAAAAGGCGACAGATCTATGTTACTCAAGCTGCTTAAAGAAATGAGCTGGAGAA	240	
Db	185	AAGAAGGCGACAGATCTATGTTTATCTCAAGCTGTTACAGAAAACGAGCTGGAG	244	
QY	241	TTTGGGCTGCGAGTGTATGTTGATGGCGCAGACGAGATGGGAGTCGTGGGTATTTC	300	
Db	245	TTTGGGCTGCGAGTGTATGTTGATGGCGCAGACGAGATGGGAGTGTAGTTATTTC	304	
QY	301	CCGAGCAACTTGTCAAGGAACACGGTGTACAGAGAGCTACAGAGAGTTCACCACC	360	
Db	305	CCGAGCAACTTGTGTGAAGGACGAGTGTATACAGGAGGCCCAAGGAGATCCCAACC	364	
QY	361	ACGATATTGACTTCTTCTGGA 383		
Db	365	ACGATATTGACTTCTTCTGTGA 387		

RESULT 4  
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LOCUS  
DEFINITION  
clone gillid01 y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gillid01 5', mRNA sequence.  
ACCESSION  
BQ564134.1  
VERSION  
BQ564134.1  
KEYWORDS  
EST.

SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 534)  
Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 11 row: d column: 01  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1..534  
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/mol\_type="mRNA"  
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/db\_xref="taxon:10090"  
/clone="gillid01"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the micro Fasttrack kit  
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library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
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from Stratagene (La Jolla, CA), according to  
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reverse transcribed using a hybrid oligo(dT) linker-primer  
that contains an Xho I site. First strand synthesis was  
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Moloney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was  
synthesized with DNA polymerase and RNase H. Complementary  
DNA was blunt ended with pfu DNA polymerase, ligated with  
EcoR I adapters in the presence of ligase and digested  
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Query Match 74.7%; Score 287; DB 13; Length 534;		Best Local Similarity 84.3%; Pred. No. 1.8e-75;	
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;			
QY 1	ATGCAAGAATATTGTTACTTTCTCCCGGCTTGTGGCTGATGTGCTGATGGA 60		
DB 3	ATGCAAGGATATTGATCTTTTCTGGGGGCTTGTGGTTCTATGTGCGGGCATGGT 62		
QY 61	ATATTATGGACGCTAGCTCCCAAGAGCTCTGCGAGATGAGTGTCTATACT 120		
DB 63	GTAATTATGGATAAATCTTCTTAAGAAGTTGTGTGCGATGAGAGTGTCTATACT 122		
QY 121	ATTTCTCTGGCTAGTGTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 180		
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QY 241	TTTTGGCTGGCAGGTTTATGCTGATGCCAGGACGAGTGGAGTCTGGGTTATTTC 300		
DB 243	TTTTGGCTGGCAGGTTTATGCTGATGCCAGGACGAGTGGAGTCTGGGTTATTTC 302		
QY 301	CCCAGGAATCTGGTCAAGGAAACAGCGTGTGTACCGAAGCTACCAAGAAATCCACCC 360		
DB 303	CCCAGCAATCTGGTGAAGGACGAGCGTGTATACCGAGGAGCCACCAAGAGATCCCAACC 362		
QY 361	ACGGATATTGACTTCTCTGTGCA 383		
DB 363	ACGGATATTGACTTCTCTGTGCA 385		
RESULT 5		BQ569741 560 bp mRNA linear EST 19-JUN-2002	
LOCUS		g1135f01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA	
DEFINITION		clone g1135f01 5', mRNA sequence.	
ACCESSION		BQ569741	
VERSION		BQ569741.1 GI:21473058	
KEYWORDS		EST.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 560)	
REFERENCE		Kachar, B.	
AUTHORS		EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing	
TITLE		Unpublished	
JOURNAL		Contact: Kachar, B.	
COMMENT		Structural Cell Biology	
		National Institute of Deafness and other Communication Disorders	
		50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA	
		Tel: 301-402-1599	
		Fax: 301-402-1765	
		Email: kachar@nidcd.nih.gov	
		Plate: 135 row: f column: 01	
		Seq primer: M13RPL reverse primer (ABI).	
FEATURES	source	Location/Qualifiers	
1..560		/organism="Mus musculus"	
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		/clone="g1135f01"	
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		/dev_stage="Post natal day 5 to 13"	
		/clone_lib="Mouse Organ of Corti cDNA pBluescript"	
		/notes="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA) according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-LV) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been preligated with the III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."	
BASE COUNT 160 a 92 c 154 g 153 t		Query Match 74.7%; Score 287; DB 13; Length 560;	
ORIGIN		Best Local Similarity 84.3%; Pred. No. 1.8e-75;	
		Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;	

QY 1 ATGCAAGAAATATTGTTACTTTTCTCCCGGCTCTGTGCTGTATGCTGTGTCATGGA 60  
 |||||  
 Db 6 ATGCAAGAAATATTGTTACTTTTCTCCCGGCTCTGTGCTGTATGCTGTGTCATGTT 65  
 |||||  
 QY 61 ATATTATGGACCGCTCTAGCTTCCAAAGCTCTGTGCAGATGATGATGCTGTCTACT 120  
 |||||  
 Db 66 GTATTATGGATAAATCTTCTCTAAGAGTTGTGTGCGATGAGGAGTGTGTCTACT 125  
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 QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTAATAATGCCCGGCTGTAGATTCATTACGTT 180  
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 QY 241 TTTTGGCTGCAGCTTATGTTGATGGCCAGACGAGATGGAGTCTGGGTATTTTC 300  
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 Db 246 TTTTGGCTGCAGCTTATGTTGATGGCCAGACGAGATGGAGTCTGGGTATTTTC 305  
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 QY 301 CCCAGGAATTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 360  
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 Db 306 CCCAGCACTTGTGTGAAGGACAGCGTGTATACCAAGGCGCCACCAAGGAGATCCCAACC 365  
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 QY 361 ACGGATATTGACTTCTTCTGGA 383  
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 Db 366 ACGGATATTGACTTCTTCTGGA 388  
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RESULT 6  
 LOCUS BQ564944  
 DEFINITION g127909.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 clone g127909 5', mRNA sequence.  
 ACCESSION BQ564944  
 VERSION BQ564944.1 GI:21468261  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Soricidae; Murinae; Mus.  
 1 (bases 1 to 608)  
 Kachar,B.  
 EST analysis of gene expression in the mouse Organ of Corti at the  
 onset of hearing  
 Unpublished  
 Contact: Kachar,B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kacharb@nidcd.nih.gov  
 Plate: 27 row: g column: 09  
 Seq primer: M13RF1 reverse primer (ABI).  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
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 /sex="male and female"  
 /dev\_stage="Post natal day 5 to 13"  
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 /note="Organ: Organ of Corti; Vector: pBluescript; The  
 organ of Corti (OC) was fine dissected from a total of 386  
 OC as follows: 102 samples from post-natal (P) day 5; 72  
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
 14 from P12 and 24 from P13. After killing animals by  
 cervical dislocation followed by decapitation, the bulla  
 was removed and opened in Leibowitz medium. The bony  
 capsule of the cochlea was chipped away, stria vascularis

## FEATURES

source  
 Query Match 74.7%; Score 287; DB 13; Length 608;  
 Best Local Similarity 84.3%; Pred. No. 1.9e-75;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
 QY 1 ATGCAAGAAATATTGTTACTTTTCTCCCGGCTCTGTGCTGTATGCTGTGTCATGGA 60  
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 Db 13 ATGCAAGGATATTGATTTCTTTCCTCGGCTGTGCTGTATGCTGTGTCATGCT 72  
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 |||||  
 Db 73 GTATTATGGATAAATCTTCTCTAAGAGTTGTGTGCGGATGAGGAGTGTGTCTACT 132  
 |||||  
 QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTAATAATGCCCGGCTGTAGATTCATTACGTT 180  
 |||||  
 Db 133 ATTTCTCTGGCAAGACAGACAGAGATTAATATGCCCGGCTGTAGTTCATCATGTC 192  
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 QY 181 AAAAAGGGCAGCAGATCTATGTCTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 240  
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 Db 193 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGTAAACAGAAACGAGCTGGAG 252  
 |||||  
 QY 241 TTTTGGCTGCAGCTTATGTTGATGGCCAGACGAGATGGAGTCTGGGTATTTTC 300  
 |||||

and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert36(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t  
 ORIGIN  
 Query Match 74.7%; Score 287; DB 13; Length 608;  
 Best Local Similarity 84.3%; Pred. No. 1.9e-75;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
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 QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTAATAATGCCCGGCTGTAGATTCATTACGTT 180  
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 QY 241 TTTTGGCTGCAGCTTATGTTGATGGCCAGACGAGATGGAGTCTGGGTATTTTC 300  
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253 TTTTGGGCTGGCAGTGTATTGTTGACCAACAGGATGAGATGGGAATTGTAGGTATTTC 312

301 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACCAAGAGTACCAAGGAAGTTCACAC 360

313 CCCAGCAACTTGGTGAAGGACAGCGTGTATACCAAGGAGGCCACCAAGGATCCCAACC 372

361 ACGGATATTGACTTCTTCTGCGA 383

373 ACGGATATTGACTTCTTCTGTGA 395

RESULT 7

BQ568471 630 bp mRNA linear EST 19-JUN-2002

LOCUS gi108g04.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

DEFINITION clone gi108g04 5', mRNA sequence.

ACCESSION BQ568471

VERSION BQ568471.1 GI:21471788

KEYWORDS Mus musculus (house mouse)

SOURCE Mus musculus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 630)

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 108 row: g column: 04

Seq primer: M3RPI reverse primer (ABI).

Location/Qualifiers

1..630

/organism="Mus musculus"

/mol\_type="mRNA"

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/db\_xref="taxon:10090"

/clone="g108g04"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the Micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested

with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 178 a 111 c 167 g 174 t

ORIGIN

Query Match 74.7%; Score 287; DB 13; Length 630;

Best Local Similarity 84.3%; Pred. No. 1.9e-75;

Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGAAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGTGTGTCATGGA 60

DB 13 ATGGCAAGAAATATTGTTACTTTTGTGGGCTTGTGTTCTATGTGCGGGCATGGT 72

QY 61 ATATTATGACCGTCTAGCTTCCAAAGAGTCTGTGCGAGATGATGAGTGTGTTACT 120

DB 73 GTATTATGATAAATCTTCTTCTAAGAGTGTGTGCGGATGAGGAGTGTGTTACT 132

QY 121 ATTCTCTGGCTAGTCTCAAGAGATTTATATCCCGGACGTAGATTCTATTACGTT 180

DB 133 ATTCTCTGGCAGAGCACAGGAAGATTACAATGCCAGACTGTAGTTTCATCGATGC 192

QY 181 AAAAAAGGCGCAGCAGATCTATGTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA 240

DB 193 AAGAAAGGCGCAGCAGATCTATGTTTACTCAAGCTGTTAAACAGAAACGAGCTGGAGAG 252

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DB 253 TTTTGGGCTGGCAGTGTATTATGTTATGTCGACGAGATGGAGTGTGTTTTC 312

QY 301 CCAGCAACTTGTGTCAGGACAGCGTGTACCAAGAGTCTACCAAGGAAGTTCACAC 360

DB 313 CCAGCAACTTGTGTCAGGAGCAGCGTGTATACCAAGGAGCCACCAAGGAGATCCCAACC 372

QY 361 ACGGATATTGACTTCTTCTGCGA 383

DB 373 ACGGATATTGACTTCTTCTGTGA 395

RESULT 8

LOCUS BB611549

DEFINITION BB611549 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110083012 5', mRNA sequence.

ACCESSION BB611549

VERSION BB611549.1 GI:15393547

BB611549 696 bp mRNA linear EST 31-AUG-2001







/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMuLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and Knaase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert-96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGTAAGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 145 a 78 c 131 g 120 t  
ORIGIN  
Query Match 74.3%; Score 285.4; DB 13; Length 474;  
Best Local Similarity 84.1%; Pred. No. 5.1e-75;  
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAAATGTTACTTCTCCCGGGCTTGTGGCTGTATGCTGTGTCAGGA 60  
DB 14 ATGGCAAGAAATGTTACTTCTTCTTCTTAATTAAGTGTGGGATGAGAGTGTCTACT 73  
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Db 194 AAGAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAG 253  
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Db 254 TTTTGGGCTGGCAGTGTATGTGTGATGCCAGGACGAGATGGGAGTTCGTGGTTATTTC 313  
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Db 314 CCCAGCACTTGGTGAAGGAGCAGCGTGTATACCAAGGAGGCGCCACCAAGGAGATCCCAACC 373  
QY 361 ACGGATATTGACTTCTTCTGCGA 383  
Db 374 ACGGATATTGACTTCTTCTGCGA 396

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VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
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JOURNAL  
COMMENT  
BQ563768 684 bp mRNA linear EST 19-JUN-2002  
gi06c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gi06c09 5', mRNA sequence.  
BQ563768  
BQ563768.1 GI:21466749  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 06 row: c column: 09  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
1. .684  
/organism="Mus musculus"  
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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to

manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-Rn) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. StrataGene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTGATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 194 a 120 c 178 g 192 t  
ORIGIN  
Query Match 74.3%; Score 285.4; DB 13; Length 684;  
Best Local Similarity 84.1%; Pred. No. 6.1e-75;  
Matches 322; Conservative 0; Mismatches 61; Indels 0; Gaps 0;  
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13 ATGGCAGGATATTGATTCTTTTGTCTTGGGGGCGCTTGTGTTCTATGTCCGGCATGGT 72  
QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTCTACT 120  
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133 ATTTCTGTGGCAGACAGAGAAATTACAATGCCCCAGACTGTAGTTTCATCATGTC 192  
QY 181 ARAAAGGCGCAGATCTATGTACTCAAGCTGTATAAAGAAATGAGCTGAGGA 240  
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193 AAGAAAGGCGCAGATCTATGTACTCAAGCTGTATAAAGAAATGAGCTGAGGA 252  
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313 CCAGAGAACTGTGTAGAGACAGCGTGTATACCGAGAGCTACCAAGAGTTCACACC 372  
QY 361 ACGGATATTGACTTCTTCTGCGA 383  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

BQ566932 409 bp mRNA linear EST 19-JUN-2002  
gi73909.v1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
Clone gi73909 5', mRNA sequence.  
BQ566932.1 GI:21470249  
BQ566932  
ESL  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar, B.  
1 (bases 1 to 409)  
ESL analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: Kachar@nidcd.nih.gov  
Plate: 73 row: g column: 09  
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Location/Qualifiers  
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/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/notes="Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RN) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000



genes are present in GenBank and have know function: 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT	191 a	77 c	109 g	112 t	1 others
ORIGIN					
Query Match	67.8%	Score	260.4	DB 13	Length 490
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Matches	306	Conservative	0	Mismatches	76; Indels 0; Gaps 0
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QY	62 TATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACTA 121				
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QY	362 CGGATATTGACTTCTCTGCGA 383				
Db	448 CGGATATTGACTTCTCTGCGA 469				

RESULT 13  
LOCUS BY232622  
DEFINITION BY232622 RIKEN full-length enriched, adult inner ear Mus musculus  
ACCESSION BY232622  
VERSION BY232622.1 GI:26413732  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Niraide, I., Osato, N., Saito, R., Suzuki, H., Yananaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzle, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pette, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempke, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wyntshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura

M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, M., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354583  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp/  
URL: http://genome.gsc.riken.go.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

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Job time : 1283.36 secs

REFERENCE 1 (bases 1 to 527)  
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.I., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G., Perlea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keale,J.W.  
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
MEDLINE 21180013  
PUBMED 11282978  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@email.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options.  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 127.462 Seconds  
(without alignments)  
8132.484 Million cell updates/sec

Title: US-10-019-455A-4

Perfect score: 384

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	384	22	AAF59065
2	384	100.0	387	24	AAH17583
3	384	100.0	426	22	AAH26341
4	384	100.0	521	24	ABL95740
5	384	100.0	521	24	ABL88251
6	384	100.0	521	24	ABK33571
7	384	100.0	891	22	AAH98228
8	384	100.0	891	22	AAH26342

9	384	100.0	923	22	AAF59083	Human MLP nucleoti
10	384	100.0	1201	22	AAH26343	Human growth regul
11	330	85.9	330	22	AAF59079	Human MLP nucleoti
12	287	74.7	384	22	AAF59068	Mouse MLP nucleoti
13	287	74.7	947	22	AAF59084	Mouse MLP nucleoti
14	285.4	74.3	384	22	AAF59098	Rat MLP nucleotide
15	252.2	65.7	330	22	AAF59080	Mouse MLP nucleoti
16	249	64.8	330	22	AAF59099	Rat MLP nucleotide
17	217.4	56.6	307	22	AAF59093	Rat MLP nucleotide
18	193.8	50.5	261	22	AAF59092	Rat MLP nucleotide
19	64.8	16.9	433	22	AAH47783	Recombinant human
20	64.8	16.9	459	16	AAQ84050	Sequence encoding
c 21	64.8	16.9	459	22	AAI70083	Melanoma inhibitor
c 22	64.8	16.9	459	22	ABD18732	Human antisense ol
c 23	63.8	16.6	555	23	ABV59229	Human prostate exp
c 24	63.2	16.5	581	16	AAQ84052	Sequence encoding
c 25	62.8	16.4	442	24	ABL63602	Breast cancer rela
c 26	62.8	16.4	442	24	ABL64012	Breast cancer rela
27	57.4	14.9	330	16	AAQ84061	Sequence encoding
28	54.2	14.1	305	16	AAQ84055	Amplified fragment
29	53.6	14.0	300	20	AAZ14828	Human cDNA encodin
30	53.6	14.0	429	22	AAZ22695	Human cDNA encodin
31	53.6	14.0	884	22	AAZ22459	Human TANGO 130 pa
32	53.6	14.0	1230	24	ABO79850	Human TANGO 130 CD
33	53.6	14.0	1263	21	AAZ51245	Human TANGO 130 po
34	53.6	14.0	1263	24	ABQ79849	Human prostate exp
35	53.6	14.0	4409	23	ABV21035	Human prostate exp
36	53.6	14.0	4409	23	ABV23751	Human prostate exp
37	53.6	14.0	4409	23	ABV26878	Human prostate exp
38	53.6	14.0	4409	23	ABV29625	Human prostate exp
39	53.6	14.0	5724	24	ABO79852	Human TANGO 130 po
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41	52	13.5	417	22	AAH99775	Human protein enco
42	46	12.0	1060	22	AAF92140	Human PRO19670 cDN
43	46	12.0	1060	24	ABZ74460	Human cDNA encodin
44	46	12.0	1060	24	ABL95738	Human angiogenesis
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#### ALIGNMENTS

#### RESULT 1

AAF59065  
ID AAF59065 standard; DNA; 384 BP.

XX AAF59065;

AC AAF59065;

DT 23-APR-2001 (first entry)

XX Human MLP nucleotide sequence SEQ ID NO:4.

DE MLP; MTA; melanoma inhibitory activity; cancer; bone disease;

KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KW cardiant; gene therapy; secretory cell function regulator; promoter;

XX inhibitor; ds.

XX Homo sapiens.

OS WO200102564-A1.

XX 11-JAN-2001.

PD 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

PI Tanaka H;

XX WPI; 2001-159271/16.

DR P-PSDB; AAB69123.  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 PS Example 1; Page 91; 111pp; Japanese.  
 XX  
 CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;  
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 Best Local Similarity 100.0%; Pred. No. 9.7e-114; Indels 0; Gaps 0;  
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 QY 361 ACGGATATTGACTTCTCTGCGAG 384  
 Db 361 ACGGATATTGACTTCTCTGCGAG 384  
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 XX  
 AC AAS17583;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE DNA encoding novel secreted protein #12.  
 XX  
 KW Secreted protein; cytostatic; immunosuppressive; vulnerary; vaccine;  
 KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
 KW human; cancer; autoimmune disease; wound healing disorder; infection;  
 KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers

CDS  
 FT 1..387  
 FT /\*tag= a  
 FT /product= "Human secreted protein"  
 XX  
 PN WO200179454-A1.  
 XX  
 PD 25-OCT-2001.  
 XX  
 XX 11-APR-2001; 2001WO-US11797.  
 PF  
 XX 13-APR-2000; 2000US-196603P.  
 PR  
 XX 24-APR-2000; 2000US-199417P.  
 PR  
 XX (SMIX ) SMITHKLINE BEECHAM CORP.  
 PA  
 XX (SMIX ) SMITHKLINE BEECHAM PLC.  
 PA  
 PI Agarwal P, Murdoch PR, Rizvi SK, Smith RP, Xiang Z;  
 XX  
 DR WPI; 2002-061975/08.  
 DR P-PSDB; AAU09871.  
 DR  
 XX New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, cancer -  
 PS Claim 2; Page 44; 92pp; English.  
 XX  
 CC The invention relates to an isolated novel secreted polypeptide (I) and  
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,  
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic  
 CC disorders, inflammatory disorders, infertility, neurological and  
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,  
 CC renal diseases, or gastrointestinal diseases. These may also be used to  
 CC treat diseases, abnormalities and disorders caused by abnormal  
 CC expression, production, function and/or metabolism of the genes, as  
 CC vaccines for inducing immunological response in a mammal, and in  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and polypeptide in cells. The polypeptides can be used  
 CC as immunogens to produce antibodies immunospecific for the polypeptides,  
 CC and to identify membrane-bound or soluble receptors. The polynucleotides  
 CC may be used as diagnostic reagents, in chromosome localisation studies,  
 CC and in tissue expression studies. The present sequence represents the  
 CC coding sequence of novel human secreted protein #12.  
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 Query Match 100.0%; Score 384; DB 24; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-114;  
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 QY 1 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 60  
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 Db 61 ATATTTATGACCGCTACCTTCCCAAGAGCTCTGTGCAGATGATGATGCTGTACT 120  
 QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTTAATATGCCCCGGACTGTAGATTCATTAAAGTT 180  
 Db 121 ATTTCTCTGGCTAGTCTCAAGAGATTTAATATGCCCCGGACTGTAGATTCATTAAAGTT 180  
 QY 181 AAAAAAGGCGCAGATCTATGTTACTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 240  
 Db 181 AAAAAAGGCGCAGATCTATGTTACTTCTCCCGGCTCTGTGGCTGTATGCTGTGCTATGGA 240  
 QY 241 TTTTGGGCTGGCAGTGTATGTTATGTTATGCTGATGCCAGGACGATGGAGTCTGGTATTTC 300  
 Db 241 TTTTGGGCTGGCAGTGTATGTTATGTTATGCTGATGCCAGGACGATGGAGTCTGGTATTTC 300  
 QY 301 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 360  
 Db 301 CCAGGAACCTTGGTCAAGGAACAGCGTGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 360





PR	22-JAN-2001;	2001US-0767609.	158	ATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCCGACTGTAGATTCAATTAACGTT	217
PR	28-FEB-2001;	2001US-0796498.	181	AAAAAGGGCAGCAGATCTATGTCTCAAACTGGTAAAGAAATGAGCTGGAGAA	240
PR	01-MAR-2001;	2001WO-US06520.	218	AAAAAGGGCAGCAGATCTATGTCTCAAACTGGTAAAGAAATGAGCTGGAGAA	277
PR	09-MAR-2001;	2001US-0802706.	241	TTTTGGCTGGCAGTGTATGTCTCAAACTGGTAAAGAAATGAGCTGGAGAA	300
PR	14-MAR-2001;	2001US-0806689.	278	TTTTGGCTGGCAGTGTATGTCTCAAACTGGTAAAGAAATGAGCTGGAGAA	337
PR	22-MAR-2001;	2001US-0816744.	301	CCCAGGAACCTTGGTCAAGGAACACCGTGTGTACCCAGGAAGCTACCAAGGAAGTCCACC	360
PR	05-APR-2001;	2001US-0828366.	338	CCCAGGAACCTTGGTCAAGGAACACCGTGTGTACCCAGGAAGCTACCAAGGAAGTCCACC	397
PR	10-MAY-2001;	2001US-0854208.	361	ACGGATATTGACTTCTTCTCGGAG	384
PR	10-MAY-2001;	2001US-0854280.	398	ACGGATATTGACTTCTTCTCGGAG	421
PR	25-MAY-2001;	2001US-0866028.			
PR	25-MAY-2001;	2001US-0866034.			
PR	25-MAY-2001;	2001WO-US17092.			
PR	30-MAY-2001;	2001US-0870574.			
PR	30-MAY-2001;	2001WO-US17443.			
PR	01-JUN-2001;	2001WO-US17800.			
PR	20-JUN-2001;	2001WO-US19692.			
PR	28-JUN-2001;	2001WO-US00000.			
XX	(GETH ) GENENTECH INC.				
PA	(BAKE)/ BAKER K P.				
PA	(FERR)/ FERRARA N.				
PA	(GERB)/ GERBER H.				
PA	(GERR)/ GERRITSEN M E.				
PA	(GODD)/ GODDARD A.				
PA	(GODO)/ GODOWSKI P J.				
PA	(GURN)/ GURNEY A L.				
PA	(HILL)/ HILLAN K J.				
PA	(MARS)/ MARSTERS S A.				
PA	(PANJ)/ PAN J.				
PA	(PAON)/ PAONI N F.				
PA	(STEP)/ STEPHAN J F.				
PA	(WATA)/ WATANABE C K.				
PA	(WILL)/ WILLIAMS P M.				
PA	(WOOD)/ WOOD W I.				
XX					
PI	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;				
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;				
PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;				
XX					
XX	WPI; 2002-171999/22.				
DR	P-PSDB; ABB95602.				
XX					
PT	One hundred and eighty seven nucleic acids encoding PRO polypeptides,				
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial				
PT	infarction), endothelial or angiogenic disorders in a mammal -				
XX					
PS	Claim 1; Fig 359; 567pp; English.				
XX					
CC	The present invention provides the protein and coding sequences of human				
CC	PRO proteins. These are useful for treating or diagnosing a				
CC	cardiovascular, endothelial or angiogenic disorder, including cardiac				
CC	hypertrophy, trauma, cancer, age-related macular degeneration,				
CC	atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,				
CC	angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour				
CC	angiogenesis (such as breast carcinoma and liver carcinoma) and wound				
CC	healing. The present sequence is a coding sequence of the invention.				
XX					
SQ	Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;				
	Query Match 100.0%; Score 384; DB 24; Length 521;				
	Best Local Similarity 100.0%; Pred. No. 1.1e-113;				
	Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1 ATGCGAAGATATTGTTACTTTCTCCCGGGTCTGTGGCTGTATGCTGTGGCATGGA	60			
DB	38 ATGCGAAGATATTGTTACTTTCTCCCGGGTCTGTGGCTGTATGCTGTGGCATGGA	97			
QY	61 ATATTATGGACCGCTAGCTTCCAGAAGCTCTGTGCAGATGATGATGTGTCTATCT	120			
DB	98 ATATTATGGACCGCTAGCTTCCAGAAGCTCTGTGCAGATGATGATGTGTCTATCT	157			
QY	121 ATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT	180			

PR	05-APR-2001; 2001US-0828366.
PR	10-MAY-2001; 2001US-0854208.
PR	10-MAY-2001; 2001US-0854280.
PR	25-MAY-2001; 2001US-0866028.
PR	25-MAY-2001; 2001US-0866034.
PR	25-MAY-2001; 2001US-0870574.
PR	30-MAY-2001; 2001US-0870574.
PR	30-MAY-2001; 2001WO-US17443.
PR	01-JUN-2001; 2001WO-US17800.
XX	(GETH ) GENENTECH INC.
PA	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
PI	Stephan JP, Watanabe CK, Williams PM, Wood WI, Ye W;
XX	WPI; 2002-090516/12.
DR	P-PSDB; ABB84996.
XX	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT	infarction), endothelial or angiogenic disorders in a mammal -
XX	Claim 2; Fig 359; 565pp; English.
XX	ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC	ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC	antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC	activities, and can be used in gene therapy. The PRO polynucleotides,
CC	proteins, agonists and antagonists are useful for treating or diagnosing
CC	a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC	e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC	deneration, arterosclerosis, hypertension, arterial restenosis,
CC	rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC	lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC	carcinoma) and wound healing. The PRO polynucleotides have applications
CC	in molecular biology, including use as hybridisation probes, and in
CC	chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC	probes used in the exemplification of the present invention.
XX	Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
SQ	
Query Match	100.0%; Score 384; DB 24; Length 521;
Best Local Similarity	100.0%; Pred. No. 1.le-113;
Matches 384; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGCAAGATATTGTACTTTCTCCCGGGTCTTGTCGTGTATGCTGTGCATGA 60
Dz	38 ATGGCAAGATATTGTACTTTCTCCCGGGTCTTGTCGTGTATGCTGTGCATGA 97
QY	61 ATATTATGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGCTGTCTATACT 120
Dz	98 ATAATTATGACCGTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGCTGTCTATACT 157
QY	121 ATTCTCTGGCTAGCTTCCAAGAAGATTAATAATCCCCGGACTGTAGATTCAATTAACGTT 180
Dz	158 ATTCTCTGGCTAGCTTCCAAGAAGATTAATAATCCCCGGACTGTAGATTCAATTAACGTT 217
QY	181 AAAAAAGGCGCAGCATCTATGTGTACTCAAAGCTGTGTAAAGAAATGAGCTGGAGAA 240
Dz	218 AAAAAAGGCGCAGCATCTATGTGTACTCAAAGCTGTGTAAAGAAATGAGCTGGAGAA 277
QY	241 TTTTGGCTGGCAGTGTATTATGTTATGCCAGACGAGATGGAGTCGTGGGTATTTC 300
Dz	278 TTTTGGCTGGCAGTGTATTATGTTATGCCAGACGAGATGGAGTCGTGGGTATTTC 337
QY	301 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTCCCACC 360
Dz	338 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTCCCACC 397
QY	361 ACGGATATTGACTTCTCTGCGAG 384
Dz	398 ACGGATATTGACTTCTCTGCGAG 421

RESULT 6  
ABK33571  
ID ABK33571 standard; cDNA; 521 BP.  
XX ABK33571;  
AC ABK33571;  
XX 08-MAY-2002 (first entry)  
XX cDNA encoding human PRO protein, Seq ID No 71.  
DE Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX Homo sapiens.  
OS WO200208288-A2.  
XX 31-JAN-2002.  
XX 29-JUN-2001; 2001WO-US21066.  
XX 20-JUL-2000; 2000US-219556P.  
PR 25-JUL-2000; 2000US-220585P.  
PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 25-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23322.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 20-FEB-2001; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Smith V, Stephan JP, Watanabe CK, Wood WI;  
XX WPI; 2002-172001/22.  
DR P-PSDB; AAU83627.  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
PT useful for treating a PRO related disorder and for diagnosing tumours  
PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
PT tumour or liver tumour -  
XX Claim 2; Figure 71; 359pp; English.  
XX The invention relates to one hundred and twenty two nucleic acids  
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
CC agonists and antagonists are useful for treating a PRO related disorder.  
CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
CC liver tumour. The PRO polypeptides are useful for stimulating the  
CC proliferation of, or gene expression, in pericyte cells, for stimulating  
CC the proliferation or differentiation of chondrocyte cells, for  
CC stimulating the release of tumour necrosis factor-alpha from human blood,  
CC for stimulating or inhibiting the proliferation of normal human dermal

CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
 CC PRO protein coding sequences of the invention.

XX  
 SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Query Match 100.0%; Score 384; DB 24; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-113;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 60  
 DB 38 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 97  
 QY 61 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 120  
 DB 98 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 157  
 QY 121 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGGAGCTGTAGATTCAATTAACGTT 180  
 DB 158 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGGAGCTGTAGATTCAATTAACGTT 217  
 QY 181 AAAAAAGGGCAGCAGATCTATGTACTCAAAAGCTGTGTAAGAAATATGAGCTGGAGAA 240  
 DB 218 AAAAAAGGGCAGCAGATCTATGTACTCAAAAGCTGTGTAAGAAATATGAGCTGGAGAA 277  
 QY 241 TTTTGGGCTGGCAGTGTATTTATGCTGATGCCAGGACGAGATGGAGTCTGGGTTATTTC 300  
 DB 278 TTTTGGGCTGGCAGTGTATTTATGCTGATGCCAGGACGAGATGGAGTCTGGGTTATTTC 337  
 QY 301 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAAGCTTACCAAGGAAGTTCCACC 360  
 DB 338 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAAGCTTACCAAGGAAGTTCCACC 397  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 DB 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 7  
 AAH98228  
 ID AAH98228 standard; cDNA; 891 BP.  
 AC AAH98228;  
 XX  
 DT 12-OCT-2001 (first entry)  
 XX Human EST-derived coding sequence SEQ ID NO: 85.  
 DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition; ss.  
 XX Homo sapiens.  
 OS  
 XX WO200154477-A2.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-US02687.  
 PF  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werthman T;

XX MPI; 2001-476164/51.  
 DR P-PSDB; AAM23569.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1; Page 236; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.

XX  
 SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Query Match 100.0%; Score 384; DB 22; Length 891;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-113;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 60  
 DB 19 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTTGCGCTGATGCTGTCATGGA 78  
 QY 61 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 120  
 DB 79 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTTACT 138  
 QY 121 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGGAGCTGTAGATTCAATTAACGTT 180  
 DB 139 ATTTCTCTGCTAGTCTCAAGAAGATTATATATGCCCCGGAGCTGTAGATTCAATTAACGTT 198  
 QY 181 AAAAAAGGGCAGCAGATCTATGTACTCAAAAGCTGTGTAAGAAATATGAGCTGGAGAA 240  
 DB 199 AAAAAAGGGCAGCAGATCTATGTACTCAAAAGCTGTGTAAGAAATATGAGCTGGAGAA 258  
 QY 241 TTTTGGGCTGGCAGTGTATTTATGCTGATGCCAGGACGAGATGGAGTCTGGGTTATTTC 300  
 DB 259 TTTTGGGCTGGCAGTGTATTTATGCTGATGCCAGGACGAGATGGAGTCTGGGTTATTTC 318  
 QY 301 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAAGCTTACCAAGGAAGTTCCACC 360  
 DB 319 CCCAGGAATTTGCTCAAGGAACAGCGTGTGTACCAAGGAAGCTTACCAAGGAAGTTCCACC 378  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 DB 379 ACGGATATTGACTTCTTCTGCGAG 402

RESULT 8  
 AAH26342  
 ID AAH26342 standard; cDNA; 891 BP.  
 AC AAH26342;  
 XX  
 DT 02-OCT-2001 (first entry)  
 XX Human growth regulatory-like polypeptide partial cDNA clone.  
 DE Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.  
 XX Homo sapiens.  
 OS  
 XX WO200155332-A2.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX

25-JAN-2001; 2001WO-US02455.  
 25-JAN-2000; 2000US-0491404.  
 02-MAY-2000; 2000US-0563786.  
 (HYSE-) HYSEQ INC.  
 Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 Drmanac RT;  
 WPI; 2001-483233/52.  
 Isolated human growth regulatory-like polypeptide useful for treating  
 e.g. Alzheimer's disease, cancer, autoimmune disorders, and nervous system  
 hyperproliferative disorders, coagulation disorders, and nervous system  
 disorders -  
 Claim 1; Page 115; 119pp; English.  
 The present sequence is that of a novel nucleic acid that was  
 assembled from human thymus cDNA library-derived Hyseq clone  
 identification number 16372272 (see AAH26341). A recursive  
 algorithm was used to extend the clone by pulling additional  
 sequences from different databases. A full-length sequence (see  
 AAH26343) encoding novel human growth regulatory-like polypeptide  
 (GRLP, see AAH2671) was subsequently obtained. Human GRLP  
 belongs to the same protein family as growth regulatory proteins,  
 growth factors, human melanoma derived growth regulatory protein  
 precursor (64% similarity and 45% identity over 111 amino acids)  
 or melanoma inhibitory activity, cattle cartilage-derived  
 retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 similarity over 126 amino acids) and other retinoic acid-sensitive  
 proteins. GRLP polypeptides and polynucleotides of the invention  
 can be used in the prophylaxis, treatment (including gene therapy)  
 and diagnosis of disorders and diseases caused by, or involving,  
 cartilage development and maintenance, inhibition of melanoma cell  
 growth and tumours, including neuroectodermal tumours such as  
 gliomas. The polynucleotides can also be used to design probes  
 and primers, for chromosome and gene mapping, in the recombinant  
 production of protein, in the generation of antisense, ribozyme and  
 peptide-nucleic acid molecules, and to produce transgenic animals.  
 Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;  
 Query Match 100.0%; Score 384; DB 22; Length 891;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-113;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGCGCTGTATGCTGTGCTATGGA 60  
 19 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGCGCTGTATGCTGTGCTATGGA 78  
 61 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTATCT 120  
 79 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTATCT 138  
 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTAATCCCGGCTCTGTATGCTGTGCTATG 180  
 139 ATTTCTCTGGCTAGTGTCTCAAGAGATTAATCCCGGCTCTGTATGCTGTGCTATG 198  
 181 AAAAAAGGGCAGCAGATCTATGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 240  
 199 AAAAAAGGGCAGCAGATCTATGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 258  
 241 TTTTGGGCTGCAGTGTATGTTATGTTGTCAGGACGAGATGGAGTCTGGTATTTC 300  
 259 TTTTGGGCTGCAGTGTATGTTGTCAGGACGAGATGGAGTCTGGTATTTC 318  
 301 CCCAGGAACCTGGTCAAGACACGGTGTGTACAGGAGCTACCAAGGAAGTTCCAC 360  
 319 CCCAGGAACCTGGTCAAGACACGGTGTGTACAGGAGCTACCAAGGAAGTTCCAC 378  
 361 ACGGATATTGACTTCTTCTCTCGGAG 384

379 ACGGATATTGACTTCTTCTCGGAG 402  
 RESULT 9  
 AAF59083  
 ID AAF59083 standard; DNA; 923 BP.  
 AC AAF59083;  
 XX 23-APR-2001 (first entry)  
 DT Human MLP nucleotide sequence SEQ ID NO:29.  
 DE MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
 XX Homo sapiens.  
 OS WO200102564-A1.  
 PN 11-JAN-2001.  
 PD 29-JUN-2000; 2000WO-JP04278.  
 PF 30-JUN-1999; 99JP-0186718.  
 PR (TAKE ) TAKEDA CHEM IND LTD.  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 DR Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX Example 1; Page 99-100; 111pp; Japanese.  
 The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;  
 SQ Query Match 100.0%; Score 384; DB 22; Length 923;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-113;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGCGCTGTATGCTGTGCTATGGA 60  
 34 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGCGCTGTATGCTGTGCTATGGA 93  
 61 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTATCT 120  
 94 ATATTATGACCGCTCTAGCTTCCAGAAGCTCTGTGCAGATGATGCTGTCTATCT 153  
 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTAATCCCGGCTCTGTATGCTGTGCTATG 180  
 154 ATTTCTCTGGCTAGTGTCTCAAGAGATTAATCCCGGCTCTGTATGCTGTGCTATG 213  
 181 AAAAAAGGGCAGCAGATCTATGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 240  
 214 AAAAAAGGGCAGCAGATCTATGTCTCAAGAGCTGTGTAAAGAAATGGAGCTGGAGAA 273

QY 241 TTTTGGGCTGGCAGTGTATGTGATGGCCAGACAGATGGAGTCGTGGTTATTTC 300  
 Db 274 TTTTGGGCTGGCAGTGTATGTGATGGCCAGACAGATGGAGTCGTGGTTATTTC 333  
 QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTTCCACACC 360  
 Db 334 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTTCCACACC 393  
 QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
 Db 394 ACGGATATTGACTTCTTCTCGGAG 417

## RESULT 10

AAH26343  
 ID AAH26343 standard; cDNA; 1201 BP.

XX AC AAH26343;

XX 02-OCT-2001 (first entry)

XX DE Human growth regulatory-like polypeptide cDNA.

XX KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
 FT CDS 33..419

FT /\*tag= a

FT sig\_peptide 33..101

FT /\*tag= b

FT mat\_peptide 102..416

FT /\*tag= c

XX WO200155332-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

XX PI Drmanac RT;

XX WPI; 2001-483233/52.

XX P-PSDB; AAB82671.

PT Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -

XX Claim 1; Page 115-116; 119pp; English.

XX The present sequence is that of a novel nucleic acid encoding  
 CC human growth regulatory-like polypeptide (GRLP, see AAB82671).  
 CC The sequence was assembled using human thymus cDNA library-derived  
 CC Hyseq clone identification number 16372272 (see AAB26341) as seed,  
 CC using software programs to pull additional sequences from Hyseq's  
 CC proprietary database containing expressed sequence tag sequences,  
 CC and by gel sequencing using primers to extend both 5' and 3' ends.  
 CC The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity and 45% identity over 111 amino acids)

CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRIP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.  
 CC They may also have cytokine and cell proliferation or  
 CC differentiation activity, stem cell growth factor activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC immunosuppressive or immunostimulant activity, activin/inhibin  
 CC activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, use in cancer diagnosis and therapy,  
 CC drug screening, receptor/ligand activity, antiinflammatory  
 CC activity, and treatment of leukaemia, nervous system disorders,  
 CC arthritis and inflammation.

XX SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;

Query Match 100.0%; Score 384; DB 22; Length 1201;

Best Local Similarity 100.0%; Pred. No. 1.6e-113;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 33 ATGGCAAGAAATATTGTACTTTCTCCCGGCTCTTGGCTGTATGTGCTGTGCATGGA 92  
 QY 61 ATATTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAAGATGATGCTGTATACT 120  
 Db 93 ATATTATGGACCGTCTAGCTTCCAAGAAGCTCTGTGCAAGATGATGCTGTATACT 152  
 QY 121 ATTTCTCTGCTAGTGTCTCAAGAAGATTAATAATGCCCGAGCTGTAGATTCAATTAACGTT 180  
 Db 153 ATTTCTCTGCTAGTGTCTCAAGAAGATTAATAATGCCCGAGCTGTAGATTCAATTAACGTT 212  
 QY 181 AAAAAAGGCGCAGCAGATCTATCTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 240  
 Db 213 AAAAAAGGCGCAGCAGATCTATCTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 272  
 QY 241 TTTTGGGCTGGCAGTGTATGTGATGCCAGGACGAGATGGAGTCGTGGGTTATTTC 300  
 Db 273 TTTTGGGCTGGCAGTGTATGTGATGCCAGGACGAGATGGAGTCGTGGGTTATTTC 332  
 QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCACCACC 360  
 Db 333 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTTCACCACC 392  
 QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
 Db 393 ACGGATATTGACTTCTTCTCGGAG 416

## RESULT 11

AAF59079

ID AAF59079 standard; DNA; 330 BP.

XX AC AAF59079;

XX DT 23-APR-2001 (first entry)

XX Human MLP nucleotide sequence SEQ ID NO:23.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
 XX OS Homo sapiens.



Db 251 TTTTGGCTGGCAGTGTATGTTGACACACAGGATGAGATGGAAATTGAGTTATTTC 310  
QY 301 CCCAGAACTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGCAAGTTCACACC 360  
Db 311 CCCAGCACTTGGTGAAGGAGAGCGGTGTATACCAAGAGGCCACCAAGAGATCCCAACC 370  
QY 361 ACGGATATTGACTTCTTCTGCGA 383  
Db 371 ACGGATATTGACTTCTTCTGCGA 393  
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ID AAF59084 standard; DNA; 947 BP.  
XX  
AC AAF59084;  
DT 23-APR-2001 (first entry)  
DE Mouse MLP nucleotide sequence SEQ ID NO:30.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
cardiant; gene therapy; secretory cell function regulator; promoter;  
inhibitor; ds.  
XX  
OS Mus musculus.  
XX  
PN WO200102564-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 29-JUN-2000; 2000WO-JP04278.  
XX  
PR 30-JUN-1999; 99JP-0196718.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
Tanaka H;  
PI WPI; 2001-159271/16.  
XX  
DR Safe, low-toxicity secretory cell function-regulatory protein and  
encoded DNA, applicable as drugs, in diagnosis and development of  
promoters and inhibitors for preventing or treating e.g. bone and joint  
diseases -  
XX  
PS Example 2; Page 100-101; 111pp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
activities, and can be used in gene therapy and as secretory cell  
function regulators. The MLP proteins and DNAs can be used in drugs, in  
the diagnosis and development of promoters and inhibitors for preventing  
or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
in the exemplification of the present invention.  
XX  
SQ Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;  
Query Match 74.7%; Score 287; DB 22; Length 947;  
Best Local Similarity 84.3%; Pred. No. 3.2e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAATATTGTTACTTTCTCCCGGCTGTGGCTGTATGCTGTGATGGA 60  
Db 11 ATGGCAAGGATATTGATTCTTTGCTTGGGGCCCTTGTGGTCTATGTGCGGGATGTT 70  
QY 61 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTACT 120  
Db 71 GTATTATGATGATAAATTCTTCTTAAGAGATTGTGTGCGATGAGGATGCTGTACT 130  
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGGAGTGTAGATTCATTAAGTT 180  
Db 131 ATTTCTCTGCAAGAGACAGAGAGATTACATGCCCCAGACTGTAGGTTTCATCGATGTC 190  
QY 181 AAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAATGAGCTGAGAA 240  
Db 191 AAGAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAATGAGCTGAGAG 250  
QY 241 TTTTGGCTGGCAGTGTGTTATGTTGATGATGCCAGGACGAGATGGAGTCGTGGTTTTC 300

Db 251 TTTTGGCTGGCAGTGTATGTTGACACACAGGATGAGATGGAAATTGAGTTATTTC 310  
QY 301 CCCAGAACTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGCAAGTTCACACC 360  
Db 311 CCCAGCACTTGGTGAAGGAGAGCGGTGTATACCAAGAGGCCACCAAGAGATCCCAACC 370  
QY 361 ACGGATATTGACTTCTTCTGCGA 383  
Db 371 ACGGATATTGACTTCTTCTGCGA 393  
RESULT 14  
AAF59084  
ID AAF59084 standard; DNA; 947 BP.  
XX  
AC AAF59084;  
DT 23-APR-2001 (first entry)  
DE Mouse MLP nucleotide sequence SEQ ID NO:30.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
cardiant; gene therapy; secretory cell function regulator; promoter;  
inhibitor; ds.  
XX  
OS Mus musculus.  
XX  
PN WO200102564-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 29-JUN-2000; 2000WO-JP04278.  
XX  
PR 30-JUN-1999; 99JP-0196718.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
Tanaka H;  
PI WPI; 2001-159271/16.  
XX  
DR Safe, low-toxicity secretory cell function-regulatory protein and  
encoded DNA, applicable as drugs, in diagnosis and development of  
promoters and inhibitors for preventing or treating e.g. bone and joint  
diseases -  
XX  
PS Example 2; Page 100-101; 111pp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
activities, and can be used in gene therapy and as secretory cell  
function regulators. The MLP proteins and DNAs can be used in drugs, in  
the diagnosis and development of promoters and inhibitors for preventing  
or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
in the exemplification of the present invention.  
XX  
SQ Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;  
Query Match 74.7%; Score 287; DB 22; Length 947;  
Best Local Similarity 84.3%; Pred. No. 3.2e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGGCAAGAATATTGTTACTTTCTCCCGGCTGTGGCTGTATGCTGTGATGGA 60  
Db 11 ATGGCAAGGATATTGATTCTTTGCTTGGGGCCCTTGTGGTCTATGTGCGGGATGTT 70  
QY 61 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTGTACT 120  
Db 71 GTATTATGATGATAAATTCTTCTTAAGAGATTGTGTGCGATGAGGATGCTGTACT 130  
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGGAGTGTAGATTCATTAAGTT 180  
Db 131 ATTTCTCTGCAAGAGACAGAGAGATTACATGCCCCAGACTGTAGGTTTCATCGATGTC 190  
QY 181 AAAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAATGAGCTGAGAA 240  
Db 191 AAGAAAGGCGACAGATCTATGTGTACTCAAGCTGTAAAGAAATGAGCTGAGAG 250  
QY 241 TTTTGGCTGGCAGTGTGTTATGTTGATGATGCCAGGACGAGATGGAGTCGTGGTTTTC 300



Db 61 ATGTTTATGGATAAACTTCTCTTAAGAAGTTGTGTGCAGATGAGGAGTGTGTCTATACC 120  
 QY 121 ATTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAAAGTT 180  
 Db 121 ATTCTCTGGCAAGACAGCAAGACTACATGCCCGGACTGTAGTTTCATCATGTC 180  
 QY 181 AAAAAGGGCAGCAGATCTATGTCTACTCAAAAGCTGTAAAGAAATGAGCTGGAGAA 240  
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 QY 301 CCCAGGAATCTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCCAAC 360  
 Db 301 CCCAGCAACTTGGTTAGAGACCAAGAGTGTACCAAGGAGGCCACCAAGGAGATTCCCAAC 360  
 QY 361 ACGGATATTGACTTCTCTCTGCGA 383  
 Db 361 ACGGATATTGACTTCTCTCTGTGA 383

## RESULT 15

AAF59080  
 ID AAF59080 standard; DNA; 330 BP.

AC AAF59080;

XX  
 XX 23-APR-2001 (first entry)

DT Mouse MLP nucleotide sequence SEQ ID NO:25.

DE MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.

XX Mus musculus.

XX WO200102564-A1.

PN 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 95JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;

XX WPI: 2001-159271/16.

DR P-PDS; AAB69127.

PT Safe low-toxicity secretory cell function-regulatory protein and  
 PI encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -

XX Claim 10; Page 98; 11pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.

XX Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

Query Match 65.7%; Score 252.2; DB 22; Length 330;  
 Best Local Similarity 85.4%; Pred. No. 3.4e-71;  
 Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 55 CATGGAATATTTATGGACCGTCTAGCTTCCAGAAGCTCTGTGCAGATGATGAGTGTGTC 114  
 Db 1 CATGGTGTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGGGATGAGGAGTGTGTC 60  
 QY 115 TATACTATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATT 174  
 Db 61 TATACTATTCTCTGGCAGAGCAGACAGGAAGATTACAATGCCCGGACTGTAGTTTCATC 120  
 QY 175 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGGTAAAAAGAAATCGAGCT 234  
 Db 121 GATGTCAAGAAAGGGCAGCAGATCTATGTTTACTCAAGCTGGTAAACAGAAACGGAGCT 180  
 QY 235 GGAGAAATTTTGGCTGGCAGTGTATTATGGTGTATGTCAGGACGAGATGGGAGTCGTGGGT 294  
 Db 181 GGAGAGTTTGGCTGGCAGTGTATTATGGTGTATGTCAGGACGAGATGGGAGTTGTAGGT 240  
 QY 295 TATTTCCCGGAACTTTGGTCAAGAAACAGCGTGTGTATCCAGGAAGCTACCAAGGAAGTT 354  
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 Job time : 129.462 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Run on: December 30, 2003, 04:08:13 ; Search time 315.339 Seconds  
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Perfect score: 384  
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Scoring table: IDENTITY\_NUC  
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
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18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	426	15	US-10-216-038-1
2	384	100.0	521	13	US-10-216-163-71
3	384	100.0	521	13	US-10-218-765-71
4	384	100.0	521	13	US-10-219-063-71
5	384	100.0	521	13	US-10-219-066-71
6	384	100.0	521	13	US-10-219-067-71
7	384	100.0	521	13	US-10-219-068-71
8	384	100.0	521	13	US-10-219-069-71
9	384	100.0	521	13	US-10-219-073-71
10	384	100.0	521	13	US-10-219-475-71
11	384	100.0	521	13	US-10-219-480-71
12	384	100.0	521	13	US-10-219-483-71
13	384	100.0	521	13	US-10-219-525-71
14	384	100.0	521	13	US-10-219-526-71
15	384	100.0	521	13	US-10-219-530-71

16	384	100.0	521	13	US-10-219-531-71	Sequence 71, Appl
17	384	100.0	521	13	US-10-219-532-71	Sequence 71, Appl
18	384	100.0	521	13	US-10-219-533-71	Sequence 71, Appl
19	384	100.0	521	13	US-10-223-081-359	Sequence 359, App
20	384	100.0	521	13	US-10-230-437-71	Sequence 71, Appl
21	384	100.0	521	13	US-10-232-228-71	Sequence 71, Appl
22	384	100.0	521	13	US-10-223-082-359	Sequence 359, App
23	384	100.0	521	15	US-10-227-884-71	Sequence 71, Appl
24	384	100.0	521	15	US-10-230-163-71	Sequence 71, Appl
25	384	100.0	521	15	US-10-230-338-71	Sequence 71, Appl
26	384	100.0	521	15	US-10-218-631-71	Sequence 71, Appl
27	384	100.0	521	15	US-10-230-414-71	Sequence 71, Appl
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29	384	100.0	521	15	US-10-218-849-71	Sequence 71, Appl
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32	384	100.0	521	15	US-10-219-076-71	Sequence 71, Appl
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ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/10216038  
; Publication No. US20030124573A1  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjastaad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1e1 Growth R  
; TITLE OF INVENTION: Polypeptides and Polynucleotides  
; FILE REFERENCE: HYS-7C1P  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (426)..(426)  
; OTHER INFORMATION: n = A, T, G, or C  
US-10-216-038-1

Query Match 100.0%; Score 384; DB 15; Length 426;  
Best Local Similarity 100.0%; Pred. No. 6.4e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Tue Dec 30 10:20:46 2003

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DB 19 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGTGCTGTGCATGGA 78
QY 61 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGAGATGAGTGTCTTACT 120
DB 79 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGAGATGAGTGTCTTACT 138
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DB 139 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 198
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QY 361 ACGGATATTGACTTCTTCTCGGAG 384
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RESULT 2
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; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71
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Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGTGCTGTGCATGGA 60
DB 38 ATGGCAAGAATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGTGCTGTGCATGGA 97
QY 61 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGAGATGAGTGTCTTACT 120
DB 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGAGATGAGTGTCTTACT 157
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 180
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
QY 181 AAAAAAGGCGAGAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCTGGAGAA 240
DB 218 AAAAAAGGCGAGAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCTGGAGAA 277
QY 241 TTTTGGGCTGGCAGTGTATGTGTATGGTATGCGCAGGAGAGATGGAGTCTGGTATTTC 300
DB 278 TTTTGGGCTGGCAGTGTATGTGTATGGTATGCGCAGGAGAGATGGAGTCTGGTATTTC 337
QY 301 CCAGAGACTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 360
DB 338 CCAGAGACTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 397
QY 361 ACGGATATTGACTTCTTCTCGGAG 384
DB 398 ACGGATATTGACTTCTTCTCGGAG 421
RESULT 3
US-10-218-765-71
; Sequence 71, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
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;  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/086392  
; PRIOR FILING DATE: 1998-05-22  
; PRIOR APPLICATION NUMBER: 60/089532  
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; PRIOR APPLICATION NUMBER: 60/090472  
; PRIOR FILING DATE: 1998-06-24  
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; PRIOR FILING DATE: 1998-06-24  
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; PRIOR APPLICATION NUMBER: 60/090695  
; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/095302  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/095318  
; PRIOR FILING DATE: 1998-08-04  
; PRIOR APPLICATION NUMBER: 60/095916  
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; PRIOR APPLICATION NUMBER: 60/097986  
; PRIOR FILING DATE: 1998-08-26  
; PRIOR APPLICATION NUMBER: 60/098544  
; PRIOR FILING DATE: 1998-08-31  
; PRIOR APPLICATION NUMBER: 60/099596  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099598  
; PRIOR FILING DATE: 1998-09-09  
; PRIOR APPLICATION NUMBER: 60/099803  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/099811  
; PRIOR FILING DATE: 1998-09-10  
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; PRIOR FILING DATE: 1998-09-10  
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; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 60/100038  
; PRIOR FILING DATE: 1998-09-11  
; PRIOR APPLICATION NUMBER: 60/100385  
; PRIOR FILING DATE: 1998-09-15  
; PRIOR APPLICATION NUMBER: 60/100390  
; PRIOR FILING DATE: 1998-09-15  
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; PRIOR FILING DATE: 1998-09-16  
; PRIOR APPLICATION NUMBER: 60/100848  
; PRIOR FILING DATE: 1998-09-18

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; PRIOR APPLICATION NUMBER: 60/100919  
; PRIOR FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/101477  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/101738  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101741  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101786  
; PRIOR FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: 60/101916  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/101922  
; PRIOR FILING DATE: 1998-09-24  
; PRIOR APPLICATION NUMBER: 60/106178  
; PRIOR FILING DATE: 1998-10-28  
; PRIOR APPLICATION NUMBER: 60/106248  
; PRIOR FILING DATE: 1998-10-29  
; PRIOR APPLICATION NUMBER: 60/106464  
; PRIOR FILING DATE: 1998-10-30  
; PRIOR APPLICATION NUMBER: 60/106905  
; PRIOR FILING DATE: 1998-11-03  
; PRIOR APPLICATION NUMBER: 60/108787  
; PRIOR FILING DATE: 1998-11-17  
; PRIOR APPLICATION NUMBER: 60/108801  
; PRIOR FILING DATE: 1998-11-17  
; PRIOR APPLICATION NUMBER: 60/108849  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: 60/112422  
; PRIOR FILING DATE: 1998-12-15  
; PRIOR APPLICATION NUMBER: 60/113296  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/113605  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/113621  
; PRIOR FILING DATE: 1998-12-23  
; PRIOR APPLICATION NUMBER: 60/115558  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115565  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/115733  
; PRIOR FILING DATE: 1999-01-12  
; PRIOR APPLICATION NUMBER: 60/119549  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: 60/123618  
; PRIOR FILING DATE: 1999-03-10  
; PRIOR APPLICATION NUMBER: 60/125259  
; PRIOR FILING DATE: 1999-03-19  
; PRIOR APPLICATION NUMBER: 60/125775  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: 60/126773  
; PRIOR FILING DATE: 1999-03-29  
; PRIOR APPLICATION NUMBER: 60/127887  
; PRIOR FILING DATE: 1999-04-05  
; PRIOR APPLICATION NUMBER: 60/130232  
; PRIOR FILING DATE: 1999-04-21  
; PRIOR APPLICATION NUMBER: 60/131022  
; PRIOR FILING DATE: 1999-04-26  
; PRIOR APPLICATION NUMBER: 60/131270  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/131291  
; PRIOR FILING DATE: 1999-04-27  
; PRIOR APPLICATION NUMBER: 60/131445  
; PRIOR FILING DATE: 1999-04-28  
; PRIOR APPLICATION NUMBER: 60/134287  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/140650  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/140723  
; PRIOR FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: 60/141037  
; PRIOR FILING DATE: 1999-06-23  
; PRIOR APPLICATION NUMBER: 60/144758

PRIOR FILING DATE: 1999-07-20  
PRIOR APPLICATION NUMBER: 60/145698 ✓  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/145222 ✓  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: 60/146963 ✓  
PRIOR FILING DATE: 1999-08-03  
PRIOR APPLICATION NUMBER: 60/149320 ✓  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/149638 ✓  
PRIOR FILING DATE: 1999-08-17  
PRIOR APPLICATION NUMBER: 60/151733 ✓  
PRIOR FILING DATE: 1999-08-31  
PRIOR APPLICATION NUMBER: 60/164418 ✓  
PRIOR FILING DATE: 1999-11-09  
PRIOR APPLICATION NUMBER: 60/166361 ✓  
PRIOR FILING DATE: 1999-11-16  
PRIOR APPLICATION NUMBER: 60/169445 ✓  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169495 ✓  
PRIOR FILING DATE: 1999-12-07  
PRIOR APPLICATION NUMBER: 60/169835 ✓  
PRIOR APPLICATION NUMBER: 60/169835

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.le-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGTCGTCATGGA 60  
DB 38 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGTCGTCATGGA 97  
QY 61 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGTCGTCATGGA 120  
DB 98 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGTCGTCATGGA 157  
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATCCCGGCTGTAGATTCATTAACTT 180  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATCCCGGCTGTAGATTCATTAACTT 217  
QY 181 AAAAAAGGGCAGCAGATCTATGTTACTCAAAAGCTGTTAAAGAAATGGAGCTGGAGAA 240  
DB 218 AAAAAAGGGCAGCAGATCTATGTTACTCAAAAGCTGTTAAAGAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGCTGGCAGTGTATGTTATGGTGATGGCCAGCAGATGGAGTCGTGGGTTATTC 300  
DB 278 TTTTGGCTGGCAGTGTATGTTATGGTGATGGCCAGCAGATGGAGTCGTGGGTTATTC 337  
QY 301 CCCAGGAACCTGGTCAAGGAACACCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 360  
DB 338 CCCAGGAACCTGGTCAAGGAACACCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 397  
QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
DB 398 ACGGATATTGACTTCTTCTCGGAG 421

## RESULT 4

US-10-219-063-71  
Sequence 71, Application US/10219063  
Publication No. US20030187202A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin I.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3530PIC24  
CURRENT APPLICATION NUMBER: US/10/219.063  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-063-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.le-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGTCGTCATGGA 60  
DB 38 ATGCGAAGATATTGTTACTTTCTCCCGGCTCTGTGGCTGTATGTCGTCATGGA 97  
QY 61 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGTCGTCATGGA 120  
DB 98 ATATTTATGGACCGCTAGCTTCCAAAGAGCTCTGTCAGATGATGTCGTCATGGA 157  
QY 121 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATCCCGGCTGTAGATTCATTAACTT 180  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATCCCGGCTGTAGATTCATTAACTT 217  
QY 181 AAAAAAGGGCAGCAGATCTATGTTACTCAAAAGCTGTTAAAGAAATGGAGCTGGAGAA 240  
DB 218 AAAAAAGGGCAGCAGATCTATGTTACTCAAAAGCTGTTAAAGAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGCTGGCAGTGTATGTTATGGTGATGGCCAGCAGATGGAGTCGTGGGTTATTC 300  
DB 278 TTTTGGCTGGCAGTGTATGTTATGGTGATGGCCAGCAGATGGAGTCGTGGGTTATTC 337  
QY 301 CCCAGGAACCTGGTCAAGGAACACCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 360  
DB 338 CCCAGGAACCTGGTCAAGGAACACCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC 397  
QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
DB 398 ACGGATATTGACTTCTTCTCGGAG 421

## RESULT 5

US-10-219-066-71  
Sequence 71, Application US/10219066  
Publication No. US20030187203A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary

APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stephan, Jean-Philippe F.  
 APPLICANT: Watanabe, Colin L.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P3530P1C27  
 CURRENT APPLICATION NUMBER: US/10/219,066  
 PRIOR FILING DATE: 2002-08-13  
 PRIOR APPLICATION NUMBER: 60/059113  
 PRIOR FILING DATE: 1997-09-17  
 PRIOR APPLICATION NUMBER: 60/062287  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/063549  
 PRIOR FILING DATE: 1997-10-28  
 PRIOR APPLICATION NUMBER: 60/064103  
 PRIOR FILING DATE: 1997-10-31  
 PRIOR APPLICATION NUMBER: 60/069873  
 PRIOR FILING DATE: 1997-12-17  
 PRIOR APPLICATION NUMBER: 60/079656  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079728  
 PRIOR FILING DATE: 1998-03-26  
 PRIOR APPLICATION NUMBER: 60/079728  
 PRIOR FILING DATE: 1998-03-27  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 246  
 SEQ ID NO 71  
 LENGTH: 521  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-219-066-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCAAGAAATATTGTACTTTTCTCCCGGGCTTGTGCTGTATGTGTCATGGA	60
Db	38	ATGGCAAGAAATATTGTACTTTTCTCCCGGGCTTGTGCTGTATGTGTCATGGA	97
QY	61	ATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGAGTGTCTATCT	120
Db	98	ATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGAGTGTCTATCT	157
QY	121	ATTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGCTGTAGATTCATTACGTT	180
Db	158	ATTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGCTGTAGATTCATTACGTT	217
QY	181	AAAAAGGCGCAGACATCTATGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA	240
Db	218	AAAAAGGCGCAGACATCTATGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA	277
QY	241	TTTTGGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGAGTCTGGGTATTTC	300
Db	278	TTTTGGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGAGTCTGGGTATTTC	337
QY	301	CCAGAACTTGGTCAAGCAAGCGTGTGTACCAAGAGCTACCAAGAAAGTTCCACC	360
Db	338	CCAGAACTTGGTCAAGCAAGCGTGTGTACCAAGAGCTACCAAGAAAGTTCCACC	397
QY	361	ACGATATTGACTTCTTCTGCGAG	384
Db	398	ACGATATTGACTTCTTCTGCGAG	421

RESULT 6  
 US-10-219-067-71  
 ; Sequence 71, Application US/10219067  
 ; Publication No. US20030187204A1  
 ; GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Gerritsen, Mary  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Smith, Victoria  
 APPLICANT: Stephan, Jean-Philippe F.  
 APPLICANT: Watanabe, Colin L.  
 APPLICANT: Wood, William I.  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P3530P1C51  
 CURRENT APPLICATION NUMBER: US/10/219,067  
 CURRENT FILING DATE: 2002-08-14  
 PRIOR APPLICATION NUMBER: 10/119,480  
 PRIOR FILING DATE: 2002-04-09  
 PRIOR APPLICATION NUMBER: 60/059113  
 PRIOR FILING DATE: 1997-09-17  
 PRIOR APPLICATION NUMBER: 60/062287  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/063549  
 PRIOR FILING DATE: 1997-10-28  
 PRIOR APPLICATION NUMBER: 60/064103  
 PRIOR FILING DATE: 1997-10-31  
 PRIOR APPLICATION NUMBER: 60/069873  
 PRIOR FILING DATE: 1997-12-17  
 PRIOR APPLICATION NUMBER: 60/078910  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: 60/079294  
 PRIOR FILING DATE: 1998-03-25  
 PRIOR APPLICATION NUMBER: 60/079656  
 PRIOR FILING DATE: 1998-03-26  
 PRIOR APPLICATION NUMBER: 60/079728  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 246  
 SEQ ID NO 71  
 LENGTH: 521  
 TYPE: DNA  
 ORGANISM: Homo Sapien  
 US-10-219-067-71

Query Match 100.0%; Score 384; DB 13; Length 521;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGCAAGAAATATTGTACTTTTCTCCCGGGCTTGTGCTGTATGTGTCATGGA	60
Db	38	ATGGCAAGAAATATTGTACTTTTCTCCCGGGCTTGTGCTGTATGTGTCATGGA	97
QY	61	ATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGAGTGTCTATCT	120
Db	98	ATATTTATGGACCGTCTAGCTTCCAAGAGCTCTGTGCAGATGATGAGTGTCTATCT	157
QY	121	ATTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGCTGTAGATTCATTACGTT	180
Db	158	ATTCTCTGGCTAGTCTCAAGAGATTATATGCCCCGGCTGTAGATTCATTACGTT	217
QY	181	AAAAAGGCGCAGACATCTATGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA	240
Db	218	AAAAAGGCGCAGACATCTATGTACTCAAAGCTGTAAAGAAATGGAGCTGAGAA	277
QY	241	TTTTGGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGAGTCTGGGTATTTC	300
Db	278	TTTTGGGCTGGCAGTGTATGTGTATGGCCAGCAGATGGAGTCTGGGTATTTC	337



Db 38 ATGGCAGATATTGTTACTTTCTCCCGGCTCTTGTGGCTGTATGTGCTGTGCATGGA 97  
QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
Db 98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157  
QY 121 ATTTCTCGGCTAGCTCAAGAAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT 180  
Db 158 ATTTCTCGGCTAGCTCAAGAAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT 217  
QY 181 AAAAAGGGCAGCAGATCTATGTACTCAAGAGCTGTAAGAGAAATGGAGCTGGAGAA 240  
Db 218 AAAAAGGGCAGCAGATCTATGTACTCAAGAGCTGTAAGAGAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGCGAGTGTATGCTGATGCGCAGGACGATGGAGTCTGGGTATTTC 300  
Db 278 TTTTGGGCTGCGAGTGTATGCTGATGCGCAGGACGATGGAGTCTGGGTATTTC 337  
QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGAAAGTTCCACC 360  
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGAAAGTTCCACC 397  
QY 361 AGGATATTGACTTCTTCTGCGAG 384  
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

## RESULT 9

US-10-219-073-71  
; Sequence 71, Application US/10219073  
; Publication No. US20030187207A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530PIC52  
; CURRENT APPLICATION NUMBER: US/10/219,073  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079810  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521

; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-073-71  
Query Match 100.0%; Score 384; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.1e-118;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCAGATATTGTTACTTTCTCCCGGCTCTTGTGGCTGTATGTGCTGTGCATGGA 60  
Db 38 ATGGCAGATATTGTTACTTTCTCCCGGCTCTTGTGGCTGTATGTGCTGTGCATGGA 97  
QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120  
Db 98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157  
QY 121 ATTTCTCGGCTAGCTCAAGAAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT 180  
Db 158 ATTTCTCGGCTAGCTCAAGAAGATTATATGCCCCGGAGCTGTAGATTCAATTAACGTT 217  
QY 181 AAAAAGGGCAGCAGATCTATGTACTCAAGAGCTGTAAGAGAAATGGAGCTGGAGAA 240  
Db 218 AAAAAGGGCAGCAGATCTATGTACTCAAGAGCTGTAAGAGAAATGGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGCGAGTGTATGCTGATGCGCAGGACGATGGAGTCTGGGTATTTC 300  
Db 278 TTTTGGGCTGCGAGTGTATGCTGATGCGCAGGACGATGGAGTCTGGGTATTTC 337  
QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGAAAGTTCCACC 360  
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCCAGGAGCTACCAAGAAAGTTCCACC 397  
QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 398 ACGGATATTGACTTCTTCTGCGAG 421

## RESULT 10

US-10-219-475-71  
; Sequence 71, Application US/10219475  
; Publication No. US20030187208A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3530PIC49  
; CURRENT APPLICATION NUMBER: US/10/219,475  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294



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; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-475-71

Query Match      100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ATGGCAAGATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGCTGTGTCATGGA 60
DB  38 ATGGCAAGATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGCTGTGTCATGGA 97

QY  61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTATACT 120
DB  98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTATACT 157

QY  121 ATTTCTGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 180
DB  158 ATTTCTGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 217

QY  181 AAAAAAGGCGACGAGATCTATGTCTCAAGAGCTGTGTAAGAAATGAGCTGGAGAA 240
DB  218 AAAAAAGGCGACGAGATCTATGTCTCAAGAGCTGTGTAAGAAATGAGCTGGAGAA 277

QY  241 TTTTGGGCTGCAGTGTATGTTATGTTGATGCCAGACAGATGGAGTCGTGGTTATTC 300
DB  278 TTTTGGGCTGCAGTGTATGTTATGTTGATGCCAGACAGATGGAGTCGTGGTTATTC 337

QY  301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGAGATTCCACC 360
DB  338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGAGATTCCACC 397

QY  361 ACGGATATTGACTTCTTCTGCGAG 384
DB  398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 11
US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-480-71

Query Match      100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 ATGGCAAGATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGCTGTGTCATGGA 60
DB  38 ATGGCAAGATATTGTTACTTTTCTCCCGGCTCTTGGCTGTATGCTGTGTCATGGA 97

QY  61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTATACT 120
DB  98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTATACT 157

QY  121 ATTTCTGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 180
DB  158 ATTTCTGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAACGTT 217

QY  181 AAAAAAGGCGACGAGATCTATGTCTCAAGAGCTGTGTAAGAAATGAGCTGGAGAA 240
DB  218 AAAAAAGGCGACGAGATCTATGTCTCAAGAGCTGTGTAAGAAATGAGCTGGAGAA 277

QY  241 TTTTGGGCTGCAGTGTATGTTATGTTGATGCCAGACAGATGGAGTCGTGGTTATTC 300
DB  278 TTTTGGGCTGCAGTGTATGTTATGTTGATGCCAGACAGATGGAGTCGTGGTTATTC 337

QY  301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGAGATTCCACC 360
DB  338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAGCTACCAAGAGATTCCACC 397

QY  361 ACGGATATTGACTTCTTCTGCGAG 384
DB  398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 12
US-10-219-483-71
; Sequence 71, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; FILE REFERENCE: P3530P1C43
; CURRENT APPLICATION NUMBER: US/10/219,483
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-483-71

Query Match      100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7,1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGCTGTATGCTGTGTCATGGA 60
Db 38 ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGCTGTATGCTGTGTCATGGA 97

QY 61 ATATTATGACCGTCTAGCTTCCCAAGAAGCTCTGTCAGATGATGAGTGTGTCTATCT 120
Db 98 ATATTATGACCGTCTAGCTTCCCAAGAAGCTCTGTCAGATGATGAGTGTGTCTATCT 157

QY 121 ATTCTCTCGGTAGTGTCTCAAGAAGATTATATGCTCCCGGACTGTAGATTCTTAACGTT 180
Db 158 ATTCTCTCGGTAGTGTCTCAAGAAGATTATATGCTCCCGGACTGTAGATTCTTAACGTT 217

QY 181 AAAAAAGGCAGACAGATCTATGTGTACTCAAAAGCTGTGTAAGAAATGGAGCTGGAGAA 240
Db 218 AAAAAAGGCAGACAGATCTATGTGTACTCAAAAGCTGTGTAAGAAATGGAGCTGGAGAA 277

QY 241 TTTTGGGCTGGCAGTGTGTTATGTTGATGTCAGGACGAGATGGAGTCTGGTATTTC 300
Db 278 TTTTGGGCTGGCAGTGTGTTATGTTGATGTCAGGACGAGATGGAGTCTGGTATTTC 337

QY 301 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCACCACC 360
Db 338 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCACCACC 397

QY 361 ACGGATATTGACTTCTTCTCGGAG 384
Db 398 ACGGATATTGACTTCTTCTCGGAG 421
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## RESULT 13

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US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication NO. US2003018721A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
```

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-525-71
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Query Match      100.0%; Score 384; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7,1e-118;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGCTGTATGCTGTGTCATGGA 60
Db 38 ATGGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGCTGTATGCTGTGTCATGGA 97

QY 61 ATATTATGACCGTCTAGCTTCCCAAGAAGCTCTGTCAGATGATGAGTGTGTCTATCT 120
Db 98 ATATTATGACCGTCTAGCTTCCCAAGAAGCTCTGTCAGATGATGAGTGTGTCTATCT 157

QY 121 ATTCTCTCGGTAGTGTCTCAAGAAGATTATATGCTCCCGGACTGTAGATTCTTAACGTT 180
Db 158 ATTCTCTCGGTAGTGTCTCAAGAAGATTATATGCTCCCGGACTGTAGATTCTTAACGTT 217

QY 181 AAAAAAGGCAGACAGATCTATGTGTACTCAAAAGCTGTGTAAGAAATGGAGCTGGAGAA 240
Db 218 AAAAAAGGCAGACAGATCTATGTGTACTCAAAAGCTGTGTAAGAAATGGAGCTGGAGAA 277

QY 241 TTTTGGGCTGGCAGTGTGTTATGTTGATGTCAGGACGAGATGGAGTCTGGTATTTC 300
Db 278 TTTTGGGCTGGCAGTGTGTTATGTTGATGTCAGGACGAGATGGAGTCTGGTATTTC 337

QY 301 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCACCACC 360
Db 338 CCCAGAACTTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCACCACC 397

QY 361 ACGGATATTGACTTCTTCTCGGAG 384
Db 398 ACGGATATTGACTTCTTCTCGGAG 421
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QY	181	AAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTTAAAGAAATGGAGCTGGAGAA	240
Db	218	AAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTTAAAGAAATGGAGCTGGAGAA	277
QY	241	TTTTGGGCTGGCAGTCTTTATGGTGATGGCCAGGACGAGATGGAGTCGTGGGTATTTC	300
Db	278	TTTTGGGCTGGCAGTCTTTATGGTGATGGCCAGGACGAGATGGAGTCGTGGGTATTTC	337
QY	301	CCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC	360
Db	338	CCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCACC	397
QY	361	ACGGATATTGACTTCTTCTGCGAG	384
Db	398	ACGGATATTGACTTCTTCTGCGAG	421

Search completed: December 30, 2003, 10:03:00  
 Job time : 318.339 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 02:01:19 ; Search time 1831.44 Seconds  
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6953.486 Million cell updates/sec

Title: US-10-019-455A-4

Perfect score: 384

Sequence: 1 atggcaagaatattgttact.....atattgactttctgtcgag 384

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 33363688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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83: /cgn2\_6/ptodata/2/pna/US6028 COMB.seq.\*

84: /cgn2\_6/ptodata/2/pna/US6029 COMB.seq.\*

85: /cgn2\_6/ptodata/2/pna/US6030 COMB.seq.\*

86: /cgn2\_6/ptodata/2/pna/US6031 COMB.seq.\*

87: /cgn2\_6/ptodata/2/pna/US6032 COMB.seq.\*

88: /cgn2\_6/ptodata/2/pna/US6033 COMB.seq.\*

89: /cgn2\_6/ptodata/2/pna/US6034 COMB.seq.\*

90: /cgn2\_6/ptodata/2/pna/US6035 COMB.seq.\*

91: /cgn2\_6/ptodata/2/pna/US6036 COMB.seq.\*

92: /cgn2\_6/ptodata/2/pna/US6037 COMB.seq.\*

93: /cgn2\_6/ptodata/2/pna/US6038 COMB.seq.\*

94: /cgn2\_6/ptodata/2/pna/US6039 COMB.seq.\*

95: /cgn2\_6/ptodata/2/pna/US6040 COMB.seq.\*

96: /cgn2\_6/ptodata/2/pna/US6041 COMB.seq.\*

97: /cgn2\_6/ptodata/2/pna/US6042 COMB.seq.\*

98: /cgn2\_6/ptodata/2/pna/US6043 COMB.seq.\*

99: /cgn2\_6/ptodata/2/pna/US6044 COMB.seq.\*

100: /cgn2\_6/ptodata/2/pna/US6045 COMB.seq.\*

101: /cgn2\_6/ptodata/2/pna/US6046 COMB.seq.\*

102: /cgn2\_6/ptodata/2/pna/US6047 COMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	384	100.0	384	44	US-10-019-455A-4
2	384	100.0	387	1	Sequence 4, Appli
3	384	100.0	387	2	Sequence 12, Appl
4	384	100.0	387	49	Sequence 12, Appl

```

5      384 100.0 426 1 PCT-US01-02455-1
6      384 100.0 426 2 PCT-US01-02455-1
7      384 100.0 426 22 US-09-528-409-107188
8      384 100.0 426 25 US-09-563-786A-1
9      384 100.0 426 39 US-09-933-524-107188
10     384 100.0 426 39 US-09-933-524A-107188
11     384 100.0 426 48 US-10-216-038-1
12     384 100.0 426 50 US-10-311-830-1
13     384 100.0 426 50 US-10-081-056-359
14     384 100.0 521 46 US-10-119-480-1
15     384 100.0 521 48 US-10-216-159A-71
16     384 100.0 521 48 US-10-216-160-71
17     384 100.0 521 48 US-10-216-162-71
18     384 100.0 521 48 US-10-216-163-71
19     384 100.0 521 48 US-10-216-164-71
20     384 100.0 521 48 US-10-216-165-71
21     384 100.0 521 48 US-10-216-166-71
22     384 100.0 521 48 US-10-216-167-71
23     384 100.0 521 48 US-10-216-168-71
24     384 100.0 521 48 US-10-218-612-71
25     384 100.0 521 48 US-10-218-631-71
26     384 100.0 521 48 US-10-218-765-71
27     384 100.0 521 48 US-10-218-784-71
28     384 100.0 521 48 US-10-218-849-71
29     384 100.0 521 48 US-10-218-930-71
30     384 100.0 521 48 US-10-218-956-71
31     384 100.0 521 48 US-10-219-003-71
32     384 100.0 521 48 US-10-219-010-71
33     384 100.0 521 48 US-10-219-060-71
34     384 100.0 521 48 US-10-219-061-71
35     384 100.0 521 48 US-10-219-062-71
36     384 100.0 521 48 US-10-219-063-71
37     384 100.0 521 48 US-10-219-064-71
38     384 100.0 521 48 US-10-219-065-71
39     384 100.0 521 48 US-10-219-066-71
40     384 100.0 521 48 US-10-219-067-71
41     384 100.0 521 48 US-10-219-068-71
42     384 100.0 521 48 US-10-219-069-71
43     384 100.0 521 48 US-10-219-070-71
44     384 100.0 521 48 US-10-219-071-71
45     384 100.0 521 48 US-10-219-072-71

```

## ALIGNMENTS

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RESULT 1
US-10-019-455A-4
; Sequence 4, Application US/10019455A
; GENERAL INFORMATION:
; APPLICANT: ITOH, YASUAKI
; APPLICANT: NISHI, KAZUNORI
; APPLICANT: OGI, KAZUHIRO
; APPLICANT: OKUBO, SHOICHI
; APPLICANT: MOGI, SHINICHI
; APPLICANT: NOGUCHI, YUKO
; TITLE OF INVENTION: NOVEL PEPTIDE AND DNA THEREOF
; FILE REFERENCE: 56804-46342
; CURRENT APPLICATION NUMBER: US/10/019,455A
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 384
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(384)
US-10-019-455A-4
Query Match 100.0%; Score 384; DB 44; Length 384;
Best Local Similarity 100.0%; Pred. No. 1.1e-107;

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Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGGCAAGAAATATGTTACTTTTCTCCCGGCTCTTGCGCTGTATGTGCTGTGATGGA 60
      1 ATGGCAAGAAATATGTTACTTTTCTCCCGGCTCTTGCGCTGTATGTGCTGTGATGGA 60
Db      1 ATGGCAAGAAATATGTTACTTTTCTCCCGGCTCTTGCGCTGTATGTGCTGTGATGGA 60
Qy      61 ATATTATGAGCCGCTAGCTTCCCAAGAGCTCTCTGCGAGATGATGAGTGTCTATACT 120
      61 ATATTATGAGCCGCTAGCTTCCCAAGAGCTCTCTGCGAGATGATGAGTGTCTATACT 120
Db      1 ATATTATGAGCCGCTAGCTTCCCAAGAGCTCTCTGCGAGATGATGAGTGTCTATACT 120
Qy      121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGCTGTAGATTCATTAACT 180
      121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGCTGTAGATTCATTAACT 180
Db      1 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGCTGTAGATTCATTAACT 180
Qy      181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240
      181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240
Db      181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240
Qy      241 TTTTGGGCTGGCAGTGTCTTATGCTGATGCGCCAGGACGAGTGGAGTCTGGGTTATTTC 300
      241 TTTTGGGCTGGCAGTGTCTTATGCTGATGCGCCAGGACGAGTGGAGTCTGGGTTATTTC 300
Db      241 TTTTGGGCTGGCAGTGTCTTATGCTGATGCGCCAGGACGAGTGGAGTCTGGGTTATTTC 300
Qy      301 CCAGAGAACTTGGTCAAGGACAGCGTGTGTACCGAGGAGCTACCAAGGAGTCCACACC 360
      301 CCAGAGAACTTGGTCAAGGACAGCGTGTGTACCGAGGAGCTACCAAGGAGTCCACACC 360
Db      301 CCAGAGAACTTGGTCAAGGACAGCGTGTGTACCGAGGAGCTACCAAGGAGTCCACACC 360
Qy      361 ACGGATATTGACTTCTTCTGCGAG 384
      361 ACGGATATTGACTTCTTCTGCGAG 384
Db      361 ACGGATATTGACTTCTTCTGCGAG 384

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## RESULT 2

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PCT-US01-11797-12
; Sequence 12, Application PC/TUS0111797
; GENERAL INFORMATION:
; APPLICANT: SMITHKLINE BEECHAM CORPORATION
; APPLICANT: SMITHKLINE BEECHAM P.L.C.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50022
; CURRENT APPLICATION NUMBER: PCT/US01/11797
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/196,603
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: 60/199,417
; PRIOR FILING DATE: 2000-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-11797-12

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Query Match 100.0%; Score 384; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.1e-107;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGGCAAGAAATATGTTACTTTTCTCCCGGCTCTTGCGCTGTATGTGCTGTGATGGA 60
      1 ATGGCAAGAAATATGTTACTTTTCTCCCGGCTCTTGCGCTGTATGTGCTGTGATGGA 60
Db      1 ATGGCAAGAAATATGTTACTTTTCTCCCGGCTCTTGCGCTGTATGTGCTGTGATGGA 60
Qy      61 ATATTATGAGCCGCTAGCTTCCCAAGAGCTCTCTGCGAGATGATGAGTGTCTATACT 120
      61 ATATTATGAGCCGCTAGCTTCCCAAGAGCTCTCTGCGAGATGATGAGTGTCTATACT 120
Db      1 ATATTATGAGCCGCTAGCTTCCCAAGAGCTCTCTGCGAGATGATGAGTGTCTATACT 120
Qy      121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGCTGTAGATTCATTAACT 180
      121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGCTGTAGATTCATTAACT 180
Db      121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGCTGTAGATTCATTAACT 180
Qy      181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240
      181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240
Db      181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA 240

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QY 241 TTTTGGGCTGGCAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
 |||||  
 Db 241 TTTTGGGCTGGCAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
 |||||  
 QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCCAACC 360  
 |||||  
 Db 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCCAACC 360  
 |||||  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||  
 Db 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||

## RESULT 3

PCT-US01-11797-12  
 ; Sequence 12, Application PC/TUS0111797  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SMITHKLINE BEECHAM CORPORATION  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP50022  
 ; CURRENT APPLICATION NUMBER: PCT/US01/11797  
 ; CURRENT FILING DATE: 2001-04-11  
 ; PRIOR APPLICATION NUMBER: 60/196,603  
 ; PRIOR FILING DATE: 2000-04-13  
 ; PRIOR FILING DATE: 2000-04-13  
 ; PRIOR FILING DATE: 2000-04-13  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 12  
 ; LENGTH: 387  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 PCT-US01-11797-12

Query Match 100.0%; Score 384; DB 2; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-107;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAATATTGTACTTTCTCCCGGGTCTTGGTGTATGTCGTGTCATGGA 60  
 |||||  
 Db 1 ATGGCAAGAATATTGTACTTTCTCCCGGGTCTTGGTGTATGTCGTGTCATGGA 60  
 |||||  
 QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTACT 120  
 |||||  
 Db 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTACT 120  
 |||||  
 QY 121 ATTTCTCTGGCTAGTCTCAAGAAATTAATATGCCCCGGACTGTAGATTCATTAAAGTT 180  
 |||||  
 Db 121 ATTTCTCTGGCTAGTCTCAAGAAATTAATATGCCCCGGACTGTAGATTCATTAAAGTT 180  
 |||||  
 QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240  
 |||||  
 Db 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240  
 |||||  
 QY 241 TTTTGGGCTGGCAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
 |||||  
 Db 241 TTTTGGGCTGGCAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
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 QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCCAACC 360  
 |||||  
 Db 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCCAACC 360  
 |||||  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||  
 Db 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||

## RESULT 4

US-10-257-174-12  
 ; Sequence 12, Application US/10257174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agarwal, Pankaj

APPLICANT: Murdoch, Paul R.  
 APPLICANT: Rizvi, Safia K.  
 APPLICANT: Smith, Randall F.  
 APPLICANT: Xiang, Zhaoying  
 TITLE OF INVENTION: NOVEL COMPOUNDS  
 FILE REFERENCE: GP50022  
 CURRENT APPLICATION NUMBER: US/10/257,174  
 CURRENT FILING DATE: 2002-10-10  
 PRIOR APPLICATION NUMBER: PCT/US01/11797  
 PRIOR FILING DATE: 2001-04-11  
 PRIOR APPLICATION NUMBER: 60/196,603  
 PRIOR FILING DATE: 2000-04-13  
 PRIOR APPLICATION NUMBER: 60/199,417  
 PRIOR FILING DATE: 2000-04-24  
 NUMBER OF SEQ ID NOS: 48  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 12  
 LENGTH: 387  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-257-174-12

Query Match 100.0%; Score 384; DB 49; Length 387;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-107;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCAAGAATATTGTACTTTCTCCCGGGTCTTGGTGTATGTCGTGTCATGGA 60  
 |||||  
 Db 1 ATGGCAAGAATATTGTACTTTCTCCCGGGTCTTGGTGTATGTCGTGTCATGGA 60  
 |||||  
 QY 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTACT 120  
 |||||  
 Db 61 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTACT 120  
 |||||  
 QY 121 ATTTCTCTGGCTAGTCTCAAGAAATTAATATGCCCCGGACTGTAGATTCATTAAAGTT 180  
 |||||  
 Db 121 ATTTCTCTGGCTAGTCTCAAGAAATTAATATGCCCCGGACTGTAGATTCATTAAAGTT 180  
 |||||  
 QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240  
 |||||  
 Db 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 240  
 |||||  
 QY 241 TTTTGGGCTGGCAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
 |||||  
 Db 241 TTTTGGGCTGGCAGTCTTTATGTCATGCGCAGACGAGATGGAGTCGTGGGTATTTC 300  
 |||||  
 QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCCAACC 360  
 |||||  
 Db 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTTCCCAACC 360  
 |||||  
 QY 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||  
 Db 361 ACGGATATTGACTTCTTCTGCGAG 384  
 |||||

## RESULT 5

PCT-US01-02455-1  
 ; Sequence 1, Application PC/TUS0102455  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc.  
 ; APPLICANT: Mize, Nancy K.  
 ; APPLICANT: Boye, Bryan J.  
 ; APPLICANT: Ford, John E.  
 ; APPLICANT: Arterburn, Matthew C.  
 ; APPLICANT: Tang, Y Tom  
 ; APPLICANT: Liu, Chenghua  
 ; APPLICANT: Drmanac, Radoje T  
 ; TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
 ; TITLE OF INVENTION: Polypeptides and Polynucleotides  
 ; FILE REFERENCE: 21272-021 (HYS-7)  
 ; CURRENT APPLICATION NUMBER: PCT/US01/02455  
 ; CURRENT FILING DATE: 2001-01-25  
 ; PRIOR APPLICATION NUMBER: US 09/563,786

PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: US 09/491,404  
PRIOR FILING DATE: 2000-01-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 1  
LENGTH: 426  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, G, or C  
PCT-US01-02455-1

Query Match 100.0%; Score 384; DB 1; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCAATGA 60  
DB 19 ATGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCAATGA 78  
QY 61 ATATTTATGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAATGATGAGTGTGCTATACT 120  
DB 79 ATATTTATGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAATGATGAGTGTGCTATACT 138  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 180  
DB 139 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 198  
QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 240  
DB 199 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 258  
QY 241 TTTTGGGCTGCGAGTGTATGTTATGTTGATGCCAGGACAGATGAGTGTGGSTTATTTTC 300  
DB 259 TTTTGGGCTGCGAGTGTATGTTATGTTGATGCCAGGACAGATGAGTGTGGSTTATTTTC 318  
QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 360  
DB 319 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 378  
QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
DB 379 ACGGATATTGACTTCTTCTCGGAG 402

RESULT 6  
PCT-US01-02455-1  
Sequence 1, Application PC/TUS0102455  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc.  
APPLICANT: Mize, Nancy K  
APPLICANT: Boyle, Bryan J  
APPLICANT: Ford, John E  
APPLICANT: Arterburn, Matthew C  
APPLICANT: Tang, Y Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Drmanac, Radoje T  
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
FILE OF INVENTION: Polypeptides and Polynucleotides  
FILE REFERENCE: 21272-021 (HYS-7)  
CURRENT APPLICATION NUMBER: PCT/US01/02455  
CURRENT FILING DATE: 2001-01-25  
PRIOR APPLICATION NUMBER: US 09/563,786  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: US 09/491,404  
PRIOR FILING DATE: 2000-01-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patent in version 3.0  
SEQ ID NO 1  
LENGTH: 426

TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, G, or C  
PCT-US01-02455-1

Query Match 100.0%; Score 384; DB 2; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCAATGA 60  
DB 19 ATGCAAGAATATTGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCAATGA 78  
QY 61 ATATTTATGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAATGATGAGTGTGCTATACT 120  
DB 79 ATATTTATGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAATGATGAGTGTGCTATACT 138  
QY 121 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 180  
DB 139 ATTTCTCTGGCTAGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCATTACGTT 198  
QY 181 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 240  
DB 199 AAAAAAGGCGACAGATCTATGTACTCAAGCTGTGTAAGAAATGAGCTGGAGAA 258  
QY 241 TTTTGGGCTGCGAGTGTATGTTATGTTGATGCCAGGACAGATGAGTGTGGSTTATTTTC 300  
DB 259 TTTTGGGCTGCGAGTGTATGTTATGTTGATGCCAGGACAGATGAGTGTGGSTTATTTTC 318  
QY 301 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 360  
DB 319 CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCACC 378  
QY 361 ACGGATATTGACTTCTTCTCGGAG 384  
DB 379 ACGGATATTGACTTCTTCTCGGAG 402

RESULT 7  
US-09-528-409-107188  
Sequence 107188, Application US/09528409  
GENERAL INFORMATION:  
APPLICANT: Drmanac, Radoje T.  
APPLICANT: Labat, Ivan  
APPLICANT: Stache-Crain, Birgit  
APPLICANT: Dickson, Mark  
APPLICANT: Jones, Lee W.  
TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
FILE REFERENCE: 774  
CURRENT APPLICATION NUMBER: US/09/528,409  
CURRENT FILING DATE: 2000-03-17  
PRIOR APPLICATION NUMBER: 60/125,453  
PRIOR FILING DATE: 1999-03-19  
NUMBER OF SEQ ID NOS: 116231  
SOFTWARE: Hy-patent.pl Version 3.1  
SEQ ID NO 107188  
LENGTH: 426  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, C or G  
US-09-528-409-107188

Query Match 100.0%; Score 384; DB 22; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



1	ATGGCAAGAAATATTGTTACTTTTCTCCCGGGCTTGTGGCTGTATGTGCTGTGATGGA	60
	QY	
19	ATGGCAAGAAATATTGTTACTTTTCTCCCGGGCTTGTGGCTGTATGTGCTGTGATGGA	78
	Db	
61	ATATTATTGGACCGCTAGCTTCCAAGAAGCTGTGCGAGATCATCAGTGTGCTATACT	120
	QY	
79	ATATTATTGGACCGCTAGCTTCCAAGAAGCTGTGCGAGATCATCAGTGTGCTATACT	138
	Db	
121	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACCTGTAGATTCATTAACT	180
	QY	
139	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACCTGTAGATTCATTAACT	198
	Db	
181	AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCTGGAGAA	240
	QY	
199	AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCTGGAGAA	258
	Db	
241	TTTTTGGGCTGGCAGTGTTATGTGTATGGTGGCCAGACAGATGGAGTCTGGGGTATTTC	300
	QY	
259	TTTTTGGGCTGGCAGTGTTATGTGTATGGTGGCCAGACAGATGGAGTCTGGGGTATTTC	318
	Db	
301	CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCACAC	360
	QY	
319	CCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCACAC	378
	Db	
361	ACGGATATTGACTTCTTCTGCGAG	384
	QY	
379	ACGGATATTGACTTCTTCTGCGAG	402
	Db	

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RESULT 8
US-09-563-786A-1
; Sequence 1, Application US/09563786A
; GENERAL INFORMATION:
; APPLICANT: Mize, Nancy K
; APPLICANT: Boyle, Bryan J
; APPLICANT: Ford, John E
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like
; TITLE OF INVENTION: Polypeptides and Polynucleotides
; FILE REFERENCE: HYS-7
; CURRENT APPLICATION NUMBER: US/09/563.786A
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(426)
; OTHER INFORMATION: n = A, T, G, or C
US-09-563-786A-1

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	Query Match	100.0%;	Score 384;	DB 25;	Length 426;
	Best Local Similarity	100.0%;	Pred. No. 1.2e-107;		
	Matches 384;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGCAAGAAATATTGTTACTTTTCTCCCGGCTTTGTGGCTGTATGTGCTGTGCATGGA	60		
Db	19	ATGGCAAGAAATATTGTTACTTTTCTCCCGGCTTTGTGGCTGTATGTGCTGTGCATGGA	78		
QY	61	ATATTATTGGACCGCTCTAGCTTCCAGAAGCTCTGTGGCAGATGATGAGTGTCTTACT	120		
Db	79	ATATTATTGGACCGCTCTAGCTTCCAGAAGCTCTGTGGCAGATGATGAGTGTCTTACT	138		
QY	121	ATTTCCTGGCTAGTGTCCAAGAGATTATTAATGCCCGGACTGTAGATTCAATTAAGCTT	180		

139	ATTTCTCTGGCTAGTGCTCAAGAGAGATTATAATGCCCGGACTGTGAGATTCATTAAACGTT	190
181	AAAAAAGGGCAGCAGACTCTATGTGTACTCAAAAGCTGGTAAAAAGAAATATGGAGCTGGAGAA	240
199	AAAAAAGGGCAGCAGACTCTATGTGTACTCAAAAGCTGGTAAAAAGAAATATGGAGCTGGAGAA	258
241	TTTTTGGGCTGGCAGTGTGTTATGGTGTATGATGCCAGGACGAGATGGGAGTCTGTGGTTATTTC	300
259	TTTTTGGGCTGGCAGTGTGTTATGGTGTATGATGCCAGGACGAGATGGGAGTCTGTGGTTATTTC	318
301	CCCAGGAACCTTGGTCAAGGAACAGCGCTGTGTACCAAGAGCTACCAAGGAAGTCTCCCAACC	360
319	CCCAGGAACCTTGGTCAAGGAACAGCGCTGTGTACCAAGAGCTACCAAGGAAGTCTCCCAACC	378
361	ACGGATATTGACTCTTCTTCGCGAG	384
379	ACGGATATTGACTCTTCTTCGCGAG	402

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RESULT 9
US-09-933-524-107188
; Sequence 107188, Application US/099333524
; GENERAL INFORMATION:
; APPLICANT: Drmanac, Radoje T.
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Dickson, Mark
; APPLICANT: Jones, Lee W.
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 774
; CURRENT APPLICATION NUMBER: US/09/933,524
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 09/528,409
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 116231
; SOFTWARE: Hy-patent.pl Version 3.1
; SEQ ID NO 107188
; LENGTH: 426
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(426)
; OTHER INFORMATION: n = A,T,C or G
US-09-933-524-107188

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Query Match	100.0%	Score 384;	DB 39;	Length 426;
Best Local Similarity	100.0%;	Pred. No. 1.2e-107;		
Matches 384;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGGCAGAAATATTGTTACTTTTCCCTCCCGGGCTCTGTGGCTGTATGTGCTGTGTCATGGA	60	
Db	19	ATGGCAGAAATATTGTTACTTTTCCCTCCCGGGCTCTGTGGCTGTATGTGCTGTGTCATGGA	78	
QY	61	ATATTATGAGACCGCTTAGCTTCCAGAGAGCTCTGTGCGAGATGATAGTGTCCTATACT	120	
Db	79	ATATTATGAGACCGCTTAGCTTCCAGAGAGCTCTGTGCGAGATGATAGTGTCCTATACT	138	
QY	121	ATTTCTCTGGCTAGTGCTCAAGAAGATTATATGCCCGGAGCTGTAGATTCAATTAACGTT	180	
Db	139	ATTTCTCTGGCTAGTGCTCAAGAAGATTATATGCCCGGAGCTGTAGATTCAATTAACGTT	198	
QY	181	AAAAAAGGCGACGAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAAATGGAGCTGGAGAA	240	
Db	199	AAAAAAGGCGACGAGATCTATGTGTACTCAAAAGCTGTGTAAAGAAAAATGGAGCTGGAGAA	258	
QY	241	TTTTTGGGCTGCGAGTGTTATGTGTATGGCCAGGACGAGATGGGAGTGTGGTGTATTTC	300	
Db	259	TTTTTGGGCTGCGAGTGTTATGTGTATGGCCAGGACGAGATGGGAGTGTGGTGTATTTC	318	
QY	301	CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCGAAGACTTACCAAGGAAGTTCGCCACC	360	

Db 319 CCCAGGAATCTGCTCAAGAACAGCGTGTACACGAGAGCTACCAAGAGATTCCACC 378  
Qy 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 10

US-09-933-524A-107188  
; Sequence 107188, Application US/09933524A  
; GENERAL INFORMATION:  
; APPLICANT: Drmanac, Radoje T.  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Dickson, Mark  
; APPLICANT: Jones, Lee W.  
; TITLE OF INVENTION: Novel Nucleic Acid Sequences Obtained  
; FILE REFERENCE: 774  
; CURRENT APPLICATION NUMBER: US/09/933,524A  
; PRIOR FILING DATE: 2001-08-20  
; PRIOR APPLICATION NUMBER: 09/528,409  
; PRIOR FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 116231  
; SOFTWARE: Hy-patent.pl Version 3.1  
; SEQ ID NO 107188  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(426)  
; OTHER INFORMATION: n = A, T, C or G  
US-09-933-524A-107188

Query Match 100.0%; Score 384; DB 39; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 60  
Db 19 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 78  
Qy 61 ATATTATGACCGCTAGCTCTCAAGAAGCTCTGTCAGATGATGAGTGTCTTACT 120  
Db 79 ATATTATGACCGCTAGCTCTCAAGAAGCTCTGTCAGATGATGAGTGTCTTACT 138  
Qy 121 ATTTCTCTGGCTAGTCTCAAGAAGATTAATATGCCCCGGACTGTAGATTCAATACGTT 180  
Db 139 ATTTCTCTGGCTAGTCTCAAGAAGATTAATATGCCCCGGACTGTAGATTCAATACGTT 198  
Qy 181 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 240  
Db 199 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 258  
Qy 241 TTTTGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 300  
Db 259 TTTTGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 318  
Qy 301 CCCAGGAATCTGTCAAGGAAACAGCGTGTATCCAGGAGCTTACCAAGGAAGTTCACCACC 360  
Db 319 CCCAGGAATCTGTCAAGGAAACAGCGTGTATCCAGGAGCTTACCAAGGAAGTTCACCACC 378  
Qy 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 11

US-10-216-038-1  
; Sequence 1, Application US/10216038  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K

; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjastaad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
; TITLE OF INVENTION: Polypeptides and Polynucleotides  
; FILE REFERENCE: HYS-7CIP  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; PRIOR FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (426)...(426)  
; OTHER INFORMATION: n = A, T, G, or C  
US-10-216-038-1

Query Match 100.0%; Score 384; DB 48; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 60  
Db 19 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTTGGCTGTATGCTGTGATGGA 78  
Qy 61 ATATTATGACCGCTAGCTCTCAAGAAGCTCTGTCAGATGATGAGTGTCTTACT 120  
Db 79 ATATTATGACCGCTAGCTCTCAAGAAGCTCTGTCAGATGATGAGTGTCTTACT 138  
Qy 121 ATTTCTCTGGCTAGTCTCAAGAAGATTAATATGCCCCGGACTGTAGATTCAATACGTT 180  
Db 139 ATTTCTCTGGCTAGTCTCAAGAAGATTAATATGCCCCGGACTGTAGATTCAATACGTT 198  
Qy 181 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 240  
Db 199 AAAAAAGGCGACAGATCTATGTACTCAAAAGCTGGTAAAGAAAATGGAGCTGGAGAA 258  
Qy 241 TTTTGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 300  
Db 259 TTTTGGCTGGCAGTGTATGGTGTATGGCCAGGACGAGTCTGGGTATTTC 318  
Qy 301 CCCAGGAATCTGTCAAGGAAACAGCGTGTATCCAGGAGCTTACCAAGGAAGTTCACCACC 360  
Db 319 CCCAGGAATCTGTCAAGGAAACAGCGTGTATCCAGGAGCTTACCAAGGAAGTTCACCACC 378  
Qy 361 ACGGATATTGACTTCTTCTGCGAG 384  
Db 379 ACGGATATTGACTTCTTCTGCGAG 402

## RESULT 12

US-10-311-830-1  
; Sequence 1, Application US/10311830  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua

APPLICANT: Drmanac, Radoje T  
TITLE OF INVENTION: Methods and Materials Relating to Novel Growth Regulatory-like  
TITLE OF INVENTION: Polypeptides and Polynucleotides  
FILE REFERENCE: 21272-021 (HVS-7)  
CURRENT APPLICATION NUMBER: US/10/311,830  
CURRENT FILING DATE: 2002-12-17  
PRIOR APPLICATION NUMBER: US 09/563,796  
PRIOR FILING DATE: 2000-05-02  
PRIOR APPLICATION NUMBER: US 09/491,404  
PRIOR FILING DATE: 2000-01-25  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 426  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)-(426)  
OTHER INFORMATION: n = A, T, G, or C  
US-10-311-830-1

Query Match 100.0%; Score 384; DB 50; Length 426;  
Best Local Similarity 100.0%; Pred. No. 1.2e-107;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGCAAGATATTTGTTACTTTTCCCTCCCGGTCTTGTGGCTGTATGCTGTGCTGATGGA	60
DB	19	ATGCAAGATATTTGTTACTTTTCCCTCCCGGTCTTGTGGCTGTATGCTGTGCTGATGGA	78
QY	61	ATATTTATGACCGTCTAGCTTCCAGAGCTCTGCGAGATGATGAGTGTCTTACT	120
DB	79	ATATTTATGACCGTCTAGCTTCCAGAGCTCTGCGAGATGATGAGTGTCTTACT	138
QY	121	ATTCTCTGCTGTAGTCTCAAGAGATTTATATGCCCGGACTGTAGATTCATTAACTT	180
DB	139	ATTCTCTGCTGTAGTCTCAAGAGATTTATATGCCCGGACTGTAGATTCATTAACTT	198
QY	181	AAAAAGGACAGATCTATGTCTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA	240
DB	199	AAAAAGGACAGATCTATGTCTCAAGAGCTGTAAAGAAATGGAGCTGGAGAA	258
QY	241	TTTGGCTGGAGTGTATATGTATGTCAGGACGAGATGCGGTGTTATTC	300
DB	259	TTTGGCTGGAGTGTATATGTATGTCAGGACGAGATGCGGTGTTATTC	318
QY	301	CCAGGAACTTGTCTCAAGACAGCTGTATCCAGGAGCTACCAAGAGTCCACC	360
DB	319	CCAGGAACTTGTCTCAAGACAGCTGTATCCAGGAGCTACCAAGAGTCCACC	378
QY	361	ACGGATATTGACTTCTTCTCGAG	384
DB	379	ACGGATATTGACTTCTTCTCGAG	402

## RESULT 13

US-10-081-056-359  
Sequence 359, Application US/10081056  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.

APPLICANT: Williams, P. Mickey  
APPLICANT: Ye, Weilan  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS  
FILE REFERENCE: P3235P1C1  
CURRENT APPLICATION NUMBER: US/10/081,056  
CURRENT FILING DATE: 2002-02-20  
PRIOR APPLICATION NUMBER: PCT/US01/21735  
PRIOR FILING DATE: 2001-07-09  
PRIOR APPLICATION NUMBER: US 60/219,556  
PRIOR FILING DATE: 2000-07-20  
PRIOR APPLICATION NUMBER: US 60/220,624  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: US 60/220,664  
PRIOR FILING DATE: 2000-07-25  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: 2000-07-28  
PRIOR APPLICATION NUMBER: US 60/222,695  
PRIOR FILING DATE: 2000-08-02  
PRIOR APPLICATION NUMBER: US 09/643,657  
PRIOR FILING DATE: 2000-08-17  
PRIOR APPLICATION NUMBER: PCT/US00/23522  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: PCT/US00/23328  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/230,978  
PRIOR FILING DATE: 2000-09-07  
PRIOR APPLICATION NUMBER: US 60/000,000  
PRIOR FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: US 09/664,610  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 09/665,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/242,922  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 09/709,238  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30952  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: PCT/US00/30873  
PRIOR FILING DATE: 2000-11-10  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: 2000-12-01  
PRIOR APPLICATION NUMBER: US 09/747,259  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/34956  
PRIOR FILING DATE: 2000-12-20  
PRIOR APPLICATION NUMBER: US 09/767,609  
PRIOR FILING DATE: 2001-01-22  
PRIOR APPLICATION NUMBER: US 09/796,498  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: 2001-02-28  
PRIOR APPLICATION NUMBER: PCT/US01/06666  
PRIOR FILING DATE: 2001-03-01  
PRIOR APPLICATION NUMBER: US 09/802,706  
PRIOR FILING DATE: 2001-03-09  
PRIOR APPLICATION NUMBER: US 09/808,689  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: US 09/816,744  
PRIOR FILING DATE: 2001-03-22  
PRIOR APPLICATION NUMBER: US 09/828,366  
PRIOR FILING DATE: 2001-04-05  
PRIOR APPLICATION NUMBER: US 09/854,208  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/854,280  
PRIOR FILING DATE: 2001-05-10  
PRIOR APPLICATION NUMBER: US 09/866,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: US 09/866,034  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: PCT/US01/17092  
PRIOR FILING DATE: 2001-05-25

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; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 359
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homosapiens
; US-10-081-056-359

Query Match      100.0%; Score 384; DB 45; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.3e-107;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGAAGATATTTACTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 60
Db 38 ATGCGAAGATATTTACTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 97
Qy 61 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120
Db 98 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
Qy 121 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGTTCATTAACGTT 180
Db 158 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGTTCATTAACGTT 217
Qy 181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAG 240
Db 218 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAG 277
Qy 241 TTTTGGGCTGGCAGTGTATGTATGTCGACGAGAGAGATGCGAGTGTGGGTTATTTC 300
Db 278 TTTTGGGCTGGCAGTGTATGTATGTCGACGAGAGAGATGCGAGTGTGGGTTATTTC 337
Qy 301 CCAGAGAACTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 338 CCAGAGAACTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 397
Qy 361 ACGGATATTGACTTCTTCTCGGAG 384
Db 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 15
US-10-216-159A-71
; Sequence 71, Application US/10216159A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 359
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homosapiens
; US-10-081-056-359

Query Match      100.0%; Score 384; DB 45; Length 521;
Best Local Similarity 100.0%; Pred. No. 1.3e-107;
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCGAAGATATTTACTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 60
Db 38 ATGCGAAGATATTTACTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGATGCTGATGGA 97
Qy 61 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 120
Db 98 ATATTTATGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
Qy 121 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGTTCATTAACGTT 180
Db 158 ATTTCTCTGCTAGTCTCAAGAGATTTATATGCCCCGGACTGTAGTTCATTAACGTT 217
Qy 181 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAG 240
Db 218 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGAGCTGTGTAAGAGAGAGAGAGAGAGAG 277
Qy 241 TTTTGGGCTGGCAGTGTATGTATGTCGACGAGAGAGATGCGAGTGTGGGTTATTTC 300
Db 278 TTTTGGGCTGGCAGTGTATGTATGTCGACGAGAGAGATGCGAGTGTGGGTTATTTC 337
Qy 301 CCAGAGAACTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 338 CCAGAGAACTTGTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 397
Qy 361 ACGGATATTGACTTCTTCTCGGAG 384
Db 398 ACGGATATTGACTTCTTCTCGGAG 421

RESULT 14
US-10-119-480-71
; Sequence 71, Application US/10119480
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C1
; CURRENT APPLICATION NUMBER: US/10/119,480
; CURRENT FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 246
; PRIOR Application removed - See File Wrapper or Palm
; SEQ ID NO 71
; LENGTH: 521

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; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-216-159A-71

Query Match 100.0%; Score 384; DB 48; Length 521;  
Best Local Similarity 100.0%; Pred. No. 1.3e-107; Indels 0; Gaps 0;  
Matches 384; Conservative 0; Mismatches 0

Qy	1	ATGGCAAGATATTTGTTACTTTCTCCCGGGTCTTTGGCTGTATGTGCTGTGATGGA	60
Db	38	ATGGCAAGATATTTGTTACTTTCTCCCGGGTCTTTGGCTGTATGTGCTGTGATGGA	97
Qy	61	ATATTTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTACT	120
Db	98	ATATTTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTACT	157
Qy	121	ATTCTCTGCTAGTCTCAAGAGATTTATATGCCCGGACTGTAGATTCAATTAACGTT	180
Db	158	ATTCTCTGCTAGTCTCAAGAGATTTATATGCCCGGACTGTAGATTCAATTAACGTT	217
Qy	181	AAAAAGGGCAGAGATCTATGTGTAATCAAGCTGGTAAAAAGAAATGGAGCTGAGAA	240
Db	218	AAAAAGGGCAGAGATCTATGTGTAATCAAGCTGGTAAAAAGAAATGGAGCTGAGAA	277
Qy	241	TTTGGGCTGGCAGTCTTTATGTGATGGCCAGGACGATGGAGTCGTGGGTTATTTC	300
Db	278	TTTGGGCTGGCAGTCTTTATGTGATGGCCAGGACGATGGAGTCGTGGGTTATTTC	337
Qy	301	CCAGGAACCTTGTCAAGGAACAGCGTGTATCCAGGAAGCTACCAAGGAAGTCCACAC	360
Db	338	CCAGGAACCTTGTCAAGGAACAGCGTGTATCCAGGAAGCTACCAAGGAAGTCCACAC	397
Qy	361	ACGGATATTGACTTCTTCTCGGAG	384
Db	398	ACGGATATTGACTTCTTCTCGGAG	421

Search completed: December 30, 2003, 09:01:32  
Job time : 1836.61 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:34:27 : Search time 31.014 Seconds  
(without alignments)  
5464.987 Million cell updates/sec

Title: US-10-019-455A-4

Perfect score: 384

Sequence: 1 atgggaagaattattgtact.....attatgactctttctgag 384

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 569979 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/prodata/2/ina/FACTUS\_COMB.seq: \*  
6: /cgn2\_6/prodata/2/ina/BACKFILES.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	64.8	16.9	459	1	US-08-578-649-1
2	63.2	16.5	581	1	US-08-578-649-4
3	57.4	14.9	330	1	US-08-578-649-18
4	54.2	14.1	205	1	US-08-578-649-8
5	40.4	10.5	596	1	US-08-578-649-24
6	40.4	10.5	3565	1	US-08-578-649-3
7	34	8.9	7218	1	US-08-232-463-14
8	33.6	8.8	1136	3	US-08-860-820-1
9	33.6	8.8	1929	3	US-09-359-161-4
10	33.6	8.8	2159	3	US-08-286-870A-7
11	32.8	8.5	6501	4	US-09-767-515-1
12	32.8	8.5	6501	4	US-09-767-515-2
13	32.2	8.4	202001	4	US-09-734-674-3
14	31.4	8.2	1944	4	US-09-252-991A-889
15	31.2	8.1	10357	4	US-08-961-527-191
16	31.2	8.1	4403765	3	US-09-103-840A-2
17	31.2	8.1	4411529	3	US-09-103-840A-1
18	30.8	8.0	1736	3	US-09-360-197-13
19	30.4	7.9	289	3	US-09-007-005-17
20	30.4	7.9	289	3	US-09-244-796-17
21	29.8	7.8	1830121	4	US-09-557-884-1
22	29.8	7.8	1830121	4	US-09-643-990A-1
23	29.6	7.7	1000	3	US-09-018-584A-38
24	29.6	7.7	319608	4	US-09-539-333D-1
25	29.6	7.7	319608	4	US-09-679-409-1
26	29.4	7.7	1497	4	US-09-220-132-94
27	29.4	7.7	2718	4	US-09-651-656-14

## ALIGNMENTS

### RESULT 1

US-08-578-649-1  
; Sequence 1, Application US/08578649

; Patent No. 5770366

; GENERAL INFORMATION:

; APPLICANT: Ulrich Bogdan

; APPLICANT: Reinhard Buttner

; APPLICANT: Brigitte Kaluza

; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/578,649

; FILING DATE: 29-July-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 43 24 247.2

; FILING DATE: 20-July-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Andrew L. Tiajolloff

; REGISTRATION NUMBER: 31,575

; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 459 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 40..432

; FEATURE:

; NAME/KEY: sig\_peptide

; LOCATION: 40..111

; FEATURE:

Sequence 14, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 3486, Ap  
Sequence 161, App  
Sequence 1, Appli  
Sequence 1171, Ap  
Sequence 10933, A  
Sequence 65, Appli  
Sequence 1, Appli  
Sequence 1, Appli  
Sequence 116, App  
Sequence 94, Appl  
Sequence 2654, Ap  
Sequence 1103, Ap  
Sequence 4, Appli

28 29.4 7.7 2718 4 US-09-650-855-14  
C 29 29.2 7.6 688 3 US-09-027-381-1  
C 30 29.2 7.6 688 4 US-09-477-071-1  
31 29.2 7.6 876 4 US-09-107-532A-3486  
32 29.2 7.6 1718 4 US-09-620-312D-161  
33 29.2 7.6 3101 2 US-08-868-786-1  
34 29.2 7.6 3489 4 US-09-134-001C-1171  
C 35 29.2 7.6 112132 4 US-09-741-150-3  
C 36 29 7.6 810 4 US-09-252-991A-10933  
37 29 7.6 2102 3 US-08-235-836C-65  
38 29 7.6 2258 1 US-07-720-589-1  
39 29 7.6 2258 2 US-08-785-190-1  
40 29 7.6 2258 5 PCT-US92-05539-1  
C 41 29 7.6 45175 4 US-09-453-702B-116  
42 28.8 7.5 1497 4 US-09-220-132-94  
43 28.8 7.5 1941 4 US-09-107-532A-2654  
44 28.6 7.4 849 4 US-09-252-991A-1103  
C 45 28.6 7.4 1518 2 US-08-929-501-4

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; NAME/KEY: mat_peptide
; LOCATION: 112..432
US-08-578-649-1

Query Match      16.9%; Score 64.8; DB 1; Length 459;
Best Local Similarity 55.6%; Pred. No. 2.3e-11;
Matches 170; Conservative 0; Mismatches 127; Indels 9; Gaps 2;

QY 23 TCCTCCGGGCTCTGTGGCTGTATGTGCTGTGATGGAATATTTATGGACCCCTAGCTT 82
Db 74 TCCTGTCTGTCTGCTCTTCGCGACCTGGTGTCAAGGGGTGTCCTATGCCCCAAGCTGGCTG 133
QY 83 CCAGAGAGCTGTGCGAGATGATGAGTGTCTATATCTATCTCTGCTAGTGTCTCAAG 142
Db 134 ACCGGAAGCTGTGTGCGGACCAAGATGACACACCTATCTCCATGGCTGTGGCCCTTC 193
QY 143 AAGATTATAATGCCCGGACTGTAGATTCATTAAAGCTTTAAAGGCGGACGAGATCTATG 202
Db 194 AGGACTACATGGCCCCCGGACTGGCGGATTCCTGACCATTCACCGGGGCCAAGTGGTATG 253
QY 203 TGTACTCAAGCTGTAAAGAAATGGAGCTGGAGATTTTGGGCTGGCAGTGTATTG 262
Db 254 TCCTCTCAAGCTG-----AAGGGCCGTGGCGGCTCTTCGGGAGGAGGCTTCAGG 307
QY 263 GTGATGCGCAGGACGAGATGGAG---TCGTGGGTATTTCCTCCAGAACTTGGCTCAAGG 319
Db 308 GAGATTACTATGAGATCTGGCTGCTCGCTGGGCTATTTCCTCCAGTAGCATTTGCCGAG 367
QY 320 AACAGC 325
Db 368 AGGACC 373

```

## RESULT 2

```

US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Flajoloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO. 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 110..499
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 110..178
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 179..499
US-08-578-649-4

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Query Match 16.5%; Score 63.2; DB 1; Length 581;

```

Best Local Similarity 54.3%; Pred. No. 8.3e-11;
Matches 175; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

QY 66 TATGGACCGCTAGCTTCCAAAGAGCTCTGTGCGAGATGATGAGTGTCTATCTATTTTC 125
Db 184 TATGCCCAAGCTGGCTGACTGGAAGCTGTGTGGGACGAGGAATGCGACCATCTATCTC 243
QY 126 TCTGGCTAGTGTCAAGAGATTATATGCCCGGAGCTGTAGATTTCATTAAAGTTAAAAA 185
Db 244 CATGGCTGTGGCCCTCCAGACTACGTGGCCCTGTATGCCGCTCTTGACTATATATAG 303
QY 186 AGGCGACGAGATCTATGTGTATCAAGAGCTGTGTAAGAAATGGAGCTGGAGAAATTTTG 245
Db 304 GGCCAAAGTGGTGTATGTCTCTTCCAAAGTTG-----AAGGGCCGTGGGCGCTTTCTG 357
QY 246 GGCTGGCAGTGTATTATGGTGTATGGCTGGCCAGGACGAGATGGGAG--TCGTGGGTATTTC 302
Db 358 GGGAGGCGAGTGTTCAGGAGGTTACTATGGAGACCTGGCAGCCGCTGGGCTATTTC 417
QY 303 CAGGAACCTTGTCAAGGACAGCGTGTGTACAGGAGCTGTGTACAGGAGCTTACCAAGAAAGTTCCCAACCAC 362
Db 418 CAGTAGCATTTGTCCGGGAGGACCTGAACTCGAACCTGGCCAAATTTGATATGAAGACCGA 477
QY 363 GGATATTGACTTCTTCTGGCGAG 384
Db 478 TCAATGGGATTTCTACTGCCAG 499

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## RESULT 3

```

US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Flajoloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO. 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid

```

```

RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994

```



```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(40..111, 40..166, 214..347, 393..503, 549
; LOCATION: ..569)
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: exon
; LOCATION: 40..166
; FEATURE:
; NAME/KEY: exon
; LOCATION: 214..347
; FEATURE:
; NAME/KEY: exon
; LOCATION: 393..503
; FEATURE:
; NAME/KEY: exon
; LOCATION: 549..569
; NAME/KEY:
; LOCATION: one-of(194, 369, 527)
; OTHER INFORMATION: /note= "N in positions 194, 369
; OTHER INFORMATION: and 527 denotes an indefinite number and sequence
; OTHER INFORMATION: of nucleotides "
US-08-578-649-24

Query Match 10.5%; Score 40.4; DB 1; Length 596;
Best Local Similarity 63.3%; Pred. No. 0.0019;
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 119 CTATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACG 178
|||||
Db 217 CTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCGGACTGCCGATTCTTGACCA 276
|||||

QY 179 TTAATAAAGGCGACGACATCTATGTCTACTCAAGCTG 216
|||||
Db 277 TTACCGGGCCCAAGTGTGTATGTCTTCTCCAAGCTG 314
|||||

RESULT 6
US-08-578-649-3
; Sequence 3, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Feife & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York

Query Match 10.5%; Score 40.4; DB 1; Length 596;
Best Local Similarity 63.3%; Pred. No. 0.0019;
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 119 CTATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACG 178
|||||
Db 217 CTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCGGACTGCCGATTCTTGACCA 276
|||||

QY 179 TTAATAAAGGCGACGACATCTATGTCTACTCAAGCTG 216
|||||
Db 277 TTACCGGGCCCAAGTGTGTATGTCTTCTCCAAGCTG 314
|||||

RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

```

```

; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 MB storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3565 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 1378..1449
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1378..1504
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1586..1719
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2804..2914
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3232..3252
; FEATURE:
; NAME/KEY:
; LOCATION: one-of(2216)
; OTHER INFORMATION: /note= "N in position 2216
; OTHER INFORMATION: denotes an indefinite number and sequence of
; OTHER INFORMATION: nucleotides"
US-08-578-649-3

Query Match 10.5%; Score 40.4; DB 1; Length 3565;
Best Local Similarity 63.3%; Pred. No. 0.0047;
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 119 CTATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACG 178
|||||
Db 1589 CTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCGGACTGCCGATTCTTGACCA 1648
|||||

QY 179 TTAATAAAGGCGACGACATCTATGTCTACTCAAGCTG 216
|||||
Db 1649 TTACCGGGCCCAAGTGTGTATGTCTTCTCCAAGCTG 1686
|||||

RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

```

NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMUI  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pt-F15  
US-08-232-463-14

[illegible]

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RESULT 8
US-08-860-820-1
; Sequence 1, Application US/08860820
; Patent No. 6245967
; GENERAL INFORMATION:
; APPLICANT: Sonnewald, Uwe
; APPLICANT: Kossmann, Jens
; APPLICANT: Bowien, Eotro
; TITLE OF INVENTION: PROCESS AND DNA MOLECULES FOR INCREASING
; TITLE OF INVENTION: THE PHOTOSYNTHESIS RATE IN PLANTS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,820  
FILING DATE: 04-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19502053.7  
FILING DATE: 13-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
LENGTH: 1136 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1121  
US-08-860-820-1

	Query Match	8.8%	Score 33.6	DB 3	Length 1136
	Best Local Similarity	56.2%	Pred. No. 0.42		
	Matches 63	Conservative 0	Mismatches 49	Indels 0	Gaps 0
Qy	226	AATGAGCTGAGAAATTTTCGGCTGCACGTGTTTATGTTGATGGCCAGACAGATGGGA	285		
Db	204	AATCAAGCCGAGAGAAGCAGGGGGCGTCAACGTCCAGGGGAAATCCAGCAGAAGCTGCAC	263		
Qy	286	GTCTGGGTGTTATTTCCCCAGGAAC TTGGTCAAGAAACAGCGTGTGTACCCAGG	337		
Db	264	GTGCTGAGCAATACACACTCTTCGCGCGTCAACAGTGGCGGGTACTCTGG	315		

RESULT 9  
US-09/359-161-4/c  
; Sequence 4, Application US/09359161A  
; Patent No. 6342656  
; GENERAL INFORMATION:  
; APPLICANT: Bradford, Kent J.  
; APPLICANT: Bahal, Peetambar  
; APPLICANT: Yang, Hong  
; APPLICANT: Cooley, Michael  
; APPLICANT: Downie, Bruce  
; APPLICANT: Gee, Oliver  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses  
; FILE REFERENCE: 023070-095900US  
; CURRENT APPLICATION NUMBER: US/09/359,161A  
; CURRENT FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1929

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; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast
; OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1)
US-09-359-161-4

Query Match      8.8%; Score 33.6; DB 4; Length 1929;
Best Local Similarity 52.9%; Pred. No. 0.54;
Matches 72; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 138 TCAAGAGATATATATGCGCGGACTGAGATTCATTAACTTAAAAAGGCGAGAGAT 197
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1793 TCTGTAAGTAGACTAGTGAAGTAACTGAAATTCATAAACCCTTAAAAAGAGAGTGAGCT 1734
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 198 CPTATCTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCTGGAGAAATTTTGGGCTGGCAGTGT 257
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1733 AGATCTCTAGGATCAAAAAGAAAAAGAGATTTGCTAGGCACCTCTGACCAAGCAGGCT 1674

QY 258 TTATGGTATGCCAG 273
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1673 GGAATTTGTTAACAAG 1658
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

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RESULT 10
US-08-286-870A-7/c
; Sequence 7, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DABY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2159
US-08-286-870A-7

Query Match      8.8%; Score 33.6; DB 3; Length 2159;
Best Local Similarity 52.1%; Pred. No. 0.57;
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 228 TGGAGCTGGAGAAATTTGGGCTGGCAGTGTATTATGGTATGCCAGGACGAGATGGGAGT 287
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2002 TGTGCTGTGTAACAGGCGGTGACCTTCTCTGGCCCTTCTCGAAGTCGTACTCGGCT 1943
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 288 CBTGGGTATTTTCCCAGGAACTTGGTCAAGGAAACAGCGTGTGTACCAAGGAGCTTACCAA 347
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1942 CGTAGTGCACCTCCACGGGACGAACTCGATGCGGTGATGACACCTCGTTGCCGCTGC 1883
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 348 GGAAGTTCACACGAGATTTGA 371
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1882 TGAAGTTCACGGCGGATGGTGA 1859
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RESULT 11
US-09-767-515-1
; Sequence 1, Application US/09767515
; Patent No. 6586207
; GENERAL INFORMATION:
; APPLICANT: Tirrell, David A
; APPLICANT: Krick, Kristi L
; TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for
; TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
; TITLE OF INVENTION: Amino Acid Analogues
; FILE REFERENCE: 30431.60S01
; CURRENT APPLICATION NUMBER: US/09/767,515
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/207,627
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PQE15-MRS
US-09-767-515-1

```

```

Query Match      8.5%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.8;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 234 TGGAGAAATTTGGGCTGGCAGTGTATTATGGTATGCCAGGACGAGATGGGAGTCTGGG 293
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2259 TGTGAGCGTGGAAAGCCGTGAATTTGGTAAACCGTGCAGAAATCATGGCCCTGGC 2318
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 294 TTATTTCCCAGGAACTTGGTCAAGGAAACAGCGTGTGTACCAAGGAGCTTACCAAGGAAGT 353
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2319 TGATCTGGCTAACCGCTATGCTGAACAGACTCCGTGGGTGGTGGCGAAACAGGAAGG 2378
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 354 TCCC 357
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2379 CCGC 2382
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 12
US-09-767-515-2
; Sequence 2, Application US/09767515
; Patent No. 6586207
; GENERAL INFORMATION:
; APPLICANT: Tirrell, David A
; APPLICANT: Krick, Kristi L
; TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for
; TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing

```

```

; TITLE OF INVENTION: Amino Acid Analogues
; FILE REFERENCE: 30431.6US01
; CURRENT APPLICATION NUMBER: US/09/767,515
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/207,627
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artifi
US-09-767-515-2

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	Query Match	8.5%;	Score 32.8;	DB 4;	Length 6501;
	Best Local Similarity	54.0%;	Pred. No. 1.8;		
	Matches 67;	Conservative 0;	Mismatches 57;	Indels 0;	Gaps 0;
Qy	234	TGGAGATTTTGGGCTGGCAGTGTTTATGFGATGGCCAGACGAGATGGAGTCGTGGG	293		
Db	2259	TGTTGAAGCGTGGGAAGACCGGTGAATTTGGTAAAGCCGTGCGCGAAATCATTGGCGCTGGC	2318		
Qy	294	TTATTTCCCGAGGAACCTTGGTCAAGGAACACAGCGTGTGTACAGGAAGCTACCAAGGAAGT	353		
Db	2319	TGATCTGGCTAACCGCTATGTCGATGAACAGGCTCCGTGGGTGCTGGCGAAACAGGAAGG	2378		
Qy	354	TCCC	357		
Db	2379	CCGC	2382		

```

RESULT 13
US-09-734-674-3
; Sequence 3, Application US/09734674
; Patent No. 6498022
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN
; TITLE OF INVENTION: NUCLEIC ACID
; TITLE OF INVENTION: AND USES THERE
; FILE REFERENCE: CL001018
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Vers
; SEQ ID NO 3
; LENGTH: 202001
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(202001)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-674-3

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	Query Match	8.4%;	Score 32.2;	DB 4;	Length 202001;
	Best local Similarity	49.7%;	Pred. No. 15;		
	Matches 82;	Conservative 0;	Mismatches 83;	Indels 0;	Gaps 0;
Qy	119	CTATTTCTCTGGCTAGTCTCAAGAGATATATATGCCCCGGACTGTAGATTCATTAAACG	178		
Db	183409	CTGAAGCTCAGGAGAGAGCTAAGGCAGAGACGTAGTCCGTGAATCATATTAGCAAGTCTGT	183468		
Qy	179	TTAAAAAGGGCAGCAGACTATGTGTACTCAAAGCTGTAATAAGAAAAATGGAGCTGGAG	238		
Db	183469	GAAGTCNAAGCCATGGGTATGGATGAACATTCCAGGAGAAAGAAAAACAGAGATGAG	183528		
Qy	239	AATTTTGGGCTGGCAGTGTTTTATGGTGATGGCCAGGACGAGATGG	283		
Db	183529	AGTCCAGGAATCCCAATGTTGAGGGCCAAATAAAGGAAGACATTG	183573		

RESULT 14  
US-09-252-991A-889/c  
; Sequence 889, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 889  
; LENGTH: 1944  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-889

	Query Match	8.2%;	Score 31.4;	DB 4;	Length 1944;
	Best Local Similarity	51.8%;	Pred. No. 2.8;		
	Matches	71;	Conservative	0;	Mismatches 66; Indels 0; Gaps 0
Qy	235	GGAGATTTTGGGCTGGCAGTGTTTATCGTCATGGCCAGACACAGATGGAGTCGTGGGT	294		
Db	420	GGGGTAGTTGTAGATGGGCCCATTTGAACCCATGGCCAGCCGAGATCGGGATCGATCAT	361		
Qy	295	TATTTCCCCCAGNACTTGGTCAAGGAACACGGTGTATCCAGGAAGCTACCAAGGAAGTT	354		
Db	360	CGGTGGCCGGAAGCTTCCGCGAGGTCCATGACTTTCAGCCGTCGATCCGAGGGCGGAT	301		
Qy	355	CCACCCACGATATTGA	371		
Db	300	CGGACCTGGGCGTGA	284		

RESULT 15  
US-08-961-527-191/c  
; Sequence 191, Application US/08961527  
; Patent No. 6420135  
; GENERAL INFORMATION:  
; APPLICANT: Charles Kunsch  
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences  
; NUMBER OF SEQUENCES: 391  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/961,527  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brookes, A. Anders  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB340P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 191:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10357 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-961-527-191

Query Match 8.1%; Score 31.2; DB 4; Length 10357;  
Best Local Similarity 55.6%; Pred. No. 7.4;  
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;  
QY 48 TGGTGTGCATGGAATATTATTTGACCGCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGA 107  
Db 1592 TGGTGACCACGAGAAAGTTTGGACGGTCTTGCTGAACAAATTCACITTTTAGAAGATTT 1533  
QY 108 GTGTGTCTACTATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGC 155  
Db 1532 GGGTGTCTCTGCAATTGCAAGTGGGTATTCCCTTTTCAGACCCCTGTTGC 1485

Search completed: December 30, 2003, 06:10:38  
Job time : 41.014 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: December 29, 2003, 22:08:26 ; Search time 1216 Seconds  
(without alignments)  
12918.830 Million cell updates/sec

Title: US-10-019-455A-10  
Perfect score: 384  
Sequence: 1 atggcaaggatattgattct.....attatgactttctgtgaa 384

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

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8: gb\_pl.\*

9: gb\_pr.\*

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11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

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19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_mam.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	384	100.0	384	6	BD010805	BD010805 Novel pol
2	384	100.0	384	6	BD093106	BD093106 Novel pol
3	384	100.0	929	10	AF243504	AF243504 Mus muscu
4	384	100.0	947	6	BD010821	BD010821 Novel pol
5	384	100.0	947	6	BD093122	BD093122 Novel pol
6	384	100.0	958	10	MMU243539	MMU243539 Mus muscu
7	384	100.0	1054	10	AF233333	AF233333 Mus muscu
8	344	89.6	384	6	BD010835	BD010835 Novel pol
9	344	89.6	384	6	BD093136	BD093136 Novel pol
10	330	85.9	330	6	BD010817	BD010817 Novel pol
11	330	85.9	330	6	BD093118	BD093118 Novel pol
12	294.8	76.8	330	6	BD010836	BD010836 Novel pol
13	294.8	76.8	330	6	BD093137	BD093137 Novel pol
14	287	74.7	384	6	BD010802	BD010802 Novel pol
15	287	74.7	384	6	BD093103	BD093103 Novel pol
16	287	74.7	521	6	AX358818	AX358818 Sequence
17	287	74.7	521	6	AX362311	AX362311 Sequence
18	287	74.7	521	6	AX454774	AX454774 Sequence
19	287	74.7	521	6	AX491252	AX491252 Sequence
20	287	74.7	846	9	AF233261	AF233261 Homo sapi
21	287	74.7	865	9	AF243505	AF243505 Homo sapi
22	287	74.7	923	6	BD010820	BD010820 Novel pol
23	287	74.7	923	6	BD093121	BD093121 Novel pol
24	287	74.7	1422	9	HSA242552	AJ242552 Homo sapi
25	267.8	69.7	307	6	BD010830	BD010830 Novel pol
26	267.8	69.7	307	6	BD093131	BD093131 Novel pol
27	252.2	65.7	330	6	BD010816	BD010816 Novel pol
28	252.2	65.7	330	6	BD093117	BD093117 Novel pol
29	233.8	60.9	261	6	BD010829	BD010829 Novel pol
30	233.8	60.9	261	6	BD093130	BD093130 Novel pol
31	178	46.4	484	5	AF233518	AF233518 Gallus ga
32	142.4	37.1	144765	2	EX510362	EX510362 Mus muscu
33	135.6	35.3	466	5	AF233519	AF233519 Rana cate
34	126	32.8	215581	2	AC106161	AC106161 Rattus no
35	114.8	29.9	232	9	HSA252325	AJ252325 Homo sapi
36	114.8	29.9	121151	9	HS705D16	AL034428 Human DNA
37	81.8	21.3	259	9	HSA252326	AJ252326 Homo sapi
38	76.4	19.9	358	9	HSA252324	AJ252324 Homo sapi
39	68.6	17.9	545	10	MMU67884	U67884 Rattus norv
40	66.2	17.2	580	10	MMU67884	X94322 M.musculus
41	66.2	17.2	581	6	A42945	A42945 Sequence 4
42	66.2	17.2	581	6	AX016788	AX016788 Sequence
43	60.2	15.7	396	9	BT007044	BT007044 Homo sapi
44	60.2	15.7	396	12	BT007775	BT007775 Synthetic
45	60.2	15.7	433	6	AX253435	AX253435 Sequence

ALIGNMENTS

RESULT 1  
BD010805  
LOCUS BD010805 384 bp DNA linear PAT 31-JAN-2002  
DEFINITION Novel polypeptide and DNA thereof.  
ACCESSION BD010805  
VERSION BD010805.1 GI:18639178  
KEYWORDS JP 2001069994-A/6.  
SOURCE Mus sp.  
ORGANISM Mus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
Yoshimura, K. and Tanaka, H.  
TITLE Novel polypeptide and DNA thereof

JOURNAL Patent: JP 2001069994-A 6 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Mus sp. (mouse)  
PN JP 2001069994-A/6  
PD 21-MAR-2001  
PF 29-JUN-2000 JP 2000195911  
PR  
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI  
SHINICHI MOGI,  
FI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC  
A61P19/08,  
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC  
G01N33/53//  
PC C12P21/08,C12N15/00,A61K37/02,C12N5/00  
CC  
FH Key Location/Qualifiers  
FT source 1..384  
FT /organism="Mus sp. (mouse)".  
FEATURES Location/Qualifiers  
source 1..384  
/organism="Mus sp."  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10095"  
BASE COUNT 98 a 68 c 111 g 107 t  
ORIGIN  
Query Match 100.0%; Score 384; DB 6; Length 384;  
Best Local Similarity 100.0%; Pred. No. 1.8e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGCAAGGATATTCATCTTTTGGTGGGGCCCTTGTGTTCTATGTCGGGGCATGGT 60  
Db 1 ATGCAAGGATATTCATCTTTTGGTGGGGCCCTTGTGTTCTATGTCGGGGCATGGT 60  
QY 61 GTATTATGATAAATCTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTTCTATACT 120  
Db 61 GTATTATGATAAATCTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTTCTATACT 120  
QY 121 ATTTCTCGGCAAGACAGAGATTCATCTTCTAAGCTGGTAAACAGAAACCGAGCTG 180  
Db 121 ATTTCTCGGCAAGACAGAGATTCATCTTCTAAGCTGGTAAACAGAAACCGAGCTG 180  
QY 181 AAGAAAGGCGACAGATCTATGTTTCTCAAGCTGGTAAACAGAAACCGAGCTGGAG 240  
Db 181 AAGAAAGGCGACAGATCTATGTTTCTCAAGCTGGTAAACAGAAACCGAGCTGGAG 240  
QY 241 TTTTGGGCTGGCAGTGTTTATGGTGACCAACAGGATGAGATGGGAATTTAGGTTAT 300  
Db 241 TTTTGGGCTGGCAGTGTTTATGGTGACCAACAGGATGAGATGGGAATTTAGGTTAT 300  
QY 301 CCCAGCACTTGGTGAAGGACAGCGTGTATACAGAGAGGCCACCAAGGATCCCAACC 360  
Db 301 CCCAGCACTTGGTGAAGGACAGCGTGTATACAGAGAGGCCACCAAGGATCCCAACC 360  
QY 361 ACGGATATTGACTTCTCTGTGAA 384  
Db 361 ACGGATATTGACTTCTCTGTGAA 384  
RESULT 2  
BD093106  
LOCUS Novel polypeptide and its DNA.  
DEFINITION BD093106  
ACCESSION BD093106.1 GI:22638694  
VERSION WO 0102564-A/6.  
KEYWORDS Mus sp.  
SOURCE Mus sp.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 384)  
REFERENCE Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,  
AUTHORS

Yoshimura,K. and Tanaka,H.  
Novel polypeptide and its DNA  
Patent: WO 0102564-A 6 11-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO  
OGI, SHOICHI OKUBO,SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,  
HIDEYUKI TANAKA  
COMMENT OS Mus sp. (mouse)  
PN WO 0102564-A/6  
PD 11-JAN-2001  
PF 29-JUN-2000 WO 2000JP004278  
PF 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI  
MOGI,  
FI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
PC C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC  
A61K38/17,  
PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088/(C12P21/  
PC 02,C12R1:19)  
CC  
FH Key Location/Qualifiers.  
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Best Local Similarity 100.0%; Pred. No. 1.8e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 361 ACGGATATTGACTTCTCTGTGAA 384  
Db 361 ACGGATATTGACTTCTCTGTGAA 384  
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LOCUS Mus musculus fibrocyte-derived protein (Fdp) mRNA ROD 26-DEC-2000  
DEFINITION AF243504  
ACCESSION AF243504  
VERSION AF243504.1 GI:11991841  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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REFERENCE 1 (bases 1 to 929)
AUTHORS Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegelings,S. and
          Petit,C.
TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
       in vitro effect on the early differentiation of the inner ear
       mesenchyme
JOURNAL J Biol. Chem. 275 (51), 40036-40041 (2000)
MEDLINE 20568254
PUBMED 10998416
REFERENCE 2 (bases 1 to 929)
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegelings,S. and Petit,C.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
       du Dr. Roux, Paris 75015, France
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BASE COUNT 260 a 156 c 220 g 293 t
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    Best Local Similarity 100.0%; Pred. No. 2e-106;
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Qy 301 CCCAGCAACTTGTGTGAGGAGCAGCGTGATACAGAGGCGCCACCAAGGAGATCCCAACC 360
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RESULT 4
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LOCUS BD010821 947 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010821

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VERSION BD010821.1 GI:18639194
KEYWORDS JP 2001069994-A/22.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 947)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
        Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 22 21-MAR-2001;
        TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Mus sp. (mouse)
        PN JP 2001069994-A/22
        PD 21-MAR-2001
        PF 29-JUN-2000 JP 2000195911
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        PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
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        PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
        PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
        A61F19/08,
        PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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RESULT 5
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LOCUS BD093122 947 bp DNA linear PAT 27-AUG-2002

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DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093122
VERSION BD093122.1 GI:22638710
KEYWORDS WO 0102564-A/22.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
JOURNAL Yoshimura, K. and Tanaka, H.
PATENT Patent: WO 0102564-A/22 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDBYUKI TANAKA
COMMENT OS Mus sp. (mouse)
PN WO 0102564-A/22
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088 // (C12P21/
PC 02, C12R1:19)
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FH Key Location/Qualifiers.
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DEFINITION (Mial gene).
ACCESSION AJ243939
VERSION AJ243939.1 GI:12619174
KEYWORDS melanoma inhibitory activity-like protein; Mial gene.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and
JOURNAL Tommerup, N.
PATENT Identification and characterization of an inner ear-expressed human
OGI, melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
polymorphism that abolishes translation
COMMENT Genomics 71 (1), 40-52 (2001)
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LOCUS Mus musculus otoraplin mRNA, complete cds.
ACCESSION AF233333
VERSION AF233333.1 GI:8927429
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 1054)
JOURNAL Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S.,
MEDLINE Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
REFERENCE A novel conserved cochlear gene, OTOR: identification, expression
AUTHORS analysis, and chromosomal mapping
JOURNAL Genomics 66 (3), 242-248 (2000)
MEDLINE 20334619
PUBMED 10873378
REFERENCE 2 (bases 1 to 1054)
AUTHORS Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S.,
TITLE Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
JOURNAL Direct Submission
SUBMITTED (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75
JOURNAL Francis Street, Boston, MA 02115, USA
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Qy      361 ACGGATATTGACTTCTTCTGTGAA 384
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RESULT 8
BD010835      384 bp DNA linear PAT 31-JAN-2002
LOCUS Novel polypeptide and DNA thereof.
ACCESSION BD010835
VERSION BD010835.1 GI:18639208
KEYWORDS JP 2001069994-A/36.
SOURCE Rattus sp.
ORGANISM Rattus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
TITLE 1 (bases 1 to 384)
JOURNAL Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
COMMENT Yoshimura,K. and Tanaka,H.
JOURNAL Novel polypeptide and DNA thereof
PATENT: JP 2001069994-A 36 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Rattus sp. (rat)
PN JP 2001069994-A/36
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
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RESULT 9  
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 DEFINITION Novel polypeptide and its DNA.  
 BD093136  
 ACCESSION BD093136.1 GI:22638724  
 VERSION WO 0102564-A/36.  
 KEYWORDS Rattus sp.  
 SOURCE Rattus sp.  
 ORGANISM Rattus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE  
 Ito.Y., Nishi.K., Ogi.K., Okubo.S., Mogi.S., Noguchi.Y.,  
 Yoshimura,K. and Tanaka.H.  
 Novel polypeptide and its DNA  
 Patent: WO 0102564-A 36 11-JAN-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO  
 OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,  
 HIDEYUKI TANAKA

COMMENT  
 OS Rattus sp. (rat)  
 PN WO 0102564-A/36  
 PD 11-JAN-2001  
 PF 29-JUN-2000 WO 2000P004278  
 PR 30-JUN-1999 JP 93P 186718  
 PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI  
 MOGI,  
 PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
 PC C12N15/12,C12N5/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00, PC  
 A61K38/17,  
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 Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGCGAGGATATTGATCTTTTCTGCTGGGGGCTTGTGGTTCTATGTGCGGGCATGGT 60  
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 ACCESSION BD010817.1 GI:18639190  
 VERSION JP 2001069994-A/18.  
 KEYWORDS Mus sp.  
 SOURCE Mus sp.  
 ORGANISM Mus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 Ito.Y., Nishi.K., Ogi.K., Okubo.S., Mogi.S., Noguchi.Y.,  
 Yoshimura,K. and Tanaka.H.  
 Novel polypeptide and DNA thereof  
 Patent: JP 2001069994-A 18 21-MAR-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD  
 OS Mus sp. (mouse)  
 PN JP 2001069994-A/18  
 PD 21-MAR-2001  
 PF 29-JUN-2000 JP 2000195911  
 PR YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI  
 SHINICHI MOGI,  
 PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
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 A61P19/08,  
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 ACCESSION BD093118  
 VERSION BD093118.1 GI:22638706  
 KEYWORDS WO 0102564-A/18.  
 SOURCE Mus sp.  
 ORGANISM Mus sp.  
 REFERENCE  
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
 Yoshimura, K. and Tanaka, H.  
 TITLE Novel polypeptide and its DNA  
 JOURNAL Patent: WO 0102564-A 18 11-JAN-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO  
 OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,  
 HIDEYUKI TANAKA  
 COMMENT OS Mus sp. (mouse)  
 PN WO 0102564-A/18  
 PD 11-JAN-2001  
 PF 29-JUN-2000 WO 2000JP004278  
 PR 30-JUN-1999 JP 99P 186718  
 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI

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 ACCESSION BD010836  
 VERSION BD010836.1 GI:18639209  
 KEYWORDS JP 2001069994-A/37.  
 SOURCE Rattus sp.  
 ORGANISM Rattus sp.

REFERENCE  
 AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
 Yoshimura, K. and Tanaka, H.  
 TITLE Novel polypeptide and DNA thereof  
 JOURNAL Patent: JP 2001069994-A 37 21-MAR-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD  
 COMMENT OS Rattus sp. (rat)  
 PN JP 2001069994-A/37  
 PD 21-MAR-2001  
 PF 29-JUN-2000 JP 2000195911  
 PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI  
 SHINICHI MOGI,  
 PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
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ACCESSION  
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AUTHORS  
TITLE  
JOURNAL  
COMMENT  
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YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
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PC A61K39/395,A61K49/16,A61P19/02,A61P19/08,A61K31/7088/(C12P21/  
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ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
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SHINICHI MOGI,  
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PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC  
A61P19/08,  
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC  
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DEFINITION
ACCESSION         BD093103
VERSION           BD093103.1 GI:22638691
KEYWORDS          WO 0102564-A/3.
SOURCE            Homo sapiens
ORGANISM          Homo sapiens

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REFERENCE
AUTHORS           Yoshimura,K. and Tanaka,H.
TITLE             Novel polypeptide and its DNA
JOURNAL           Patent: WO 0102564-A 3 11-JAN-2001;
                  TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO
                  OGI, SHOICHI OKUBO, SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
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COMMENT
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PN               WO 0102564-A/3
PD               11-JAN-2001
PF               29-JUN-2000 WO 2000JP004278
PR               30-JUN-1999 JP 99P 186718
PI               YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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#### SUMMARIES

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6	384	100.0	608	13	BQ564944
7	384	100.0	630	13	BQ568471
8	384	100.0	696	10	BB611549
9	382.4	99.6	474	13	BQ565637
10	382.4	99.6	684	13	BQ563768
11	366.2	95.4	409	13	BQ566932
12	347.8	90.6	490	13	BQ565411
13	340.4	88.6	365	13	BY232622
14	300	78.1	604	13	BQ567343
15	260	67.7	280	13	BQ568785
16	244	63.5	485	13	BQ565179
17	204	53.1	588	13	BQ566776
18	196	51.0	795	13	BU748241
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DEFINITION  
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VERSION  
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KEYWORDS  
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SOURCE  
Mus musculus (house mouse)  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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1 (bases 1 to 398)  
Kachar, B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
JOURNAL  
COMMENT  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: KacharB@nidcd.nih.gov  
Plate: 143 row: b column: 10  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers

1. .398  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /sex="male and female"  
 /dev\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the Micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert36(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t  
 ORIGIN

Query Match 100.0%; Score 394; DB 13; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-106;  
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGCAAGGATATTTGATCTTTTGGTGGGGCCCTTGTGTCTTATGTCCGGCATGGT 60



epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 143 a 83 c 135 g 127 t  
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 QY 61 GTATTTATGATAAATCTTCTTAACAAGTTGTCGGATGAGGATGTCCTACT 120  
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 QY 67 GTATTTATGATAAATCTTCTTAACAAGTTGTCGGATGAGGATGTCCTACT 126  
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 gi109c02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus CDNA  
 clone gl109c02 5', mRNA sequence.  
 ACCSSION BQ568498  
 VERSION BQ568498.1 GI:21471815  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Kachar, B.  
 EST analysis of gene expression in the mouse Organ of Corti at the  
 onset of hearing  
 Unpublished  
 CONTACT: Kachar, B.  
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 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kacharbenidded.nih.gov  
 Plate: 109 row: c column: 02  
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 FEATURES  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:10090"  
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 /sex="male and female"  
 /dbv\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated

over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN

Query Match 100.0%; Score 384; DB 13; Length 514;

Best Local Similarity 100.0%; Pred. NO. 4.1e-106;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GTATTATGATAAATCTTCTTCTAAGAAGTTGTGTCGGATGAGGAGTGTCTATACT 120
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QY 361 ACGGATATTGACTTCTCTGTGAA 384
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RESULT 4

BQ564134

LOCUS

DEFINITION

g11d01.y1 Mouse Organ of Corti cdna pBluescript Mus musculus cDNA

clone g11d01 5', mRNA sequence.

ACCESSION

BQ564134

VERSION

BQ564134.1

KEYWORDS

BQ564134 534 bp mRNA linear EST 19-JUN-2002

g11d01.y1 Mouse Organ of Corti cdna pBluescript Mus musculus cDNA

clone g11d01 5', mRNA sequence.

ACCESSION

BQ564134

VERSION

BQ564134.1

KEYWORDS

EST.

# SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 534)

Kachar,B.

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished

Contact: Kachar,B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kacharbenidcd.nih.gov

Plate: 11 row: d column: 01

Seq primer: M13RPL reverse primer (ABI).

Location/Qualifiers

1..534

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="g11d01"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cdna pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The

organ of Corti (OC) was fine dissected from a total of 386

OC as follows: 102 samples from post-natal (P) day 5; 72

from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;

14 from P12 and 24 from P13. After killing animals by

cervical dislocation followed by decapitation, the bulla

was removed and opened in Leibowitz medium. The bony

capsule of the cochlea was chipped away, stria vascularis

and spiral ligament were removed and the sensory

epithelium was carefully dissected out of the modiolus.

Total RNA was extracted using the micro Fasttrack kit

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according

to manufacturer's instructions. Reverse transcription and

library construction were carried out with the Uni-Zap XR

vector kit (catalog # 237211, Stratagene) and Uni-Zap XR

Gigapack III Gold Cloning kit (catalog # 237612), both

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reverse transcribed using a hybrid oligo(dT) linker-primer

that contains an Xho I site. First strand synthesis was

primed with the linker- primer and transcribed using

Moloney murine leukemia virus reverse transcriptase

(MMLV-RT) and 5-methyl dCTP. The second strand was

synthesized with DNA polymerase and RNase H. Complementary

DNA was blunt ended with Pfu DNA polymerase, ligated with

EcoR I adapters in the presence of ligase and digested

with Xho I. The cDNA was sequentially size fractionated

over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)

columns to enrich for cDNAs greater than 400bp and 1000 bp

, respectively. The cDNA was then directionally ligated to

the Uni-ZAP XR vector, which had been predigested with

EcoR I and Xho I. The phagemid was packaged with Gigapak

III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the

yield of the phage library was estimated to be 11,100,000

recombinants. Stratagene's ExAssist Interference

resistance helper phage (catalogue # 211203) was adopted

to rescue plasmid DNA from the phages. Upon plating of the

rescued library, individual cDNA clones were selected and

grown in 96-well, 2 ml growth plate. Plasmid DNA was

purified from 200 ul of saturated culture with the

Concert96(TM) plasmid purification kit (Invitrogen,

Carlsbad, CA) as instructed by the manufacturer. ESTs from

the 5' end of the cDNA clones were generated with the

universal M13 reverse primer (CAGGAACAGCTATGACC) and 25%

strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 155 a 87 c 148 g 144 t

Query Match 100.0%; Score 384; DB 13; Length 534;

Best Local Similarity 100.0%; Pred. No. 4.2e-106; Mismatches 0; Indels 0; Gaps 0; Matches 384; Conservative 0;

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QY 1 ATGCAAGGATATGATCTTTTCTGGGGCCCTTGGTTCTATGCGGGCATGGT 60
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QY 121 ATTCTCTGCAAGACAGGAGATTACAATCCCGAGCTGTAGTTTCATCGATGTC 180
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QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAGCTGTTACAGAAAACGGAGCTGGAGAG 240
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DB 183 AAGAAAGGGCAGCAGATCTATGTTTACTCCAGCTGTTACAGAAAACGGAGCTGGAGAG 242
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QY 241 TTTTGGCTGGCAGTGTATGTTGACACAGAGATGAGATGGAATGTAGTTATTC 300
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QY 301 CCAGCAACTTGGTGAAGGACGACGCTGTATACAGAGAGCCACCAAGGAGATCCCAACC 360
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DB 303 CCAGCAACTTGGTGAAGGACGACGCTGTATACAGAGAGCCACCAAGGAGATCCCAACC 362
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QY 361 ACGGATATGACTTCTCTGTGAA 384
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## RESULT 5

BQ569741

LOCUS

DEFINITION BQ569741 560 bp mRNA linear EST 19-JUN-2002  
 Clone g1135f01.1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA

ACCESSION BQ569741

VERSION BQ569741.1 GI:21473058

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 560)

Kachar, B.

EST analysis of gene expression in the mouse Organ of Corti at the

onset of hearing

Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 135 row: f column: 01

Seq primer: M13RPI reverse primer (ABI).

## FEATURES

source

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 /mol\_type="mRNA"  
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 /dev\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /notes="Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's Exassist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 160 a 92 c 154 g 153 t

ORIGIN

Query Match 100.0%; Score 384; DB 13; Length 560;

Best Local Similarity 100.0%; Pred. No. 4.3e-106;

Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Dbb 366 ACGGATATGACTTCTTCTGTGAA 389

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DEFINITION  
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clone gi27903 5', mRNA sequence.

ACCESSION  
BQ564944  
VERSION  
BQ564944.1  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 608)  
Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar,B.  
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National Institute of Deafness and other Communication Disorders  
50/4243 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 27 row: 9 column: 09  
Seq primer: M13Rpi reverse primer (ABI).

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/sex="male and female"  
/dev\_stage="post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis

and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the micro Fasttrack kit  
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
to manufacturer's instructions. Reverse transcription and  
library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both  
from Stratagene (La Jolla, CA, USA), according to  
manufacturer's instructions. Briefly: 1.5 ug mRNA was  
reverse transcribed using a hybrid oligo(dT) linker-primer  
that contains an Xho I site. First strand synthesis was  
primed with the linker-primer and transcribed using  
Moloney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was  
synthesized with DNA polymerase and RNase H. Complementary  
DNA was blunt ended with Pfu DNA polymerase, ligated with  
EcoR I adapters in the presence of ligase and digested  
with Xho I. The cDNA was sequentially size fractionated  
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)  
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)  
columns to enrich for cDNAs greater than 400bp and 1000 bp  
, respectively. The cDNA was then directionally ligated to  
the Uni-Zap XR vector, which had been pre-digested with  
EcoR I and Xho I. The phagemid was packaged with Gigapak  
III Gold and, upon titration on XL1 Blue MRF' cells, the  
yield of the phage library was estimated to be 11,100,000  
recombinants. Stratagene's Exsist Interference  
resistance helper phage (catalogue # 211203) was adopted  
to rescue plasmid DNA from the phages. Upon plating of the  
rescued library, individual cDNA clones were selected and  
grown in 96-well, 2 ml growth plate. Plasmid DNA was  
purified from 200 ul of saturated culture with the  
Concer96(TM) plasmid purification kit (Invitrogen,  
Carlsbad, CA) as instructed by the manufacturer. ESTs from  
the 5' end of the cDNA clones were generated with the  
universal M13 reverse primer (CAGGAACAGCTATGACC) and 25%  
strength BigDye terminator sequencing chemistry (Applied  
Biosystems, Foster City, CA). Sequencing reactions were  
performed on MJ Tetrad thermal cyclers (MJ Research,  
Walham, MA), and analyzed on 3700 automated capillary  
sequencers using POP5 polymer (Applied Biosystems, Foster  
City, CA). The frequency distribution of the library is  
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;  
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of  
genes are present in GenBank and have known function; 23%  
have hits in GenBank, but do not have assigned function;  
12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t  
ORIGIN  
Query Match 100.0%; Score 384; DB 13; Length 608;  
Best Local Similarity 100.0%; Pred. No. 4.5e-106;  
Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGCAAGGATATGATCTTTCTTCTGGGGCCCTTGCTTCATGTCGGGCGCATGGT 60  
Dbb 13 ATGCAAGGATATGATCTTTCTTCTGGGGCCCTTGCTTCATGTCGGGCGCATGGT 72  
Qy 61 GTATTATGATATAACTTCTTCTTAAGAGTTGTGCGGATAGGAGTGTCATACT 120  
Dbb 73 GTATTATGATATAACTTCTTCTTAAGAGTTGTGCGGATAGGAGTGTCATACT 132  
Qy 121 ATTTCTCTGGCAAGACAGACAGAGATACAAATGCCAGACTGTAGGTTTCATCGATGTC 180  
Dbb 133 ATTTCTCTGGCAAGACAGACAGAGATACAAATGCCAGACTGTAGGTTTCATCGATGTC 192  
Qy 181 AAGAAAGGCGACAGATCTATGTTTATCTCCAGCTGTAAACAGAAACCGGAGTGGAGAG 240  
Dbb 193 AAGAAAGGCGACAGATCTATGTTTATCTCCAGCTGTAAACAGAAACCGGAGTGGAGAG 252  
Qy 241 TTTTGGGCTGCAGTGTATGTTTATGTTGACCCAGAGATGAGTGGGAATGTAGGTTATTTTC 300

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Db      253 TTTTGGCTGGCAGTGTATTATGGTGACCACGAGATGAGATGGGAATTGTAGGTTATTC 312
QY      301 CCCAGCAACTTGGTGAAGGAGCAGCGGTGTATACAGAGAGCCCAAGGAGATCCCAACC 360
      |||
Db      313 CCCAGCAACTTGGTGAAGGAGCAGCGGTGTATACAGAGAGCCCAAGGAGATCCCAACC 372
QY      361 ACGGATATTGACTTCTCTCTGAA 384
Db      373 ACGGATATTGACTTCTCTGTGAA 396

RESULT 7
LOCUS   BQ568471
DEFINITION gi108g04.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi108g04 5', mRNA sequence.
ACCESSION BQ568471
VERSION   BQ568471.1 GI:21471788
KEYWORDS EST.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 630)
Kachar,B.
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished
Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharbenid@nid.nih.gov
Plate: 108 row: g column: 04
Seq primer: M13Rpl reverse primer (ABI).

FEATURES
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1..630
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
/clone="gi108g04"
/sex="male and female"
/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested

```

with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xli Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12.3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 178 a 111 c 167 g 174 t

ORIGIN

Query Match 100.0%; Score 384; DB 13; Length 630;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-106;  
 Matches 384; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1  ATGCGAAGGATATTGATTTCTTTGCTGGGGGCTTGTCTTCTATCTGCGGGCATGGT 60
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QY      121  ATTTCTTGGCAGAGACACAGAGATTAACAATGCCCCAGACTGTAGGTTTCATCGATGC 180
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QY      181  AAGAAAGGCGCAGAGATCTATGTTTACTCCAAAGCTGTACAGAAACGGAGCTGGAGAG 240
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Db      253  TTTTGGCTGGCAGTGTATTATGTTGACCAAGGATGAGATGGGAATTGTAGGTTATTTC 312
QY      301  CCAGCAACTTGGTGAAGGAGCAGCGGTGTATACAGAGAGCCCAAGGAGATCCCAACC 360
Db      313  CCAGCAACTTGGTGAAGGAGCAGCGGTGTATACAGAGAGCCCAAGGAGATCCCAACC 372
QY      361  ACGGATATTGACTTCTCTCTGAA 384
Db      373  ACGGATATTGACTTCTCTGTGAA 396

RESULT 8
LOCUS   BB611549
DEFINITION BB611549 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110083012 5', mRNA sequence.
ACCESSION BB611549
VERSION   BB611549.1 GI:15393547

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/clone lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTAGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 145 a 78 c 131 g 120 t  
 ORIGIN  
 Query Match 99.6%; Score 382.4; DB 13; Length 474;  
 Best Local Similarity 99.7%; Pred. No. 1.2e-105;  
 Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 ATGCAAGGATATGATCTTTGCTGGGGCCCTTGTTCTATGTCGGGCAATGGT 60  
 Db 14 ATGCAAGGATATGATCTTTGCTGGGGCCCTTGTTCTATGTCGGGCAATGGT 73  
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 QY 121 ATTTCTGCGAAGACACAGGAAGATTACAATGCCCCAGACTGTAGTTTCATCGATGTC 180

Db 134 ATTTCTCTGCGAAGACACAGGAAGATTACAATGCCCCAGACTGTAGTTTCATCGATGTC 193  
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 QY 361 ACGGATATTGACTTCTTCTGTGAA 384  
 Db 374 ACGGATATTGACTTCTTCTGTGAA 397

RESULT 10  
 BQ563768

LOCUS  
 DEFINITION

BQ563768 684 bp mRNA linear EST 19-JUN-2002  
 gi06c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 clone gi06c09 5', mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS

BQ563768  
 BQ563768.1 GI:21466749  
 EST.

SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Kachar, B.  
 1 (bases 1 to 684)

REFERENCE  
 AUTHORS  
 TITLE

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
 Unpublished  
 Contact: Kachar, B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kacharbeniddc.nih.gov  
 Plate: 06 row: c column: 09  
 Seq primer: M13RP1 reverse primer (ABI).

JOURNAL  
 COMMENT

Location/Qualifiers  
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 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
 /clone="gi06c09"  
 /sex="male and female"  
 /dev\_stage="Post natal"  
 /note="Organ: Organ of Corti; Vector: pBluescript"  
 /organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to

FEATURES  
 source

1. 684  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="BALB/c"  
 /db\_xref="taxon:10090"  
 /clone="gi06c09"  
 /sex="male and female"  
 /dev\_stage="Post natal"  
 /note="Organ: Organ of Corti; Vector: pBluescript"  
 /organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to



manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAAACAGCTAGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

194 a 120 c 178 g 192 t

BASE COUNT  
ORIGIN

Query Match 99.6%; Score 382.4; DB 13; Length 684;  
Best Local Similarity 99.7%; Pred. No. 1.5e-105;  
Matches 383; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTCATCTTTCTTCTGGGGCCCTTGTGGTCTATGTCCGGGATGGT 60  
DB 13 ATGGCAGGATATTCATCTTTCTTCTGGGGCCCTTGTGGTCTATGTCCGGGATGGT 72

QY 61 GTATTATGGATAAATCTTTCTTCTAAGAGTTGTGTGGGATGAGAGTGTCTATACT 120  
DB 73 GTATTATGGATAAATCTTTCTTCTAAGAGTTGTGTGGGATGAGAGTGTCTATACT 132

QY 121 ATTTCTTGGCAAGGACAGAGATTAATGTCCTCAAGCTGGTAAACAGAAACCGAGCTGAGAG 180  
DB 133 ATTTCTTGGCAAGGACAGAGATTAATGTCCTCAAGCTGGTAAACAGAAACCGAGCTGAGAG 192

QY 181 AAGAAGGGCAGCAGATCTATGTTTCTCAAGCTGGTAAACAGAAACCGAGCTGAGAG 240  
DB 193 AAGAAGGGCAGCAGATCTATGTTTCTCAAGCTGGTAAACAGAAACCGAGCTGAGAG 252

QY 241 TTTTGGGCTGGCAGTGTATGTTGTCACACAGGATGAGATGGGATTTAGTTATTTC 300  
DB 253 TTTTGGGCTGGCAGTGTATGTTGTCACACAGGATGAGATGGGATTTAGTTATTTC 312

QY 301 CCAGCAACTTGGTGAAGGACAGCGTGTATACCGAGGCGCCACCAAGGAGATCCCAACC 360  
DB 313 CCAGCAACTTGGTGAAGGACAGCGTGTATACCGAGGCGCCACCAAGGAGATCCCAACC 372

QY 361 ACGGATATTGACTTCTTCTGTGAA 384  
DB 373 ACGGATATTGACTTCTTCTGTGAA 396

RESULT 11  
LOCUS BQ566932  
DEFINITION gi73g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi73g09.5', mRNA sequence.  
ACCESSION BQ566932  
VERSION BQ566932.1 GI:21470249  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 409)  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharbenidod.nih.gov  
Plate: 73 row: 9 column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
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/db\_xref="taxon:10090"  
/clone="gi73g09"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000



recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT	102 a	75 c	121 g	111 t
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Query Match	95.4%	Score 366.2;	DB 13;	Length 409;
Best Local Similarity	99.0%;	Pred. No. 9.9e-101;		
Matches 379;	Conservative 0;	Mismatches 3;	Indels 1;	Gaps 1;
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Qy	61	GTATTTATGGATAAATCTTCTTAAGAAGTTGTGCG-GGATCAGGAGTGTGCTATAC	119	
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Db	147	TATTTCTCTGCAAGACACAGGAGATTACAATGCCCGACACTGTAGTTTCATCGATGT	206	
Qy	180	CAAGAAAGGGCAGCAGATCTATGTTTACTCAAGCTGTGTAAACAGAAACCGAGTGGAGA	239	
Db	207	CAAGAAAGGGCAGCAGATCTATGTTTACTCAAGCTGTGTAAACAGAAACCGAGTGGAGA	266	
Qy	240	GTTTTGGCTGGCAGTGTATGTTGTGACCCAGCAGTGCAGATGCGAATTCAGGTTATT	299	
Db	267	GTTTTGGCTGGCAGTGTATGTTGTGACCCAGCAGTGCAGATGCGAATTCAGGTTATT	326	
Qy	300	CCCCAGCAACTTGTGAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATCCCAAC	359	
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Qy	360	CACGGATATTGACTTCTTCTGTG 382		
Db	387	CACGGTATTGACTTCTTCTGTG 409		

RESULT 12  
BQ565411  
LOCUS  
DEFINITION gi37b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi37b12 5', mRNA sequence. 490 bp linear EST 19-JUN-2002  
ACCESSION BQ565411  
VERSION BQ565411.1 GI:21468728  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 490)  
AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL COMMENT

Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 37 row: b column: 12  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
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OC as follows: 102 samples from post-natal (P) day 5 of 386 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and the Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on Xli Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of

FEATURES source

genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT	191 a	77 c	109 g	112 t	1 Others
ORIGIN					
Query Match	90.6%	Score	347.8;	DB 13;	Length 490;
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				Gaps	0;
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QY	70	GATTAACCTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTCTATCTATCTTCTCTG	129		
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QY	190	CAGCAGATCTATGTTTACTCCAGCTGTGTACAGAAACGGAGCTGGAGGTTTGGGCT	249		
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QY	250	GCAGTGTATTGTTGACCAACAGGATGAGATGGGAATTTAGTGTATTTCGCCAGCAAC	309		
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QY	310	TTGTGAAGGACAGCGTGTATACAGAGGACCAAGGAGATCCCAACCGGATATT	369		
Db	396	TTGTGAAGGACAGCGTGTATACAGAGGACCAAGGAGATCCCAACCGGATATT	455		
QY	370	GACTTCTTCTGGAA	384		
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BY232622 RIKEN full-length enriched, adult inner ear Mus musculus  
cDNA clone F930026J20 5', mRNA sequence.  
BY232622  
EST.  
Mus musculus (house mouse)  
Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 365)  
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,  
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,  
Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,  
Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,  
Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani,  
L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest,  
A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,  
Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,  
Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierzki, R. M.,  
King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, R. B., Lyons,  
P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki,  
H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertes, G.,  
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Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,  
B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou,  
M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Tesdale,  
R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,  
Watanabe, Y., Wells, C., Wilming, L. G., Wyszynski, B. A., Yanagisawa,  
M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,  
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura

M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,  
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sakai, D., Shibata,  
K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,  
E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
12466851  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp/  
URL: http://genome.gsc.riken.go.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane,  
T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A.,  
Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K.,  
Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami,  
M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct  
Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with  
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National  
Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose  
assistance we gratefully acknowledge. Please visit our web site  
(http://genome.gsc.riken.go.jp) for further details.

FEATURES  
source

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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 604)

REFERENCE Kachar,B.  
 AUTHORS EST analysis of gene expression in the mouse Organ of Corti at the  
 TITLE onset of hearing  
 JOURNAL Unpublished  
 COMMENT Contact: Kachar,B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kacharbenidc@nih.gov  
 Plate: 88 row: d column: 08  
 Seq primer: M13RP1 reverse primer (ABI).

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 OC as follows: 102 samples from post-natal (P) day 5; 72  
 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
 14 from P12 and 24 from P13. After killing animals by  
 cervical dislocation followed by decapitation, the bulla  
 was removed and opened in Leibowitz medium. The bony  
 capsule of the cochlea was chipped away, stria vascularis  
 and spiral ligament were removed and the sensory  
 epithelium was carefully dissected out of the modiolus.  
 Total RNA was extracted using the micro Fasttrack kit  
 (catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
 to manufacturer's instructions. Reverse transcription and  
 library construction were carried out with the Uni-Zap XR  
 vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
 Gigapack III Gold Cloning kit (catalog # 237612), both  
 from Stratagene (La Jolla, CA, USA), according to  
 manufacturer's instructions. Briefly: 1.5 ug mRNA was  
 reverse transcribed using a hybrid oligo(dT) linker-primer  
 that contains an Xho I site. First strand synthesis was  
 primed with the linker- primer and transcribed using  
 Moloney murine leukemia virus reverse transcriptase  
 (MMLV-RT) and 5-methyl dCTP. The second strand was

synthesized with DNA polymerase and RNase H. Complementary  
 DNA was blunt ended with Pfu DNA polymerase, ligated with  
 EcoR I adapters in the presence of ligase and digested  
 with Xho I. The cDNA was sequentially size fractionated  
 over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)  
 and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)  
 columns to enrich for cDNAs greater than 400bp and 1000 bp  
 , respectively. The cDNA was then directionally ligated to  
 the Uni-Zap XR vector, which had been predigested with  
 EcoR I and Xho I. The phagemid was packaged with Gigapak  
 III Gold and, upon titration on Xli Blue MRF' cells, the  
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 recombinants. Stratagene's ExAssist Interference  
 resistance helper phage (catalogue # 211203) was adopted  
 to rescue plasmid DNA from the phages. Upon plating of the  
 rescued library, individual cDNA clones were selected and  
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 purified from 200 ul of saturated culture with the  
 Concert96(TM) plasmid purification kit (Invitrogen,  
 Carlsbad, CA) as instructed by the manufacturer. ESTs from  
 the 5' end of the cDNA clones were generated with the  
 universal M13 reverse primer (CAGGAACAGCTATGACC) and 25x  
 strength BigDye terminator sequencing chemistry (Applied  
 Biosystems, Foster City, CA). Sequencing reactions were  
 performed on MJ Tetrad thermal cyclers (MJ Research,  
 Waltham, MA), and analyzed on 3700 automated capillary  
 sequencers using POP5 polymer (Applied Biosystems, Foster  
 City, CA). The frequency distribution of the library is  
 as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;  
 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of  
 genes are present in GenBank and have known function; 23%  
 have hits in GenBank, but do not have assigned function;  
 12% are uncharacterized ESTs and 20% are unidentified."

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ORIGIN

Query Match 78.1%; Score 300; DB 13; Length 604;  
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BQ568785

LOCUS

DEFINITION g114f04.y2 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 clone g114f04 5', mRNA sequence.

ACCESSION BQ568785

VERSION BQ568785.1 GI:21472102

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Tue Dec 30 10:20:36 2003

REFERENCE 1 (bases 1 to 280)  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 114 row: f column: 04  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack Kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xli Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25<sup>th</sup> strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary

sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT	72 a	44 c	85 g	79 t
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Query Match	67.7%	Score 260;	DB 13;	Length 280;
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Job time : 1280.36 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 127,462 Seconds  
(without alignments)  
8132.484 Million cell updates/sec

Title: US-10-019-455A-10  
Perfect score: 384  
Sequence: 1 atggcaaggattgtcttcttcttctgtgaa 384

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues  
Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :				N Geneseq 19Jun03:*			
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				2: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*			
				3: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*			
				4: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT.*			
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				20: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*			
				21: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT.*			
				22: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*			
				23: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*			
				24: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*			
				25: /SIDSI1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	384	100.0	384	22 AAF59068	Mouse MLP nucleoti
2	384	100.0	947	22 AAF59084	Mouse MLP nucleoti
3	344	89.6	384	22 AAF59098	Rat MLP nucleotide
4	330	85.9	330	22 AAF59080	Mouse MLP nucleoti
5	294.8	76.8	330	22 AAF59099	Rat MLP nucleotide
6	287	74.7	384	22 AAF59065	Human MLP nucleoti
7	287	74.7	387	24 AAF59065	DNA encoding novel
8	287	74.7	426	22 AAF59065	Human growth regul

9	287	74.7	521	24 ABL95740	Human angiogenesis
10	287	74.7	521	24 ABL88251	Human PRO9873 cDNA
11	287	74.7	521	24 ABK33571	cDNA encoding huma
12	287	74.7	891	22 AAH98228	Human EST-derived
13	287	74.7	891	22 AAH26342	Human growth regul
14	287	74.7	923	22 AAF59083	Human MLP nucleoti
15	287	74.7	1201	22 AAH26343	Human growth regul
16	267.8	69.7	307	22 AAF59093	Rat MLP nucleotide
17	252.2	65.7	330	22 AAF59079	Human MLP nucleoti
18	233.8	60.9	261	22 AAF59092	Rat MLP nucleotide
19	66.2	17.2	581	16 AAQ84052	Sequence encoding
20	60.2	15.7	433	22 AAH47783	Recombinant human
21	60.2	15.7	459	16 AAQ84050	Sequence encoding
22	60.2	15.7	459	22 AAI70083	Melanoma inhibitor
23	60.2	15.7	459	22 AAD18732	Human antisenase ol
24	60.2	15.7	555	23 ABV59229	Human prostate exp
25	58.6	15.3	442	24 ABL63602	Breast cancer rela
26	58.6	15.3	442	24 ABL64012	Breast cancer rela
27	55.2	14.4	330	16 AAQ84061	Sequence encoding
28	52.6	13.7	305	16 AAQ84055	Amplified fragment
29	47.2	12.3	300	20 AAZ14828	Human gene express
30	47.2	12.3	417	22 AAH99775	Human protein enco
31	47.2	12.3	429	22 AAS22695	Human cDNA encodin
32	47.2	12.3	884	22 AAS22459	Human cDNA encodin
33	47.2	12.3	1060	22 AAF92140	Human PRO19670 cDN
34	47.2	12.3	1060	24 ABS74460	Human cDNA encodin
35	47.2	12.3	1060	24 ABL95738	Human angiogenesis
36	47.2	12.3	1060	24 ABL88249	Human PRO19670 cDN
37	47.2	12.3	1060	25 ACAS7963	Human PRO19670 cDN
38	47.2	12.3	1060	25 ACAS8892	cDNA encoding huma
39	47.2	12.3	1060	25 ACAG0445	Novel human secret
40	47.2	12.3	1060	25 ACAG3455	cDNA encoding huma
41	47.2	12.3	1060	25 ACAG3455	Human cDNA encodin
42	47.2	12.3	1060	25 ABX98433	Novel human secret
43	47.2	12.3	1060	25 ABX98935	Human secreted/tra
44	47.2	12.3	1060	25 ACAG05980	Human PRO polynucl
45	47.2	12.3	1060	25 ABX78808	Human PRO polynucl

ALIGNMENTS

RESULT 1

AAF59068

ID AAF59068 standard; DNA; 384 BP.

XX AAF59068;

AC AAF59068;

XX 23-APR-2001 (first entry)

XX Mouse MLP nucleotide sequence SEQ ID NO:10.

DE MLP; MTA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.

OS Mus musculus.

XX WO200102564-A1.

PN 11-JAN-2001.

PD 29-JUN-2000; 2000WO-JP04278.

PF 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

PI Tanaka H;

XX WPI; 2001-159271/16.



KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
OS Rattus sp.  
XX  
PN WO200102564-A1.  
XX  
XX 11-JAN-2001.  
XX  
XX 29-JUN-2000; 2000WO-JP04278.  
XX  
XX 30-JUN-1999; 99JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
XX WPI; 2001-159271/16.  
DR P-PSDB; AAB69130.  
XX  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
XX Claim 13; Page 105-106; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;  
SQ  
Query Match 89.6%; Score 344; DB 22; Length 384;  
Best Local Similarity 93.5%; Pred. No. 1.3e-100;  
Matches 359; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 1 ATGCGAAGATATGATCTTTGCTTGGGGCTTGTGTTCTATGTCGCGGCGATGGT 60  
DB 1 ATGCGAAGATATGATCTTTGCTTGGGGCTTGTGTTCTATGTCGCGGCGATGGC 60  
QY 61 GTATTATGATATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTCTATACT 120  
DB 61 ATGTTATGATATAAACTTTCTTCTAAGAAGTTGTGCGAGTGTGTTGTTCTATACC 120  
QY 121 ATTTCTCTGCGACAGACAGGAGATTAACAATGCCCGACATGTTAGTTTCATGATGTC 180  
DB 121 ATTTCTCTGCGACAGACAGGAGATTAACAATGCCCGACATGTTAGTTTCATCAATGTC 180  
QY 181 AAGAAAGGCGACAGATCTATGTTTCTCAAGCTGTTAACAAGACGAGCTGGAGAG 240  
DB 181 AAGAAAGGCGACAGATCTATGTTTCTCAAGCTGTTAACAAGATGAGCTGGGGCA 240  
QY 241 TTTTGGGCTGGCAGTGTATGTTGTCACACAGATGAGATGGAATTTAGTTTATTTTC 300  
DB 241 TTCTGGGCTGGCAGTGTATGTTGTCACACAGATGAGATGGAATTTGGGTTATTTTC 300  
QY 301 CCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCGCCACCAAGGATCCCCAAC 360  
DB 301 CCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCGCCACCAAGGATTTCCAAAC 360  
QY 361 ACGGATATTCAGTCTTCTCTGGA 384  
DB 361 ACGGATATTCAGTCTTCTCTGGA 384

RESULT 4  
AAF59080  
ID AAF59080 standard; DNA; 330 BP.  
XX  
XX AAF59080;  
AC  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Mouse MLP nucleotide sequence SEQ ID NO:25.  
XX  
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.  
XX  
XX Mus musculus.  
OS  
XX  
PN WO200102564-A1.  
XX  
XX 11-JAN-2001.  
XX  
XX 29-JUN-2000; 2000WO-JP04278.  
XX  
XX 30-JUN-1999; 99JP-0186718.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX  
XX WPI; 2001-159271/16.  
DR P-PSDB; AAB69127.  
XX  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
XX Claim 10; Page 98; 111pp; Japanese.  
XX  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
XX Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;  
SQ  
Query Match 85.9%; Score 330; DB 22; Length 330;  
Best Local Similarity 100.0%; Pred. No. 3.9e-96;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 55 CATGGTGTTATTTATGATATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTC 114  
DB 1 CATGGTGTTATTTATGATATAAACTTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTGTC 60  
QY 115 TATATCTATTTCTCTGCGACAGACAGGAGATTAACAATGCCCGACATCTAGTTTCATC 174  
DB 61 TATATCTATTTCTCTGCGACAGACAGGAGATTAACAATGCCCGACATCTAGTTTCATC 120  
QY 175 GATGTCAGAAAGGCGACGATCTATGTTTCTCAAGCTGTTAACAAGACGAGCT 234  
DB 121 GATGTCAGAAAGGCGACGATCTATGTTTCTCAAGCTGTTAACAAGACGAGCT 180  
QY 235 GGAGAGTTTGGGCTGGCAGTGTATGTTGTCACACAGATGAGATGGAATTTAGGT 294  
DB 181 GGAGAGTTTGGGCTGGCAGTGTATGTTGTCACACAGATGAGATGGAATTTAGGT 240  
QY 295 TATTTCCCGACCAACTTGGTGAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATC 354

Db	241	TATTTCCCGAGCACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACAGGAGATC	300
QY	355	CCAACACGGATATTGACTTCTTCTGTGAA	384
Db	301	CCAACACGGATATTGACTTCTTCTGTGAA	330
RESULT 5			
AAF59099	standard; DNA; 330 BP.		
ID	AAF59099		
XX	AAF59099;		
AC	AAF59099;		
XX	23-APR-2001 (first entry)		
DT	Rat MLP nucleotide sequence SEQ ID NO:48.		
XX	MLP; MIA; melanoma inhibitory activity; cancer; bone disease;		
XX	joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;		
KW	cardiant; gene therapy; secretory cell function regulator; promoter;		
KW	inhibitor; ds.		
XX	Rattus sp.		
OS	WO200102564-A1.		
XX	11-JAN-2001.		
XX	29-JUN-2000; 2000WO-JP04278.		
PF	30-JUN-1999; 99JP-0186718.		
XX	(TAKE ) TAKEDA CHEM IND LTD.		
XX	Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;		
PI	Tanaka H;		
PI	WPI; 2001-159271/16.		
DR	P-PSDB; AAB69131.		
XX	Safe, low-toxicity secretory cell function-regulatory protein and		
PT	encoded DNA, applicable as drugs, in diagnosis and development of		
PT	promoters and inhibitors for preventing or treating e.g. bone and joint		
PT	diseases -		
XX	Claim 12; Page 107; 111pp; Japanese.		
PS	The present invention describes novel MLP proteins and their encoding		
CC	DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant		
CC	activities, and can be used in gene therapy and as secretory cell		
CC	function regulators. The MLP proteins and DNAs can be used in drugs, in		
CC	the diagnosis and development of promoters and inhibitors for preventing		
CC	or treating bone and joint diseases as well as pathologic angiogenesis.		
CC	AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used		
CC	in the exemplification of the present invention.		
XX	Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;		
SQ	Query Match 76.8%; Score 294.8; DB 22; Length 330;		
	Best Local Similarity 93.3%; Pred. No. 8.7e-85;		
	Matches 308; Conservative 0; Mismatches 22; Indels 0; Gaps 0;		
QY	55	CATGGTGTATTTATGGATAAATTTCTCTAAGAAAGTTGTGCGGATGAGAGTGTGTC	114
Db	1	CATGGCATGTTTATGGATAAATTTCTCTAAGAAAGTTGTGCGGATGAGAGTGTGTC	60
QY	115	TATACATTTCTCTGACAGACGACAGGAGTATTAATGCCAGACTGTAGGTTTCATC	174
Db	61	TATACATTTCTCTGACAGACGACAGGAGTATTAATGCCAGACTGTAGGTTTCATC	120
QY	175	GATGTCAAGAAAGGCGACAGATCTATGTTTACTCCAAGCTGTGTACAGAAAACGGAGCT	234
Db	1	GATGTCAAGAAAGTATTGTTACTTCTCCCGGCTCTTGTGGCTGTATGTCTGTCATGGA	60
Db	121	AATGTCAAGAAAGGCGACAGATCTATGTTTATTTCCAGCTGTGTAAACAGAAATGGAGCT	180
QY	235	GGAGAGTTTGGGCTGGCAGTGTATGTGTACCAACAGGATCAGATGGGAATTGTAGGT	294
Db	181	GGGGCATTTCTGGGCTGGCAGTGTATGTGTACCAACAGGATCAGATGGGAATTGTGGGT	240
QY	295	TATTTCCCGAGCACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATC	354
Db	241	TATTTCCCGAGCACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATT	300
QY	355	CCAACACGGATATTGACTTCTTCTGTGAA	384
Db	301	CCAACACGGATATTGACTTCTTCTGTGAA	330
RESULT 6			
AAF59065	standard; DNA; 384 BP.		
ID	AAF59065		
XX	AAF59065;		
AC	AAF59065;		
XX	23-APR-2001 (first entry)		
DT	Human MLP nucleotide sequence SEQ ID NO:4.		
XX	MLP; MIA; melanoma inhibitory activity; cancer; bone disease;		
XX	joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;		
KW	cardiant; gene therapy; secretory cell function regulator; promoter;		
KW	inhibitor; ds.		
XX	Homo sapiens.		
OS	WO200102564-A1.		
XX	11-JAN-2001.		
XX	29-JUN-2000; 2000WO-JP04278.		
PF	30-JUN-1999; 99JP-0186718.		
XX	(TAKE ) TAKEDA CHEM IND LTD.		
XX	Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;		
PI	Tanaka H;		
PI	WPI; 2001-159271/16.		
DR	P-PSDB; AAB69123.		
XX	Safe, low-toxicity secretory cell function-regulatory protein and		
PT	encoded DNA, applicable as drugs, in diagnosis and development of		
PT	promoters and inhibitors for preventing or treating e.g. bone and joint		
PT	diseases -		
XX	Example 1; Page 91; 111pp; Japanese.		
PS	The present invention describes novel MLP proteins and their encoding		
CC	DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant		
CC	activities, and can be used in gene therapy and as secretory cell		
CC	function regulators. The MLP proteins and DNAs can be used in drugs, in		
CC	the diagnosis and development of promoters and inhibitors for preventing		
CC	or treating bone and joint diseases as well as pathologic angiogenesis.		
CC	AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used		
CC	in the exemplification of the present invention.		
XX	Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;		
SQ	Query Match 74.7%; Score 287; DB 22; Length 384;		
	Best Local Similarity 84.3%; Pred. No. 3e-82;		
	Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;		
QY	1	ATGGCAAGGATATTGATTCTTTTGTGTGGGCGCTTGTGGTCTATGTGCGGGCATGGT	60
Db	1	ATGGCAAGGATATTGATTCTTTTGTGTGGGCGCTTGTGGTCTATGTGCGGGCATGGT	60



QY	61	GGATTATGGATAAACTTCTTCTAAGAAAGTTGTGTGGGATGAGGAGTGTGCTATACT	120
Db	61	ATATTATGGACCGTCTAGCTTCCAAGAAAGCTGTGTGCAGATGATGAGTGTGCTATACT	120
QY	121	ATTCTCTGGCAGAGCAGGAGATTACAATGCCCGACGTAGGTTTCATCGATGTC	180
Db	121	ATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAAGTT	180
QY	181	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGTGTACAGAAACCGAGCTGGAGAG	240
Db	181	AAAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGTGTAAAGAAATGAGCTGGAGAA	240
QY	241	TTTTGGCTGGCAGTGTATGTTGACCCACAGATGAGATGGAAATTTAGGTTATTTTC	300
Db	241	TTTTGGCTGGCAGTGTATGTTGATGGCGCAGACGAGATGGGATGGGTTATTTTC	300
QY	301	CCAGCAACTTGTGTAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC	360
Db	301	CCAGGAACTTGTGTAAGGAAACAGCGTGTATACCAGGAAGTACCAAGGAAGTTCCACC	360
QY	361	ACGATATTGACTTCTTCTGTGA 383	
Db	361	ACGATATTGACTTCTTCTGCGA 383	
RESULT 7			
AAH17583			
ID	AAH17583	standard; cDNA; 387 BP.	
XX	AAH17583;		
AC	AAH17583;		
XX	26-FEB-2002	(first entry)	
XX		DNA encoding novel secreted protein #12.	
XX		Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine;	
XX		antiinflammatory; neuroprotective; nephrotropic; cardiovascular;	
XX		human; cancer; autoimmune disease; wound healing disorder; infection;	
XX		haematopoietic disorder; inflammatory disorder; infertility;	
XX		neurological disease; psychiatric disease; cardiovascular disease;	
XX		respiratory disease; renal; gastrointestinal; ss.	
OS		Homo sapiens.	
XX			
XX	Key	Location/Qualifiers	
PH	CDS	1..387	
FT		/*tag= a	
FT		/product= "Human secreted protein"	
XX			
PN	WO200179454-A1.		
XX			
XX	25-OCT-2001.		
XX	11-APR-2001;	2001WO-US11797.	
XX	13-APR-2000;	2000US-196603P.	
PR	24-APR-2000;	2000US-199417P.	
XX		(SMIK ) SMITHKLINE BEECHAM CORP.	
PA		(SMIK ) SMITHKLINE BEECHAM PLC.	
XX			
XX	Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;		
XX			
XX	WPI; 2002-061975/08.		
DR	P-PSDB; AAU09871.		
XX			
XX	New secreted proteins or polypeptides, useful for treating e.g. cancer,		
PT	autoimmune diseases, wound healing disorder, infections, haematopoietic		
PT	disorders, inflammatory disorders, infertility, cancer -		
XX			
XX	Claim 2; Page 44; 92pp; English.		
XX			
CC	The invention relates to an isolated novel secreted polypeptide (I) and		
CC	polynucleotide (II). (I) and (II) are useful for treating cancer,		
CC	autoimmune diseases, wound healing disorder, infections, haematopoietic		
CC	disorders, inflammatory disorders, infertility, neurological and		
CC	psychiatric diseases, cardiovascular diseases, these may also be used to		
CC	renal diseases, or gastrointestinal diseases. These may also be used to		
CC	treat diseases, abnormalities and disorders caused by abnormal		
CC	expression, production, function and/or metabolism of the genes, as		
CC	vaccines for inducing immunological response in a mammal, and in		
CC	screening methods for detecting the effect of added compounds on the		
CC	production of mRNA and polypeptide in cells. The polypeptides can be used		
CC	as immunogens to produce antibodies immunospecific for the polypeptides,		
CC	and to identify membrane-bound or soluble receptors. The polynucleotides		
CC	may be used as diagnostic reagents, in chromosome localisation studies,		
CC	and in tissue expression studies. The present sequence represents the		
CC	coding sequence of novel human secreted protein #12.		
XX			
SQ	Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;		
	Query Match	74.7%; Score 287; DB 24; Length 387;	
	Best Local Similarity	84.3%; Pred. No. 3.1e-82;	
	Matches 323; Conservative	0; Mismatches 60; Indels 0; Gaps 0;	
QY	1	ATGCGAAGGATATTGATTTCTTTGCTGGGGCTTTGTTCTATGTCGCGGATGGT	60
Db	1	ATGCGAAGGATATTGTTTCTTCTCCCGGCTTTGTTGCTGTATGCTGTGATGGA	60
QY	61	GTATTTATGGATAAATTTCTTTCTAAGAAAGTTGTGTGCGGATGAGGAGTGTCTATACT	120
Db	61	ATATTTATGGACCGTCTAGCTTCCAAGAAAGCTCTGTGCGATGATGATGTTCTATCT	120
QY	121	ATTTCTCTGGCAAGACACAGGAGATTACAATGCCCGGAGCTGTAGGTTTCATCGATGTC	180
Db	121	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAAGCCCGGACTGTAGATTCAATTAAGTT	180
QY	181	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGTGTAAACAGAAACCGAGCTGGAGAG	240
Db	181	AAAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGTGTAAAGAAATGAGCTGGAGAA	240
QY	241	TTTTGGCTGGCAGTGTATGTTGACCCACAGATGAGATGGAAATTTAGGTTATTTTC	300
Db	241	TTTTGGCTGGCAGTGTATGTTGATGGCGCAGACGAGATGGGATGGGTTATTTTC	300
QY	301	CCAGCAACTTGTGTAAGGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATCCCAACC	360
Db	301	CCAGGAACTTGTGTAAGGAAACAGCGTGTATACCAGGAAGTACCAAGGAAGTTCCACC	360
QY	361	ACGATATTGACTTCTTCTGTGA 383	
Db	361	ACGATATTGACTTCTTCTGCGA 383	
RESULT 8			
AAH26341			
ID	AAH26341	standard; cDNA; 426 BP.	
XX	AAH26341;		
AC	AAH26341;		
XX	02-OCT-2001	(first entry)	
DT		Human growth regulatory-like polypeptide clone 16372272.	
XX			
XX	Growth regulatory-like polypeptide; human; cartilage; melanoma;		
KW	neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;		
KW	ss.		
XX			
OS	Homo sapiens.		
XX			
XX	WO200155332-A2.		
PN			
PD	02-AUG-2001.		
XX			
XX	25-JAN-2001; 2001WO-US02455.		



```
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI: 2002-171999/22.
DR P-PSDB; ABB95602.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 1; Fig 359; 567pp; English.
XX
XX The present invention provides the protein and coding sequences of human
CC PRO proteins. These are useful for treating or diagnosing a
CC cardiovascular, endothelial or angiogenic disorder, including cardiac
CC hypertrophy, trauma, cancer, age-related macular degeneration,
CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC healing. The present sequence is a coding sequence of the invention.
XX
XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
SQ
Query Match 74.7%; Score 287; DB 24; Length 521;
Best Local Similarity 84.3%; Pred. No. 3.5e-82;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
Qy 1 ATGGCAAGGATATTGATCTTTTCCTGGGGCCCTGTGGTCTCTATGTCGGGCGCATGGT 60
Db 38 ATGGCAAGAAATATTGTACTTTTCTCCCGGGTCTTGGGCTGTATGCTGTGCATGGA 97
Qy 61 GTATTTATGGATAAACTTTCTTCAAGAAAGTTGTGCGGATGAGGAGTGTGTCTATACT 120
Db 98 ATATTTATGGACCGCTAGCTTCCCAAGAGCTCTGTGCAGATGATGATGTGTCTATACT 157
Qy 121 ATTTCTCTGGCAAGACACAGAGATTAATATGCCCGAGCTAGTTCATCGATGTC 180
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTAATATGCCCGAGCTAGTTCATTAACGTT 217
Qy 181 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAG 240
Db 218 AAAAAAGGCGACAGATCTATGTTACTCAAGCTGGTAAGAAAGAAATGGAGCTGGAGAA 277
Qy 241 TTTTGGGCTGCGAGTGTATTTATGGTGACCAACAGATGAGATGGGAATTTGATAGTTATTC 300
Db 278 TTTTGGGCTGCGAGTGTATTTATGGTGATGGCCAGGACGAGATGGGAGTCTGGGTATTTTC 337
Qy 301 CCCGACACTTGGTGAAGGACGAGCTGTATACAGGAGGCCACCAAGGAGATCCCAACC 360
Db 338 CCCGAGCACTTGGTGAAGGACGAGCTGTATACAGGAGGCCACCAAGGAGATTCCTCCACC 397
Qy 361 ACGGATATTGACTTCTTCTGTGA 383
Db 398 ACGGATATTGACTTCTTCTGTGA 420
RESULT 10
ABL88251
ID ABL88251 standard; cDNA; 521 BP.
XX
XX ABL88251;
AC
XX
XX 16-MAY-2002 (first entry)
DT
```

```
XX DE
XX Human PRO9873 cDNA sequence SEQ ID NO:359.
XX
XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200200690-A2.
XX
XX 03-JAN-2002.
XX
XX 20-JUN-2001; 2001WO-US19692.
XX
XX 23-JUN-2000; 2000US-213637P.
XX 20-JUL-2000; 2000US-219556P.
XX 25-JUL-2000; 2000US-220624P.
XX 28-JUL-2000; 2000US-220664P.
XX 02-AUG-2000; 2000US-2220710.
XX 17-AUG-2000; 2000US-222695P.
XX 23-AUG-2000; 2000US-0643657.
XX 24-AUG-2000; 2000WO-US23352.
XX 07-SEP-2000; 2000WO-US23328.
XX 18-SEP-2000; 2000US-230978P.
XX 18-SEP-2000; 2000US-0664610.
XX 18-SEP-2000; 2000US-0665350.
XX 24-OCT-2000; 2000US-242922P.
XX 08-NOV-2000; 2000US-0709238.
XX 08-NOV-2000; 2000WO-US30952.
XX 10-NOV-2000; 2000WO-US30873.
XX 01-DEC-2000; 2000US-0747259.
XX 20-DEC-2000; 2000WO-US34956.
XX 22-JAN-2001; 2001US-0767609.
XX 28-FEB-2001; 2001US-0796498.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-MAR-2001; 2001WO-US06666.
XX 09-MAR-2001; 2001US-0802706.
XX 14-MAR-2001; 2001US-0808689.
XX 22-MAR-2001; 2001US-0816744.
XX 05-APR-2001; 2001US-0828366.
XX 10-MAY-2001; 2001US-0854208.
XX 10-MAY-2001; 2001US-0854280.
XX 25-MAY-2001; 2001US-0866028.
XX 25-MAY-2001; 2001US-0866034.
XX 25-MAY-2001; 2001WO-US17092.
XX 30-MAY-2001; 2001US-0870574.
XX 30-MAY-2001; 2001WO-US17443.
XX 01-JUN-2001; 2001WO-US17800.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI: 2002-090516/12.
XX P-PSDB; ABB84996.
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 2; Fig 359; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC
```

CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
CC activities, and can be used in gene therapy. The PRO polynucleotides,  
CC proteins, agonists and antagonists are useful for treating or diagnosing  
CC a cardiovascular endothelial or angiogenic disorder in a mammal,  
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
CC degeneration, atherosclerosis, hypertension, arterial restenosis,  
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
CC carcinoma) and wound healing. The PRO polynucleotides have applications  
CC in molecular biology, including use as hybridisation probes, and in  
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
CC probes used in the exemplification of the present invention.  
XX  
SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
Query Match 74.7%; Score 287; DB 24; Length 521;  
Best Local Similarity 84.3%; Pred. No. 3.5e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGGCATGGT 60  
Db ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGGCATGG 97  
QY 61 GTATTATCGATAAATCTTCTCAAGAGTGTGTGCGGATGAGGAGTGTCTATCT 120  
Db GTATTATCGACCGCTAGCTTCAAGAGCTCTGTGCGAGATGAGTGTCTATCT 157  
QY 121 ATTTCTCTGGCAGACACAGGAGATTACAATGCCCGAGCTGTAGTTCATCGATGTC 180  
Db ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCGGACTGTAGTTCATTAACGTT 217  
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAACTGGTAACAGAAACCGAGCTGGAG 240  
Db AAAAAAGGGCAGCAGATCTATGTTGTACTCAAGCTGGTAAAGAAATGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGCGAGTGTATTGTGTGACACCGAGATGAGATGGGAATTGTAGTATTTC 300  
Db TTTTGGGCTGCGAGTGTATTGTGTGACGACGAGATGGGAGTGTGGTATTTC 337  
QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGGCCACCAAGGAGATCCCAACC 360  
Db CCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAATGCCACC 397  
QY 361 ACGGATATTGACTTCTTCTGTGA 383  
Db ACGGATATTGACTTCTTCTGCGA 420  
RESULT 11  
ABK33571  
ID ABK33571 standard; cDNA; 521 BP.  
XX AC ABK33571;  
XX  
XX  
DT 08-MAY-2002 (first entry)  
XX  
XX cDNA encoding human PRO protein, Seq ID No 71.  
DE  
XX Human; secreted protein; PRO; tumour; lung cancer; colon cancer;  
KW breast cancer; prostate tumour; rectal tumour; liver tumour;  
KW pericyte cell proliferation; chondrocyte cell proliferation;  
KW tumour necrosis factor-alpha; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200208288-A2.  
XX  
XX 31-JAN-2002.  
XX  
XX 29-JUN-2001; 2001WO-US21066.  
XX  
XX 20-JUL-2000; 2000US-219556P.  
XX  
XX 25-JUL-2000; 2000US-220585P.

PR 25-JUL-2000; 2000US-220605P.  
PR 25-JUL-2000; 2000US-220607P.  
PR 25-JUL-2000; 2000US-220624P.  
PR 25-JUL-2000; 2000US-220638P.  
PR 25-JUL-2000; 2000US-220664P.  
PR 25-JUL-2000; 2000US-220666P.  
PR 26-JUL-2000; 2000US-220893P.  
PR 28-JUL-2000; 2000WO-US20710.  
PR 23-AUG-2000; 2000WO-US23522.  
PR 24-AUG-2000; 2000WO-US23328.  
PR 15-SEP-2000; 2000US-000000P.  
PR 10-NOV-2000; 2000WO-US30873.  
PR 28-NOV-2000; 2000US-253646P.  
PR 01-DEC-2000; 2000WO-US32678.  
PR 20-DEC-2000; 2000US-0747259.  
PR 28-DEC-2000; 2000WO-US34956.  
PR 28-FEB-2001; 2001WO-US06520.  
PR 10-MAY-2001; 2001US-0854280.  
PR 25-MAY-2001; 2001WO-US17092.  
XX (GETH ) GENENTECH INC.  
PA  
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;  
PI  
XX WPI: 2002-172001/22.  
XX P-PSDB; AAU83627.  
DR  
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
XX such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
XX tumour or liver tumour -  
XX  
XX Claim 2; Figure 71; 359pp; English.  
XX  
XX The invention relates to one hundred and twenty two nucleic acids  
XX encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
XX encode human secreted proteins. The PRO nucleic acids, polypeptides,  
XX agonists and antagonists are useful for treating a PRO related disorder.  
XX The PRO polypeptides are useful for diagnosing tumours, especially lung  
XX cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
XX liver tumour. The PRO polypeptides are useful for stimulating the  
XX proliferation of, or gene expression in, pericyte cells, for stimulating  
XX the proliferation or differentiation of chondrocyte cells, for  
XX stimulating the release of tumour necrosis factor-alpha from human blood,  
XX for stimulating or inhibiting the proliferation of normal human dermal  
XX fibroblast cells. The PRO polypeptide may also be used as molecular  
XX weight markers and for tissue typing. The PRO nucleic acids have  
XX applications in molecular biology, including use as hybridisation probes,  
XX and in chromosome and gene mapping. ABK33536-ABK33657 represent human  
XX PRO protein coding sequences of the invention.  
XX  
SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;  
Query Match 74.7%; Score 287; DB 24; Length 521;  
Best Local Similarity 84.3%; Pred. No. 3.5e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGGCATGGT 60  
Db ATGGCAAGGATATTGATCTTTGCTTGGGGGCTTGTGCTTATGTCGGGGCATGG 97  
QY 61 GTATTATCGATAAATCTTCTCAAGAGTGTGTGCGGATGAGGAGTGTCTATCT 120  
Db GTATTATCGACCGCTAGCTTCAAGAGCTCTGTGCGAGATGAGTGTCTATCT 157  
QY 121 ATTTCTCTGGCAGACACAGGAGATTACAATGCCCGAGCTGTAGTTCATCGATGTC 180  
Db ATTTCTCTGGCTAGTGTCTCAAGAGATTATAATGCCCGGACTGTAGTTCATTAACGTT 217  
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAACTGGTAACAGAAACCGAGCTGGAG 240  
Db AAAAAAGGGCAGCAGATCTATGTTGTACTCAAGCTGGTAAAGAAATGAGCTGGAGAA 277

QY 241 TTTTGGCTGGCAGTCTTTATGCTGACCCAGCAGATGAGATGGAAATTTAGTTATTTTC 300  
 DB 278 TTTTGGCTGGCAGTCTTTATGCTGATGGCCAGCAGATGGAGTCGTGGGTATTTTC 337  
 QY 301 CCAGCAACTTGGTGAAGGAGCAGCGTGATACAGGAGGCCACCAAGAGATCCCAACC 360  
 DB 338 CCAGGAACTTGGTCAAGGAAACAGCGTGATACAGGAAGCTACCAAGGAAGTTCCACC 397  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 DB 398 ACGGATATTGACTTCTTCTGTGA 420

RESULT 12  
 AAH98228  
 ID AAH98228 standard; cDNA; 891 BP.  
 AC AAH98228;  
 XX  
 DT 12-OCT-2001 (first entry)  
 DE Human EST-derived coding sequence SEQ ID NO: 85.  
 XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
 KW diagnostics; forensic test; gene mapping; genetic disorder;  
 KW biodiversity; gene therapy; nutrition; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200154477-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-US02687.  
 XX  
 PR 25-JAN-2000; 2000US-0491404.  
 PR 17-JUL-2000; 2000US-0617746.  
 PR 03-AUG-2000; 2000US-0631451.  
 PR 15-SEP-2000; 2000US-0663870.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
 XX  
 DR WPI; 2001-476164/51.  
 DR P-PSDB; AAM23569.  
 XX  
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising  
 PT antibodies and research use -  
 XX  
 PS Claim 1; Page 236; 1275pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of novel  
 CC proteins from a variety of organisms, including human, dog, cat, horse,  
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
 CC from the organism of interest. They can be used in diagnostics,  
 CC forensics, gene mapping, identification of mutations, to assess  
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA  
 CC of the invention.  
 XX  
 SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;  
 XX

Query Match 74.7%; Score 287; DB 22; Length 891;  
 Best Local Similarity 84.3%; Pred. No. 4.4e-82;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGATATTGATTTCTTTGCTGGGGCCTTGTGTTCTATGTGCGGGCATGGT 60  
 DB 19 ATGGCAAGATATTGTTACTTTCTCCCGGGCTTTGTGCTGTATGTGTGTCATGGA 78

QY 61 GTATTTATGGATAAACTTTCTTCTTAAGAAGTTGTGTCCGATGAGGAGTGTCTTACT 120  
 DB 79 ATATTTATGGACCGTCTAGCTTCCAAAGAAGCTCTGTGCAGATGATGAGTGTCTACT 138  
 QY 121 ATTTCCTCTGCAAGAGCAGCAGGAAGATTACAATGCCCCAGACTGTAGTTTCATCGATGTC 180  
 DB 139 ATTTCCTCTGCTAGTCTCTCAGGAAGATTATATGCCCCGACCTGTAGATTCNTTAACGTT 198  
 QY 181 AAGAAAGGCGAGCAGATCTATGTTTACTCCAGCTGGTAAACAGAAACCGAGCTGGAGAG 240  
 DB 199 AAAAAAGGCGAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAAGAAATGCGAGCTGGAGAA 258  
 QY 241 TTTTGGCTGGCAGTCTTTATGCTGACCCAGCAGATGAGATGGAAATTTAGTTATTTTC 300  
 DB 259 TTTTGGCTGGCAGTCTTTATGCTGATGGCCAGCAGATGGAGTCGTGGGTATTTTC 318  
 QY 301 CCAGCAACTTGGTGAAGGAGCAGCGTGATACAGGAGGCCACCAAGAGATCCCAACC 360  
 DB 319 CCAGGAACTTGGTCAAGGAAACAGCGTGATACAGGAAGCTACCAAGGAAGTTCCACC 378  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 DB 379 ACGGATATTGACTTCTTCTGTGA 401

RESULT 13  
 AAH26342  
 ID AAH26342 standard; cDNA; 891 BP.  
 AC AAH26342;  
 XX  
 DT 02-OCT-2001 (first entry)  
 DE Human growth regulatory-like polypeptide partial cDNA clone.  
 XX  
 KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200155332-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 PF 25-JAN-2001; 2001WO-US02455.  
 XX  
 PR 25-JAN-2000; 2000US-0491404.  
 PR 02-MAY-2000; 2000US-0563786.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;  
 PI  
 XX WPI; 2001-483233/52.  
 XX  
 XX Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -  
 XX  
 PS Claim 1; Page 115; 119pp; English.  
 XX  
 CC The present sequence is that of a novel nucleic acid that was  
 CC assembled from human thymus cDNA library-derived Hyseq clone  
 CC identification number 16372272 (see AAH26341). A recursive  
 CC algorithm was used to extend the clone by pulling additional  
 CC sequences from different databases. A full-length sequence (see  
 CC AAH26343) encoding novel human growth regulatory-like polypeptide  
 CC (GRIP, see AAH82671) was subsequently obtained. Human GRIP  
 CC belongs to the same protein family as growth regulatory proteins,

```
CC growth factors, human melanoma derived growth regulatory protein
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and maintenance, inhibition of melanoma cell
CC cartilage development and tumours, including neuroectodermal tumours such as
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Query Match 74.7%; Score 287; DB 22; Length 891;
Best Local Similarity 84.3%; Pred. No. 4.4e-82;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTTATGTCGCGGATCGT 60
DB 19 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTTATGTCGCGATGGA 78

QY 61 GTATTATGGATAAATCTTCTTCTAAGAGTGTGTCGGGATGAGAGTGTCTTATCT 120
DB 79 ATATTATGGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGTCTTATCT 138

QY 121 ATTTCTCTGGCAAGACACAGAGATTAATGCCCCAGAGCTGTAGGTTTCATCGATGTC 180
DB 139 ATTTCTCTGGCTAGTGTCTCAAGAGATTAATGCCCCGAGCTGTAGATTCAATACGTT 198

QY 181 AAGAAAGGCGACAGATCTATGTTTACTCCAGAGCTGTAAACAGAAAACGAGCTGGAGAG 240
DB 199 AAAAAGGCGACAGATCTATGTTGACTCAAGAGCTGTAAAGAAAATGGAGCTGGAGAA 258

QY 241 TTTTGGGCTGGCAGGTTTATGTCACACAGGATGAGATGGGAATGTAGGTTTATTTTC 300
DB 259 TTTTGGGCTGGCAGGTTTATGTTGATGTCACAGGACGAGATGGGAGTCTGGGTTATTTTC 318

QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATCCCAACC 360
DB 319 CCCAGCAACTTGGTGAAGGACAGCGTGTGTACAGGAGGCTACCAAGGAAGTCCCAACC 378

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 379 ACGGATATTGACTTCTTCTGTGA 401

RESULT 14
AAF59083
ID AAF59083 standard; DNA; 923 BP.
XX
AC AAF59083;
XX
DT 23-APR-2001 (first entry)
XX
DE Human MLP nucleotide sequence SEQ ID NO:29.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
OS Homo sapiens.
XX
XX WC200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JF04278.
XX
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```
PR 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 1; Page 99-100; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

Query Match 74.7%; Score 287; DB 22; Length 923;
Best Local Similarity 84.3%; Pred. No. 4.5e-82;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTTATGTCGCGGATCGT 60
DB 34 ATGGCAAGGATATTGATTCTTTTGGCTTGGGGCCCTTGGTCTTATGTCGATGGA 93

QY 61 GTATTATGGATAAATCTTCTTCTAAGAGTGTGTCGGATGAGAGTGTCTTATCT 120
DB 94 ATATTATGGACCGCTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGTCTTATCT 153

QY 121 ATTTCTCTGGCAAGACACAGAGATTAATGCCCCAGAGCTGTAGGTTTCATCGATGTC 180
DB 154 ATTTCTCTGGCTAGTGTCTCAAGAGATTAATGCCCCGAGCTGTAGATTCAATACGTT 213

QY 181 AAGAAAGGCGACAGATCTATGTTTACTCCAGAGCTGTAAACAGAAAACGAGCTGGAGAG 240
DB 214 AAAAAGGCGACAGATCTATGTTGACTCAAGAGCTGTAAAGAAAATGGAGCTGGAGAA 273

QY 241 TTTTGGGCTGGCAGTGTATGTTGTCACCAAGGATGAGATGGGAATGTAGGTTTATTTTC 300
DB 274 TTTTGGGCTGGCAGTGTATGTTGTCACCAAGGATGAGATGGGAGTCTGGGTTATTTTC 333

QY 301 CCCAGCAACTTGGTGAAGGAGCGGTGTATACAGGAGGCCACCAAGGAGATCCCAACC 360
DB 334 CCCAGCAACTTGGTGAAGGAGCGGTGTGTACAGGAGGCTTACCAAGGAAGTCCCAACC 393

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 394 ACGGATATTGACTTCTTCTGTGA 416

RESULT 15
AAH26343
ID AAH26343 standard; cDNA; 1201 BP.
XX
XX AC AAH26343;
XX
XX 02-OCT-2001 (first entry)
XX
XX Human growth regulatory-like polypeptide cDNA.
XX
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KW ss.
```

XX OS Homo sapiens.  
XX PH Key Location/Qualifiers  
XX FT CDS 33..419  
XX FT sig\_peptide /\*tag= a  
XX FT mat\_peptide 33..101  
XX FT 102..416 /\*tag= b  
XX FT /\*tag= c  
XX PN WO200155332-A2.  
XX PD 02-AUG-2001.  
XX PF 25-JAN-2001; 2001WO-US02455.  
XX PR 25-JAN-2000; 2000US-0491404.  
XX PR 02-MAY-2000; 2000US-0563786.  
XX PA (HYSEQ-) HYSEQ INC.  
XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
XX PI Drmanac RT;  
XX DR WPI; 2001-483233/52.  
XX DR P-PSDB; AAB82671.  
XX PT Isolated human growth regulatory-like polypeptide useful for treating  
XX PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
XX PT hyperproliferative disorders, coagulation disorders, and nervous system  
XX PT disorders -  
XX PS Claim 1; Page 115-116; 119pp; English.  
XX CC The present sequence is that of a novel nucleic acid encoding  
XX CC human growth regulatory-like polypeptide (GRLP, see AAB82671).  
XX CC The sequence was assembled using human thymus cDNA library-derived  
XX CC Hyseq clone identification number 16372272 (see AAB26341) as seed,  
XX CC using software programs to pull additional sequences from Hyseq's  
XX CC proprietary database containing expressed sequence tag sequences,  
XX CC and by gel sequencing using primers to extend both 5' and 3' ends.  
XX CC The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
XX CC belongs to the same protein family as growth regulatory proteins,  
XX CC growth factors, human melanoma derived growth regulatory protein  
XX CC precursor (64% similarity and 45% identity over 111 amino acids)  
XX CC or melanoma inhibitory activity, cattle cartilage-derived  
XX CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
XX CC similarity over 126 amino acids) and other retinoic acid-sensitive  
XX CC proteins. GRLP polypeptides and polynucleotides of the invention  
XX CC can be used in the prophylaxis, treatment (including gene therapy)  
XX CC and diagnosis of disorders and diseases caused by, or involving,  
XX CC cartilage development and maintenance, inhibition of melanoma cell  
XX CC growth and tumours, including neuroectodermal tumours such as  
XX CC gliomas. The polynucleotides can also be used to design probes  
XX CC and primers, for chromosome and gene mapping, in the recombinant  
XX CC production of protein, in the generation of antisense, ribozyme and  
XX CC peptide-nucleic acid molecules, and to produce transgenic animals.  
XX CC They may also have cytokine and cell proliferation or  
XX CC differentiation activity, stem cell growth factor activity,  
XX CC haematopoiesis regulating activity, tissue growth activity,  
XX CC immunosuppressive or immunostimulant activity, activin/inhibin  
XX CC activity, chemotactic/chemokinetic activity, haemostatic and  
XX CC thrombolytic activity, use in cancer diagnosis and therapy,  
XX CC drug screening, receptor/ligand activity, antiinflammatory  
XX CC activity, and treatment of leukaemia, nervous system disorders,  
XX CC arthritis and inflammation.  
XX SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;

Query Match 74.7%; Score 287; DB 22; Length 1201;  
Best Local Similarity 84.3%; Pred. No. 5.1e-82;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTCTTTTCCTTGGGGCCTTGTGGTTCTATGTGCGGCGCATGCT 60  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 92  
QY 61 GTATTATGGATAAACTTTCTTTAAGAAGTTGTGTGCGGATGAGGAGTGTCTTATACT 120  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 152  
QY 93 ATATTATGGACCGCTTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTCTTATACT 152  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 180  
QY 121 ATTTCTCTGGCAAGACACAGAGATTAATAATGCCCCAGACTGTAGTTCATCGATGTC 180  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 212  
QY 181 AAGAAAGGCGACAGATCTATGTTTACTCCAGCTGGTAAACAGAAAACGGAGCTGGAGAG 240  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 272  
QY 241 TTTTGGGCTGGCAGTGTATTATGTGTGACCCAGGATGAGATGGGAATTTGTAGTTATTTC 300  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 332  
QY 273 TTTTGGGCTGGCAGTGTATTATGTGTGATGGCCAGGACGAGATGGGATCGTGGTTATTTC 332  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 360  
QY 301 CCCAGCAACTTTGGTGAAGGACGCGGTATATACAGGAGGCCACCAAGGAGATCCCAACC 360  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 392  
QY 361 ACGGATATTGACTTCTTCTGTGA 383  
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 415

Search completed: December 30, 2003, 02:14:32  
Job time : 128.462 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 04:08:13 ; Search time 315.339 Seconds  
(without alignments)  
4172.254 Million cell updates/sec

Title: US-10-019-455A-10  
Perfect score: 384  
Sequence: 1 atggcaagatattgattct.....atattgactctctgtgaa 384

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2244575 seqs, 1713117285 residues

Total number of hits satisfying chosen parameters: 4489150

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications NA:\*
- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
  - 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
  - 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
  - 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
  - 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
  - 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
  - 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
  - 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
  - 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
  - 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
  - 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
  - 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
  - 13: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq2:\*
  - 14: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
  - 15: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
  - 16: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
  - 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
  - 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	287	74.7	426	15	US-10-216-038-1
2	287	74.7	521	13	Sequence 71, Appl
3	287	74.7	521	13	Sequence 71, Appl
4	287	74.7	521	13	Sequence 71, Appl
5	287	74.7	521	13	Sequence 71, Appl
6	287	74.7	521	13	Sequence 71, Appl
7	287	74.7	521	13	Sequence 71, Appl
8	287	74.7	521	13	Sequence 71, Appl
9	287	74.7	521	13	Sequence 71, Appl
10	287	74.7	521	13	Sequence 71, Appl
11	287	74.7	521	13	Sequence 71, Appl
12	287	74.7	521	13	Sequence 71, Appl
13	287	74.7	521	13	Sequence 71, Appl
14	287	74.7	521	13	Sequence 71, Appl
15	287	74.7	521	13	Sequence 71, Appl

16	287	74.7	521	13	US-10-219-531-71
17	287	74.7	521	13	US-10-219-532-71
18	287	74.7	521	13	US-10-219-533-71
19	287	74.7	521	13	US-10-223-081-359
20	287	74.7	521	13	US-10-230-437-71
21	287	74.7	521	13	US-10-232-228-71
22	287	74.7	521	13	US-10-233-082-359
23	287	74.7	521	15	US-10-227-884-71
24	287	74.7	521	15	US-10-230-163-71
25	287	74.7	521	15	US-10-230-338-71
26	287	74.7	521	15	US-10-218-631-71
27	287	74.7	521	15	US-10-230-414-71
28	287	74.7	521	15	US-10-216-159A-71
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33	287	74.7	521	15	US-10-230-434-71
34	287	74.7	521	15	US-10-219-003-71
35	287	74.7	521	15	US-10-219-075-71
36	287	74.7	521	15	US-10-219-464-71
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39	287	74.7	521	15	US-10-219-481-71
40	287	74.7	521	15	US-10-230-260-71
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42	287	74.7	521	15	US-10-232-233-71
43	287	74.7	521	15	US-10-216-165-71
44	287	74.7	521	15	US-10-218-956-71
45	287	74.7	521	15	US-10-219-468-71

ALIGNMENTS

RESULT 1  
US-10-216-038-1  
; Sequence 1, Application US/10216038  
; Publication No. US20030124573A1  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Aterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjastaad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1el Growth i  
; FILE REFERENCE: HVS-7CIP  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; PRIOR FILING DATE: 2002-08-08  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 426  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (426)..(426)  
; OTHER INFORMATION: n = A, T, G, or C  
US-10-216-038-1

Query Match 74.7%; Score 287; DB 15; Length 426;  
Best Local Similarity 84.3%; Pred. No. 7.1e-87;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;



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QY 1 ATGCGAAGATATTGATCTTTTGGTGGGGCCTTGGTCTATGTGCCGGGATGGT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
19 ATGCGAAGATATTGATCTTTTCCCGGGTCTTGGGCTGTATGTCTGTGATGGA 78
QY 61 GTATTATGGATAAACTTTCTTCTAAGAAAGTTGTGTGCGGATGAGAGTGTCTATACT 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
79 ATATTATGACCGTCTAGCTTCCAAAGAGCTGTGTGAGATGATGAGTGTCTATACT 138
QY 121 ATTTCTCTGCGAAGACACAGGAAGATTACAATGCCCGGACAGTGTATGATGTC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
139 ATTTCTCTGCTAGTCTCAAGAAAGATTATAATGCCCGGACGTGTAGATTCAATACGTT 198
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAGAGCTGTAAACAGAAAAACGAGCTGGAGAG 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
199 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAAAATGAGCTGGAGAA 258
QY 241 TTTTGGGCTGGCAGTGTATGTGTACACCGAGATGAGATGGAAATGTAGTTATTTC 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
259 TTTTGGGCTGGCAGTGTATGTGTATGGTGATGGCCAGGACGATGGGATCGTGGGTTATTTC 318
QY 301 CCCAGCAACTTGTGTGAAGAGCAGCGTGTATACCGAGGGCCACCAAGAGATCCCAACC 360
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
319 CCCAGCAACTTGTGTGAAGAGCAGCGTGTATACCGAGGGCCACCAAGAGATCCCAACC 378
QY 361 ACGGATATTGACTTCTCTGTGA 383
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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## RESULT 2

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US-10-216-163-71
; Sequence 71, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246

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## ; SEQ ID NO 71

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; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-216-163-71

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Query Match 74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7,9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 1 ATGCGAAGATATTGATCTTTTGGTGGGGCCTTGGTCTATGTGCCGGGATGGT 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
38 ATGCGAAGATATTGATCTTTTCCCGGGTCTTGGGCTGTATGTCTGTGATGGA 97
QY 61 GTATTATGGATAAACTTTCTTCTAAGAAAGTTGTGTGCGGATGAGAGTGTCTATACT 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
98 ATATTATGACCGTCTAGCTTCCAAAGAGCTGTGTGAGATGATGAGTGTCTATACT 157
QY 121 ATTTCTCTGCGAAGACACAGGAAGATTACAATGCCCGGACAGTGTATGATGTC 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
158 ATTTCTCTGCTAGTCTCAAGAAAGATTATAATGCCCGGACGTGTAGATTCAATACGTT 217
QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAGAGCTGTAAACAGAAAAACGAGCTGGAGAG 240
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218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAAAATGAGCTGGAGAA 277
QY 241 TTTTGGGCTGGCAGTGTATGTGTACACCGAGATGAGATGGAAATGTAGTTATTTC 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
278 TTTTGGGCTGGCAGTGTATGTGTATGGTGATGGCCAGGACGATGGGATCGTGGGTTATTTC 337
QY 301 CCCAGCAACTTGTGTGAAGAGCAGCGTGTATACCGAGGGCCACCAAGAGATCCCAACC 360
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338 CCCAGCAACTTGTGTGAAGAGCAGCGTGTATACCGAGGGCCACCAAGAGATCCCAACC 397
QY 361 ACGGATATTGACTTCTCTGTGA 383
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
398 ACGGATATTGACTTCTCTGCGA 420

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## RESULT 3

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US-10-218-765-71
; Sequence 71, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-12
; PRIOR FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 1997-10-17
; PRIOR FILING DATE: 1997-10-28
; PRIOR FILING DATE: 1998-03-20
; PRIOR FILING DATE: 1998-03-25
; PRIOR FILING DATE: 1998-03-26
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246

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PRIOR APPLICATION NUMBER: 60/100911	PRIOR FILING DATE: 1998-09-17	PRIOR APPLICATION NUMBER: 60/101477	PRIOR FILING DATE: 1998-09-23	PRIOR APPLICATION NUMBER: 60/101738	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101741	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101786	PRIOR FILING DATE: 1998-09-25	PRIOR APPLICATION NUMBER: 60/101916	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/101922	PRIOR FILING DATE: 1998-09-24	PRIOR APPLICATION NUMBER: 60/106178	PRIOR FILING DATE: 1998-10-28	PRIOR APPLICATION NUMBER: 60/106248	PRIOR FILING DATE: 1998-10-29	PRIOR APPLICATION NUMBER: 60/106464	PRIOR FILING DATE: 1998-10-30	PRIOR APPLICATION NUMBER: 60/106905	PRIOR FILING DATE: 1998-11-03	PRIOR APPLICATION NUMBER: 60/108787	PRIOR FILING DATE: 1998-11-17	PRIOR APPLICATION NUMBER: 60/108801	PRIOR FILING DATE: 1998-11-17	PRIOR APPLICATION NUMBER: 60/108849	PRIOR FILING DATE: 1998-11-18	PRIOR APPLICATION NUMBER: 60/112422	PRIOR FILING DATE: 1998-12-15	PRIOR APPLICATION NUMBER: 60/113296	PRIOR FILING DATE: 1998-12-22	PRIOR APPLICATION NUMBER: 60/113605	PRIOR FILING DATE: 1998-12-23	PRIOR APPLICATION NUMBER: 60/113621	PRIOR FILING DATE: 1998-12-23	PRIOR APPLICATION NUMBER: 60/115558	PRIOR FILING DATE: 1999-01-12	PRIOR APPLICATION NUMBER: 60/115565	PRIOR FILING DATE: 1999-01-12	PRIOR APPLICATION NUMBER: 60/115733	PRIOR FILING DATE: 1999-01-12	PRIOR APPLICATION NUMBER: 60/119549	PRIOR FILING DATE: 1999-02-10	PRIOR APPLICATION NUMBER: 60/123618	PRIOR FILING DATE: 1999-03-10	PRIOR APPLICATION NUMBER: 60/125259	PRIOR FILING DATE: 1999-03-19	PRIOR APPLICATION NUMBER: 60/125775	PRIOR FILING DATE: 1999-03-23	PRIOR APPLICATION NUMBER: 60/126773	PRIOR FILING DATE: 1999-03-29	PRIOR APPLICATION NUMBER: 60/127887	PRIOR FILING DATE: 1999-04-05	PRIOR APPLICATION NUMBER: 60/130232	PRIOR FILING DATE: 1999-04-21	PRIOR APPLICATION NUMBER: 60/131022	PRIOR FILING DATE: 1999-04-26	PRIOR APPLICATION NUMBER: 60/131270	PRIOR FILING DATE: 1999-04-27	PRIOR APPLICATION NUMBER: 60/131291	PRIOR FILING DATE: 1999-04-27	PRIOR APPLICATION NUMBER: 60/131445	PRIOR FILING DATE: 1999-04-28	PRIOR APPLICATION NUMBER: 60/134287	PRIOR FILING DATE: 1999-05-14	PRIOR APPLICATION NUMBER: 60/140650	PRIOR FILING DATE: 1999-06-22	PRIOR APPLICATION NUMBER: 60/140723	PRIOR FILING DATE: 1999-06-22	PRIOR APPLICATION NUMBER: 60/141037	PRIOR FILING DATE: 1999-06-23	PRIOR APPLICATION NUMBER: 60/144758
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; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/145698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: 60/146222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835
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Query Match 74.7%; Score 287; DB 13; Length 521;

Best Local Similarity 84.3%; Pred. No. 7.9e-87; Mismatches 60; Indels 0; Gaps 0;

Matches 323; Conservative 0;

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QY 1 ATGGCAAGGATATTGATCTTTTGTCTGGGGCCCTTGTGGTCTATGTCCGGGCATGGT 60
DB 38 ATGGCAAGATATTGATCTTTTCTCCCGGCTTGTGGCTATGTCTGTGCATGGA 97

QY 61 GTATTTATGATAAACTTTCTTCAAGAGATTGTGTGGGATGAGAGTGTGTCTATCT 120
DB 98 ATATTTATGACCGTCTAGCTTCCAAAGAGATTATATGCCCCGACTGTAGATTCAATACGTT 157

QY 121 ATTTCTCTGCAAGACACAGGAGATTACAATGCCCGCCAGACTGTAGTTCATCGATGC 180
DB 158 ATTTCTCTGGCTAGTGTATGTGTGATGGCCAGGACGAGATGGAGTCGTGGGTATTTC 217

QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGGTAAACAGAAACGAGCTGGAGAG 240
DB 218 AAAAAAGGGCAGCAGATCTATGTTACTCAAGAGCTGTGTCAAGAAATGGAGCTGGAGAA 277

QY 241 TTTTGGGCTGGCAGTGTATATGTGTACCCAGGATGAGATGGGAATTTGTAGTTATTTC 300
DB 278 TTTTGGGCTGGCAGTGTATATGTGTGATGGCCAGGACGAGATGGAGTCGTGGGTATTTC 337

QY 301 CCCAGCAACTTGTGTGAAGCAGCGTGTATACCAAGGAGCCACCAAGGAGATCCCAACC 360
DB 338 CCAGGAACCTTGTGTGAAGCAGCGTGTATACCAAGGAGCTACCAAGGAGTTCCACC 397

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 398 ACGGATATTGACTTCTTCTGCGA 420
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#### RESULT 4

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US-10-219-063-71
; Sequence 71, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME

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; FILE REFERENCE: P3530PIC24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-063-71
```

Query Match 74.7%; Score 287; DB 13; Length 521;

Best Local Similarity 84.3%; Pred. No. 7.9e-87; Mismatches 60; Indels 0; Gaps 0;

Matches 323; Conservative 0;

```
QY 1 ATGGCAAGGATATTGATCTTTTGTCTGGGGCCCTTGTGGTCTATGTCCGGGCATGGT 60
DB 38 ATGGCAAGATATTGATCTTTTCTCCCGGCTTGTGGCTATGTCTGTGCATGGA 97

QY 61 GTATTTATGATAAACTTTCTTCAAGAGATTGTGTGGGATGAGAGTGTGTCTATCT 120
DB 98 ATATTTATGACCGTCTAGCTTCCAAAGAGCTGTGTCAAGAAATGGAGCTGGAGAA 157

QY 121 ATTTCTCTGCAAGACACAGGAGATTACAATGCCCGCCAGACTGTAGTTCATCGATGC 180
DB 158 ATTTCTCTGGCTAGTGTATGTGTGATGGCCAGGACGAGATGGAGTCGTGGGTATTTC 217

QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGGTAAACAGAAACGAGCTGGAGAG 240
DB 218 AAAAAAGGGCAGCAGATCTATGTTACTCAAGAGCTGTGTCAAGAAATGGAGCTGGAGAA 277

QY 241 TTTTGGGCTGGCAGTGTATATGTGTACCCAGGATGAGATGGGAATTTGTAGTTATTTC 300
DB 278 TTTTGGGCTGGCAGTGTATATGTGTGATGGCCAGGACGAGATGGAGTCGTGGGTATTTC 337

QY 301 CCCAGCAACTTGTGTGAAGCAGCGTGTATACCAAGGAGCCACCAAGGAGATCCCAACC 360
DB 338 CCAGGAACCTTGTGTGAAGCAGCGTGTATACCAAGGAGCTACCAAGGAGTTCCACC 397

QY 361 ACGGATATTGACTTCTTCTGTGA 383
DB 398 ACGGATATTGACTTCTTCTGCGA 420
```

#### RESULT 5

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US-10-219-066-71
; Sequence 71, Application US/10219066
; Publication No. US20030187203A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
```



Db 158 ATTTCTGCTAGTGTCTCAAGAAGATTATATGCCCCGAGCTGTAGATTCAATTAAGTT 217  
 QY 181 AAGAAAGGGCAGCAGATCTATGTTTACTCAAGCTGGTAACAGAAACGAGCTGGAGAG 240  
 Db 218 AAAAAAGGGCAGCAGATCTATGTTTACTCAAGCTGGTAACAGAAACGAGCTGGAGAA 277  
 QY 241 TTTTGGGCTGGCAGTGTATGTTGTCACCAAGATGAGATGGGAATTTAGTGTATTTTC 300  
 Db 278 TTTTGGGCTGGCAGTGTATGTTGTCACCAAGATGAGATGGGAATTTAGTGTATTTTC 337  
 QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGAGAGCCCAAGAGGATCCCAACC 360  
 Db 338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCCAACC 397  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 Db 398 ACGGATATTGACTTCTTCTGTGA 420

RESULT 8  
 US-10-219-069-71  
 ; Sequence 71, Application US/10219069  
 ; Publication No. US20030187206A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PLC40  
 ; CURRENT APPLICATION NUMBER: US/10/219,069  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-069-71

Query Match 74.7%; Score 287; DB 13; Length 521;  
 Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTTCTTTGCTGGGGGCTTGTGTTCTATGTGCGGGCATGGT 60  
 Db 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGGCTGTATGTGCTGTGCAATGA 97  
 QY 61 GTATTTATGATTAACCTTTCTTCAAGAGTTGTGCGGATGAGGAGTGTCTATACT 120  
 Db 98 ATATTTATGACCGTCTAGCTTCCAGAGCTCTGTGCAGATGATGATGTGTCTACT 157  
 QY 121 ATTTCTCTGCAGAGCACAGGAGATTACAATGCCCGGCTTGTGTTCTATGTGCGGGCATGGT 180

QY 301 CCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGCCACCAAGGAGATCCCAACC 360  
 Db 338 CCCAGGAACTTGGTCAAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTTCCCAACC 397  
 QY 361 ACGGATATTGACTTCTTCTGTGA 383  
 Db 398 ACGGATATTGACTTCTTCTGTGA 420

RESULT 7  
 US-10-219-068-71  
 ; Sequence 71, Application US/10219068  
 ; Publication No. US20030187205A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Gerritsen, Mary  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stephan, Jean-Philippe F.  
 ; APPLICANT: Watanabe, Colin L.  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3530PLC31  
 ; CURRENT APPLICATION NUMBER: US/10/219,068  
 ; CURRENT FILING DATE: 2002-08-13  
 ; PRIOR APPLICATION NUMBER: 10/119,480  
 ; PRIOR FILING DATE: 2002-04-09  
 ; PRIOR APPLICATION NUMBER: 60/059113  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/062287  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/063549  
 ; PRIOR FILING DATE: 1997-10-28  
 ; PRIOR APPLICATION NUMBER: 60/064103  
 ; PRIOR FILING DATE: 1997-10-31  
 ; PRIOR APPLICATION NUMBER: 60/069873  
 ; PRIOR FILING DATE: 1997-12-17  
 ; PRIOR APPLICATION NUMBER: 60/078910  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: 60/079294  
 ; PRIOR FILING DATE: 1998-03-25  
 ; PRIOR APPLICATION NUMBER: 60/079656  
 ; PRIOR FILING DATE: 1998-03-26  
 ; PRIOR APPLICATION NUMBER: 60/079728  
 ; PRIOR FILING DATE: 1998-03-27  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 246  
 ; SEQ ID NO 71  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-219-068-71

Query Match 74.7%; Score 287; DB 13; Length 521;  
 Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
 Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATTGATTTCTTTGCTGGGGGCTTGTGTTCTATGTGCGGGCATGGT 60  
 Db 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGGCTGTATGTGCTGTGCAATGA 97  
 QY 61 GTATTTATGATTAACCTTTCTTCAAGAGTTGTGCGGATGAGGAGTGTCTATACT 120  
 Db 98 ATATTTATGACCGTCTAGCTTCCAGAGCTCTGTGCAGATGATGATGTGTCTACT 157  
 QY 121 ATTTCTCTGCAGAGCACAGGAGATTACAATGCCCGGCTTGTGTTCTATGTGCGGGCATGGT 180

Db 38 ATGCGCAAGAATATGTGTACTTTTCCCTCCGGGCTTGTGGCTGTATGTCTGTGCAATGGA 97  
QY 61 GTATTATGATAAACTTTCTTCTTAAGAAAGTGTGTGCGGATGAGGAGTGTGTCTTACT 120  
Db 98 ATATTATGACCGCTAGCTTCCCAAGAGCTCTGTGCAGATGATGAGTGTGTCTTACT 157  
QY 121 ATTTCTCTGCGCAAGAGACAGGAGATTACAATGCCCCGACAGTGTAGTTCATCGATGTC 180  
Db 158 ATTTCTCTGCGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 181 AAGAAAGGCGAGCAGATCTATGTTTACTCCAAGCTGTGTAACAGAAACCGAGCTGGAGAG 240  
Db 218 AAAAAAGGCGAGCAGATCTATGTTTACTCCAAGCTGTGTAACAGAAATGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTATGTTTATGTTGACCAACAGATGAGATGGAAATGTAGTATTTC 300  
Db 278 TTTTGGGCTGGCAGTGTATGTTTATGTTGATGGCAGGAGATGGAGTGGTGGTATTTC 337  
QY 301 CCAGCAACTTGTGAAGGAGCAGCGTGTATACCAAGGCGCCACCAAGGAGATCCCAACC 360  
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTATACCAAGGAAGCTACCAAGGAAGTTCACCACC 397  
QY 361 ACGGATATTGACTTCTTCTGTGA 383  
Db 398 ACGGATATTGACTTCTTCTGGA 420

RESULT 9  
US-10-219-073-71  
; Sequence 71, Application US/10219073  
; Publication No. US20030187207A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C52  
; CURRENT APPLICATION NUMBER: US/10/219,073  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521

TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-219-073-71  
Query Match 74.7%; Score 287; DB 13; Length 521;  
Best Local Similarity 84.3%; Pred. No. 7.9e-87;  
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;  
QY 1 ATGCGCAAGATATTGATTTCTTTTGGGGGCTTGTGGTCTTATGTCGCGGCGCATGGT 60  
Db 38 ATGCGCAAGAATATGTGTACTTTTCCCTCCGGGCTTGTGGCTGTATGTCTGTGCAATGGA 97  
QY 61 GTATTATGATAAACTTTCTTCTTAAGAAAGTGTGTGCGGATGAGGAGTGTGTCTTACT 120  
Db 98 ATATTATGACCGCTAGCTTCCCAAGAGCTCTGTGCAGATGATGAGTGTGTCTTACT 157  
QY 121 ATTTCTCTGCGCAAGAGACAGGAGATTACAATGCCCGGACTGTAGTTCATCGATGTC 180  
Db 158 ATTTCTCTGCGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAATTAACGTT 217  
QY 181 AAGAAAGGCGAGCAGATCTATGTTTACTCCAAGCTGTGTAACAGAAACCGAGCTGGAGAG 240  
Db 218 AAAAAAGGCGAGCAGATCTATGTTTACTCCAAGCTGTGTAACAGAAATGAGCTGGAGAA 277  
QY 241 TTTTGGGCTGGCAGTGTATGTTTATGTTGACCAACAGATGAGATGGAAATGTAGTATTTC 300  
Db 278 TTTTGGGCTGGCAGTGTATGTTTATGTTGATGGCAGGAGATGGAGTGGTGGTATTTC 337  
QY 301 CCAGCAACTTGTGAAGGAGCAGCGTGTATACCAAGGCGCCACCAAGGAGATCCCAACC 360  
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGTGTATACCAAGGAAGCTACCAAGGAAGTTCACCACC 397  
QY 361 ACGGATATTGACTTCTTCTGTGA 383  
Db 398 ACGGATATTGACTTCTTCTGGA 420  
RESULT 10  
US-10-219-475-71  
; Sequence 71, Application US/10219475  
; Publication No. US20030187208A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C49  
; CURRENT APPLICATION NUMBER: US/10/219,475  
; PRIOR FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294

```
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-475-71

Query Match          74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATGATCTTTTGGTGGGGCCCTTGTGCTATGTCGCGGCATGCT 60
Db 38 ATGGCAAGATATGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 97

QY 61 GTATTATGGAATAAATCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTCTATACT 120
Db 98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157

QY 121 ATTTCTCTGGCAAGACAGAGATTACAAATGCCCGACAGCTGTAGGTTCAATCGATGC 180
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAATTAACGTT 217

QY 181 AAGAAAGGCGACAGATCTATGTTTCTTCCAGAGCTGTAAACAGAAACGGAGCTGGAG 240
Db 218 AAAAAAGGCGACAGATCTATGTTTCTTCCAGAGCTGTAAAGAGAAATGGAGCTGGAG 277

QY 241 TTTTGGGCTGGCAGTGTATGTTGTCACACAGGATGAGATGGGAATTTAGGTTATTTTC 300
Db 278 TTTTGGGCTGGCAGTGTATGTTGTCACACAGGATGAGATGGGACTCTGGGTTATTTTC 337

QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 360
Db 338 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 397

RESULT 11
US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-480-71

Query Match          74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 ATGGCAAGGATATGATCTTTTGGTGGGGCCCTTGTGCTATGTCGCGGCATGCT 60
Db 38 ATGGCAAGATATGTTACTTTTCTCCCGGGTCTTGTGGCTGTATGCTGTGCATGGA 97

QY 61 GTATTATGGAATAAATCTTCTTAAGAAGTTGTGCGGATGAGGAGTGTCTATACT 120
Db 98 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157

QY 121 ATTTCTCTGGCAAGACAGAGATTACAAATGCCCGACAGCTGTAGGTTCAATCGATGC 180
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAATTAACGTT 217

QY 181 AAGAAAGGCGACAGATCTATGTTTCTTCCAGAGCTGTAAACAGAAACGGAGCTGGAG 240
Db 218 AAAAAAGGCGACAGATCTATGTTTCTTCCAGAGCTGTAAAGAGAAATGGAGCTGGAG 277

QY 241 TTTTGGGCTGGCAGTGTATGTTGTCACACAGGATGAGATGGGAATTTAGGTTATTTTC 300
Db 278 TTTTGGGCTGGCAGTGTATGTTGTCACACAGGATGAGATGGGACTCTGGGTTATTTTC 337

QY 301 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 360
Db 338 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 397

RESULT 12
US-10-219-483-71
; Sequence 71, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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Tue Dec 30 10:20:36 2003

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, FILE REFERENCE: P3530PIC43
, CURRENT APPLICATION NUMBER: US/10/219,483
, CURRENT FILING DATE: 2002-08-13
, PRIOR APPLICATION NUMBER: 10/119,480
, PRIOR FILING DATE: 2002-04-09
, PRIOR APPLICATION NUMBER: 60/059113
, PRIOR FILING DATE: 1997-09-17
, PRIOR APPLICATION NUMBER: 60/062287
, PRIOR FILING DATE: 1997-10-17
, PRIOR APPLICATION NUMBER: 60/063549
, PRIOR FILING DATE: 1997-10-28
, PRIOR APPLICATION NUMBER: 60/064103
, PRIOR FILING DATE: 1997-10-31
, PRIOR APPLICATION NUMBER: 60/069873
, PRIOR FILING DATE: 1997-12-17
, PRIOR APPLICATION NUMBER: 60/078910
, PRIOR FILING DATE: 1998-03-20
, PRIOR APPLICATION NUMBER: 60/079294
, PRIOR FILING DATE: 1998-03-25
, PRIOR APPLICATION NUMBER: 60/079656
, PRIOR FILING DATE: 1998-03-26
, PRIOR APPLICATION NUMBER: 60/079728
, PRIOR FILING DATE: 1998-03-27
, Remaining PRIOR Application data removed
, NUMBER OF SEQ ID NOS: 246
, SEQ ID NO 71
, LENGTH: 521
, TYPE: DNA
, ORGANISM: Homo Sapien
, US-10-219-483-71

```

Query Match	74.78;	Score 287;	DB 13;	Length 521;
Best Local Similarity	84.3%;	Pred. No. 7.9e-87;		
Matches 323;	Conservative 0;	Mismatches 60;	Indels 0;	Gaps 0;
Qy	1	ATGCGAAGGATATTGATCTTTTGGCTTGGGGCCCTTGGTTCATGTGCCGGCATGGT	60	
Db	38	ATGCGAAGATATTGTTACTTTTCTCCCGGCTCTGTGGCTGTATGTGCTGTGCATGGA	97	
Qy	61	GTATTTATGGANAAACTTTCTTCTAAGAAGTTGTGTGGGATGAGGAGTGTCTCTACT	120	
Db	98	ATATTTATGGACCGCTAGCTTCCAGAAGCTCTGTGCAGATGATGAGTGTGTCTACT	157	
Qy	121	ATTTCTCTGGCAGAGCAGACAGGAAGATTACAAATGCCCCAGACTGTAGTTCATCGATCTC	180	
Db	158	ATTTCTCTGGCTAGTGCTCAAGAAGATTATTAATGCCCCGAGCTGTAGATTCATTAAAGTT	217	
Qy	181	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGTTAACAGAAACCGAGCTGGAGAG	240	
Db	218	AAAAAAGGCAGCAGACTATGTGTACTCAAAAGCTGGTAAAGAAAAATGGAGCTGGAGAA	277	
Qy	241	TTTTGGGCTGGCAGTGTTATGGTGACCAACAGAGATGAGATCGGNAATTGTAGGTATTTC	300	
Db	278	TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCTGTGGGTATTTC	337	
Qy	301	CCGAGCAACTTGGTGAAGGACGACGGTGTATACAGGAGGGCCACCAAGGAGATCCCAACC	360	
Db	338	CCGAGCAACTTGGTCAAGGAACGGGTGTGTACCAAGGAAGCTACCAAGGAAGTCCCACC	397	
Qy	361	ACGGATATTGACTTCTTCTGTGA	383	
Db	398	ACGGATATTGACTTCTTCTGTGA	420	

RESULT 13  
US-10-219-525-71  
; Sequence 71, Application US/10219525  
; Publication No. US2003018721A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey

```

1  ; APPLICANT: Godowski, Paul J.
2  ; APPLICANT: Grimaldi, J. Christopher
3  ; APPLICANT: Gurney, Austin L.
4  ; APPLICANT: Smith, Victoria
5  ; APPLICANT: Stephan, Jean-Philippe F.
6  ; APPLICANT: Watanabe, Colin L.
7  ; APPLICANT: Wood, William I.
8  ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
9  ; FILE REFERENCE: P3530PIC29
10 ; CURRENT APPLICATION NUMBER: US/10/219,525
11 ; CURRENT FILING DATE: 2002-08-13
12 ; PRIOR APPLICATION NUMBER: 10/119,480
13 ; PRIOR FILING DATE: 2002-04-09
14 ; PRIOR APPLICATION NUMBER: 60/059113
15 ; PRIOR FILING DATE: 1997-09-17
16 ; PRIOR APPLICATION NUMBER: 60/062287
17 ; PRIOR FILING DATE: 1997-10-17
18 ; PRIOR APPLICATION NUMBER: 60/063549
19 ; PRIOR FILING DATE: 1997-10-28
20 ; PRIOR APPLICATION NUMBER: 60/064103
21 ; PRIOR FILING DATE: 1997-10-31
22 ; PRIOR APPLICATION NUMBER: 60/069873
23 ; PRIOR FILING DATE: 1997-12-17
24 ; PRIOR APPLICATION NUMBER: 60/078910
25 ; PRIOR FILING DATE: 1998-03-20
26 ; PRIOR APPLICATION NUMBER: 60/079294
27 ; PRIOR FILING DATE: 1998-03-25
28 ; PRIOR APPLICATION NUMBER: 60/079656
29 ; PRIOR FILING DATE: 1998-03-26
30 ; PRIOR APPLICATION NUMBER: 60/079728
31 ; PRIOR FILING DATE: 1998-03-27
32 ; Remaining prior Application data removed - See File Wrapper or PALM.
33 ; NUMBER OF SEQ ID NOS: 246
34 ; SEQ ID NO 71
35 ; LENGTH: 521
36 ; TYPE: DNA
37 ; ORGANISM: Homo Sapien
38 ; US-10-219-525-71

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Query Match	74.78;	Score 287;	DB 13;	Length 521;
Best Local Similarity	84.31;	Pred. No. 7.9e-87;		
Matches 323;	Conservative 0;	Mismatches 60;	Indels 0;	Gaps 0;
Qy	1	ATGCGAAGGATATTGATCTTTTCTGGGGCCCTTGTTCTATGTGCCGGGCATGGT	60	
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Qy	61	GTATTTATGGATAAACTTTTCTTAAGAAGTTGTGCGGATGAGGAGTGTGTCTATACT	120	
Db	98	ATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGTCTATACT	157	
Qy	121	ATTTCTCTGGCAAGACGACAGGAAGATTACAATGCCCAGACTGTAGGTTTCATCGATGTC	180	
Db	158	ATTTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCATTAAACGT	217	
Qy	181	AAGAAAGGCGACGAGATCTATGTTTATCTCCAAGCTGGTAAACAGAAAACGAGCTGGAGAG	240	
Db	218	AAAAAGGCGACGAGATCTATGTGTACTCAAAGCTGGTAAAGAAGAAATGGAGCTGGAGAA	277	
Qy	241	TTTTGGGCTGGCAGTGTATTAGTTGACCAACAGATGAGATGGGNAATGTAGGTTATTTC	300	
Db	278	TTTTGGGCTGGCAGTGTATTAGTTGATGGCCAGACGAGATGGGAGTCTGGGGTTATTTC	337	
Qy	301	CCACGAACTTGGTGAAGGACGACGCTGTATACCAGGAGGGCCACCAAGGAGATCCCAACC	360	
Db	338	CCACGAACTTGGTCAAGBAACGCTGTATACCAGGAGACTCAAGGAAGATCCCACC	397	
Qy	361	ACGGATATTGACTTCTTCTGTGA	383	
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us-10-019-455a-10.rnpb

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RESULT 14
US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-526-71

Query Match      74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 ATGCGAAGGATATTGATTTCTTTGCTGGGGCCCTTGGTTCATGTGCGGGCATGGT 60
Db 38 ATGCGAAGAATATTGTTACTTTCTCCCGGCTTGTGGCTGTATGTGCTGATGGA 97

Qy 61 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGATAGAGGAGTGTCTACT 120
Db 98 ATATTTATGGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTGTCTACT 157

Qy 121 ATTTCTCTGGCAAGACAGAGATTAACATCCCGACTGTAGCTTTCATCGATGTC 180
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGACTGTAGATTCAATACGTT 217

Qy 181 AAGAAAGGCGACAGATCTATGTTTACTCCAAAGCTGTGTAACAGAAAACGAGCTGGAG 240
Db 218 AAAAAGGCGACAGATCTATGTTACTCAAGCTGTGTAAGAAATGGAGCTGGAG 277

Qy 241 TTTTGGGCTGGCAGTGTGTTATGTTGACCAACAGAGATGAGTGGAAATGTAGGTTATTC 300
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Qy 301 CCCAGCAACTTGGTGAAGGACGCGTGTATACAGGAGGCGCACCAAGGAGATCCCAACC 360
Db 338 CCCAGGAACTTGGTCAAGGAAACGCGTGTATCCAGGAGGTACCAAGGAGTTCCCAACC 397

Qy 361 ACGGATATTGACTTCTTCTGTGA 383
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RESULT 15
US-10-219-530-71
; Sequence 71, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-530-71

Query Match      74.7%; Score 287; DB 13; Length 521;
Best Local Similarity 84.3%; Pred. No. 7.9e-87;
Matches 323; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 1 ATGCGAAGGATATTGATTTCTTTGCTGGGGCCCTTGGTTCATGTGCGGGCATGGT 60
Db 38 ATGCGAAGAATATTGTTACTTTCTCCCGGCTTGTGGCTGTATGTGCTGATGGA 97

Qy 61 GTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGCGGATAGAGGAGTGTCTACT 120
Db 98 ATATTTATGGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGATGTGTCTACT 157

Qy 121 ATTTCTCTGGCAAGACAGAGATTAACATCCCGACTGTAGCTTTCATCGATGTC 180
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGACTGTAGATTCAATACGTT 217
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Job time : 316.339 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:34:27 ; Search time 31.014 Seconds  
(without alignments)  
5464.987 Million cell updates/sec

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Perfect score: 384  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Match Length	DB ID	Description
		Match	Length			
1	66.2	17.2	581	1	US-08-578-649-4	Sequence 4, Appli
2	60.2	15.7	459	1	US-08-578-649-1	Sequence 1, Appli
3	55.2	14.4	330	1	US-08-578-649-18	Sequence 18, Appli
4	52.6	13.7	305	1	US-08-578-649-8	Sequence 8, Appli
5	35.6	9.3	596	1	US-08-578-649-24	Sequence 24, Appli
6	35.6	9.3	3565	1	US-08-578-649-3	Sequence 3, Appli
7	34.4	9.0	2644	4	US-09-399-913-35	Sequence 35, Appli
8	34.4	9.0	2644	4	US-09-298-731-35	Sequence 35, Appli
9	34.4	9.0	7218	1	US-08-232-463-14	Sequence 14, Appli
C 10	32.6	8.5	5822	3	US-08-899-595-4	Sequence 4, Appli
11	32.6	8.5	5822	3	US-08-899-595-5	Sequence 5, Appli
12	32.2	8.4	202001	4	US-09-734-674-3	Sequence 3, Appli
C 13	31.8	8.3	654	4	US-09-280-116-57	Sequence 57, Appli
C 14	31.8	8.3	683	3	US-09-088-651-3	Sequence 3, Appli
C 15	31.8	8.3	980	4	US-09-023-942A-30	Sequence 30, Appli
C 16	31.8	8.3	1109	3	US-09-088-651-1	Sequence 1, Appli
C 17	31.8	8.3	1109	3	US-09-088-651-6	Sequence 6, Appli
C 18	31.8	8.3	1110	4	US-09-386-653A-1	Sequence 1, Appli
C 19	31.8	8.3	1130	4	US-09-386-653A-8	Sequence 8, Appli
C 20	31.8	8.3	1212	4	US-09-620-312D-431	Sequence 431, App
C 21	31.8	8.3	1751	4	US-09-453-702B-223	Sequence 223, App
22	31.6	8.2	464	4	US-09-615-192A-236	Sequence 236, App
23	31	8.1	2949	3	US-08-433-522A-1	Sequence 1, Appli
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25	31	8.1	2949	3	US-08-942-046-1	Sequence 1, Appli
26	31	8.1	2950	3	US-08-433-522A-5	Sequence 5, Appli
27	31	8.1	2950	3	US-09-135-166-5	Sequence 5, Appli

28	31	8.1	2950	3	US-08-942-046-5	Sequence 5, Appli
29	31	8.1	2984	3	US-08-433-522A-3	Sequence 3, Appli
30	31	8.1	2984	3	US-09-135-166-3	Sequence 3, Appli
31	31	8.1	2984	3	US-08-942-046-3	Sequence 3, Appli
32	31	8.1	2987	3	US-08-433-522A-55	Sequence 55, Appli
33	31	8.1	2987	3	US-09-135-166-55	Sequence 55, Appli
34	31	8.1	2987	3	US-08-942-046-55	Sequence 55, Appli
C 35	30.8	8.0	1778	1	US-08-416-870C-3	Sequence 3, Appli
36	30.4	7.9	8789	1	US-08-328-254-5	Sequence 5, Appli
37	30.4	7.9	10136	1	US-08-353-700-2	Sequence 2, Appli
38	30.4	7.9	10136	5	PCT-US95-16216-2	Sequence 48, Appli
39	30.4	7.9	25002	4	US-08-961-527-48	Sequence 105, App
C 40	30	7.8	13158	2	US-08-687-080-105	Sequence 132, App
C 41	30	7.8	36412	4	US-08-311-731A-132	Sequence 4920, Ap
C 42	29.8	7.8	1500	4	US-09-252-991A-4920	Sequence 4922, Ap
43	29.8	7.8	1620	4	US-09-252-991A-4922	Sequence 35, Appli
C 44	29.8	7.8	2800	3	US-08-714-918-35	Sequence 35, Appli
C 45	29.8	7.8	2800	3	US-09-265-315-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1  
US-08-578-649-4  
; Sequence 4, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tajoloff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 581 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 110..499  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 110..178  
; FEATURE:

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; NAME/KEY: mat peptide
; LOCATION: 179..499
US-08-578-649-4

Query Match      17.2%; Score 66.2; DB 1; Length 581;
Best Local Similarity 54.4%; Pred. No. 6.2e-12;
Matches 181; Conservative 0; Mismatches 143; Indels 9; Gaps 2;

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Db 169 CAGGCGTATCGAGCTATGCCAAGCTGGCTGACTGGAAGCTGTGTGGACGAGGAATG 228
QY 111 TGTCTATATCTATTTCTTGGCAAGACAGACAGAGATTAACATGCCCCAGACTGTAGTT 170
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QY 171 CATGATGTCAGAAAGGCGAGCAGATCTATGTTTACTCCAAAGCTGGTAAACAGAAACGG 230
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QY 231 AGCTGGAGAGTTTGGGCTGGCAGTGTATTTATGGTGACCAACAGGATGAGTGGGA--AT 287
Db 343 TGGGCGCTTCTTGGGAGGCGAGTGTTCAGGGAGGTTACTATGAGACCTGGCAGCCCG 402
QY 288 TGTAGTTATTTCCCAACAATTGGTGAAGAGCAGCGGTATACACAGGAGGCCACCAA 347
Db 403 CCTGGCTATTTCCCACTAGCAATTGTCCGGGAGGACCTGAACCTCGAAACCTGGCAAAAT 462
QY 348 GGAGATCCCAACACGGATATGACTTCTTCTG 380
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RESULT 2
US-08-578-649-1
; Sequence 1, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloiff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
;

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 40..432
; FEATURE:
; NAME/KEY: sig peptide
; LOCATION: 40..111
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 112..432
US-08-578-649-1

Query Match      15.7%; Score 60.2; DB 1; Length 459;
Best Local Similarity 56.8%; Pred. No. 5e-10;
Matches 154; Conservative 0; Mismatches 108; Indels 9; Gaps 2;

QY 58 GGTCTATTTATGGATAAACTTTCTTAAGAAGTTGTGTGGGATGAGGAGTGTCTAT 117
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QY 178 GTCAAGAAAGGCGACGACATCTATGTTTACTCCAAAGCTGTAACAGAAAACGGAGCTGGA 237
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RESULT 3
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloiff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
;

```

```
;
; TELEPHONE: (212) 688-3200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 7..327
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 4..6
; OTHER INFORMATION: /function= "Startcodon Met"
;
US-08-578-649-18

Query Match 14.4%; Score 55.2; DB 1; Length 330;
Best Local Similarity 55.5%; Pred. No. 1.8e-08;
Matches 152; Conservative 0; Mismatches 113; Indels 9; Gaps 2;

QY 55 CATGGCTATTATTGGATAAACTTTCTTAAGAAGTTGTGCGGATGAGGAGTGTGTC 114
Db 1 CATATGGGCAATGCCAAATAGCAGATCGTAATATGTGCAGATCAGGAGTGCGAC 60
QY 115 TATATATTCTCTCGCAAGACACAGGAAGATTACAAATGCCCCAGACTGTAGATTTCATC 174
Db 61 CACCTTATCTCCATGGCTGTGGCCCTTCAGGACTACATGCCCCCGACTGCCGATTCCTG 120
QY 175 GATGTCGAAGAAGGGGACGAGATCTATGTTTACTCCAGCTGGTAAACAGAAACGGAGCT 234
Db 121 ACCATTACCCGGGCGCAAGTGGTGTATGTTCTTCCAAAGCTG-----AAGGGCCGTGGG 174
QY 235 GGAGAGTTTGGGCTGGCAGTGTATTGTCACCAACAGGATGAGATGGGAATT---GTA 291
Db 175 CGGCTCTCTGGGAGCAGCGTTTCAGGAGATTACTATGGAGATCTGGCTGTCGCTCGCTG 234
QY 292 GGTATTTCCTCCAGCAACTTGGTGAAGGAGCAGC 325
Db 235 GGCTATTTCCTCCAGTAGCATTGTCGAGAGGACC 268

RESULT 4
US-08-578-649-8
; Sequence 8, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:

;
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: join(1..29, 277..305)
; OTHER INFORMATION: /function= "Primer"
;
US-08-578-649-8

Query Match 13.7%; Score 52.6; DB 1; Length 305;
Best Local Similarity 57.3%; Pred. No. 1.2e-07;
Matches 138; Conservative 0; Mismatches 94; Indels 9; Gaps 2;

QY 88 AAGTTGTGTCGGATGAGGAGTGTCTATACTATTCTCTGGCAAGACACAGGAAGAT 147
Db 7 AAGTTTTCGGGATCAGGATGCAGCCACCTATCTCCATGGCTGTGGCCCTTCAGGAC 66
QY 148 TACAATGCCCGACACTGTAGGTTTCATGATGTCAAGAAAGGCGCAGCATCTATGTTTAC 207
Db 67 TACATGGCCCCGACTGCCGATTCTTGACCAATTCACCGGGGCCCAAGTGGTGTATGTTCTTC 126
QY 208 TCCAAGCTGTACAGAAACGGAGCTGGAGAGTTTGGGCTGGCAGTGTATTGTTGAC 267
Db 127 TCCAAGCTG-----AAGGGCCGTGGCGGCTCTTCTGGGAGGCGCAGCGTTCAGGGAGAT 180
QY 268 CACCAGATGAGATGGGAATT---GTAGGTTATTTCCTCCAGCACTTGGTGAAGGAGCAG 324
Db 181 TACTATGAGATCTGGTTCGCTCGCTCGCTGGCTATTTCCTCCAGTAGCATTTGTCGAGAGGAC 240
QY 325 C 325
Db 241 C 241

RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
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; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
; EARLIER FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: USSN 09/350,614
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 09/350,874
; EARLIER FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 2644
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (49)..(816)
;
US-09-399-913-35

Query Match          9.0%; Score 34.4; DB 4; Length 2644;
Best Local Similarity 52.1%; Pred. No. 0.28;
Matches 100; Conservative 0; Mismatches 91; Indels 1; Gaps 1;

QY      187  GGGCAGCAGATCTATTGTTTACTCCAGCTCGTTAACAGAAAACGGAGCTCGAGAGTTTGG 246
Db      1940  GGATTGAGGCCACTGTTTAACTTAACTGGAGCTAGCCCTGAGGGCTGGGACCTGTGA 1999

QY      247  GCTGGCAGTGTTTATGTGTGACCCACGAGTAGATGGGAATTGTAGTATTATTTCCCGAGC 306
Db      2000  CCAGGCCAACAGGTCAGACAGACCCCTCAGGAGGAGA-GAGAGCTGTTCTGTGCTCCCGAGGC 2058

QY      307  AACTTGGTGAAGGACGCGGTGTATACAGGAGGCCCAAGGAGATCCCAACCCACCGAT 366
Db      2059  CTCGCCCAGAGGNACAGTGTCCCAAGAAGCATGTTTCTTGGAGGAACATCCCCACAAA 2118

QY      367  ATTGACTTCTTC 378
Db      2119  GTACATTCCATC 2130

```

247 GCTGGCAGTGTTTATGGTGACCAACAGGATGAGATGGGAATTCTAGTATTATTTCCCCAGC 306  
 2000 CCAGGCCAACAGGTCAGCAGACCCCTCAGGAGGAGA-GAGAGCTGTCTCTGCTCTCCCCAGGC 2058  
 307 AACTTGGTGAAGAGCAGCGGTGTATACCAAGGAGGCCACCAAGGAGATCCCAACACAGGAT 366  
 2059 CTCGCCCAGAGGAACAGTGTCCCAAGAGCATGTTTCTTGGAGGAACATCCCCACAAAA 2118  
 367 ATTGACTTCTTC 378  
 2119 GTACATTCCATC 2130

Db

RESULT 9  
 US-08-232-463-14/c  
 ; Sequence 14, Application US/08232463  
 ; Patent No. 5670367  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DORNER, F.  
 ; APPLICANT: SCHEIFLINGER, F.  
 ; APPLICANT: FALKNER, F. G.  
 ; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
 ; NUMBER OF SEQUENCES: 52  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 1800 Diagonal Road, Suite 500  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22313-0299  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/232,463  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/935,313  
 ; FILING DATE:  
 ; APPLICATION NUMBER: EP 91 114 300.6  
 ; FILING DATE: 26-AUG-1991  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BENT, Stephen A.  
 ; REGISTRATION NUMBER: 29,768  
 ; REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (703)836-9300  
 ; TELEFAX: (703)683-4109  
 ; TELEX: 899149  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7218 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; CLONE: pTZgpt-F15  
 ; US-08-232-463-14

	Query Match	9.0%	Score 34.4;	DB 1;	Length 7218;
	Best Local Similarity	2.9%;	Pred. No. 0.43;		
	Matches	8;	Conservative 157;	Mismatches 113;	Indels 0;
	Gaps	0;			
Qy	85	AAGAAGTTGTGCGGATGAGAGTGTCTATCTATCTTCTGCGCAAGACACAGAA	144		
Db	1333	RR	1274		
Qy	145	GATTACAATGCCACAGCTGAGTTTCATCGATGCAAGAAGGCGACAGATCATGTT	204		
Db	1273	RR	1214		





Db

3757

GTACCTCCAGTAAAGAGGGGTGAGGAGATGCAAAACACCCCGAGCAAGAGGTTGGA

3816

QY

228

CGGAGCTGGAGAGTTTGGGTGGCAGTGTATTATGTGACACACAGGATGAGATGGGAAT

287

Db

3817

GGAGGAGAGAGGAGGAGGAGGAGGAGTGTACTATCCCGAGGACGGTGGT

3876

QY

288

TGTAGTTATTTCCTCCAGCAACTTGGTGAAGGACGAGGTGTATACAGAGGGCCACAA

347

Db

3877

GGAATAATAGTGCAGAGTCACAGGTAAAGAGGGGCGAGGGGAACAGGAGCACGACTA

3936

QY

348

GGA

350

Db

3937

GGA

3939

RESULT 12

US-09-734-674-3

; Sequence 3, Application US/09734674

; Patent No. 6498022

; GENERAL INFORMATION:

; APPLICANT: WEI, Ming-Hui et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CLO01018

; CURRENT APPLICATION NUMBER: US/09/734,674

; CURRENT FILING DATE: 2000-12-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 202001

; TYPE: DNA

; ORGANISM: Human

; NAME/KEY: misc feature

; LOCATION: (1)...(202001)

; OTHER INFORMATION: n = A,T,C or G

US-09-734-674-3

Query Match

Best Local Similarity

Matches

82;

Conservative

0;

Mismatches

83;

Indels

0;

Gaps

0;

QY

119

CTATTCTCTGCAAGACACAGGAGATTACATGCCCCAGACTGTAGTTCATCGATG

178

Db

183409

CTAGAACTCAGGAGAGAGTAAAGGAGAGACGTCAGTCCGTGGTAAATCATTAGCAAGTCTGT

183468

QY

179

TCAAGAAAGGCGAGCAGATCTATGTTTACTCCAAGCTGTACAGAAACCGAGCTGGAG

238

Db

183469

GAAAGTCAAGCCATGGGTATGGATGAACTATTCAGGAGAAAGAAACAGAGATGAG

183528

QY

239

AGTTTGGGCTGGCAGTGTATTATGTGACCCAGAGATGATGG

283

Db

183529

AGTCCAGGAATCCCAATGTTGAGGGGCAATAAAGAGAGATG

183573

RESULT 13

US-09-280-116-57/c

; Sequence 57, Application US/09280116A

; Patent No. 6331427

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs

; FILE REFERENCE: 5800-24, 035800/176965

; CURRENT APPLICATION NUMBER: US/09/280,116A

; CURRENT FILING DATE: 1999-03-26

; NUMBER OF SEQ ID NOS: 268

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 57

; LENGTH: 654

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-280-116-57/c

Query Match

Best Local Similarity

Matches

54;

Conservative

0;

Mismatches

37;

Indels

0;

Gaps

0;

QY

252

CAGTGTATTATGTGACACAGGATGAGATGGGAATTGTAGTTATTTCCTCCAGCAACTT

311

Db

625

CGGTGCTCTTGTCTGTAGACGAGGTTCACCTTGGGTGTGTCATGATGGGCACAGGAGTT

566

FEATURE:

; OTHER INFORMATION: trypsin-like serine proteases

US-09-280-116-57

Query Match

Best Local Similarity

Matches

54;

Conservative

0;

Mismatches

37;

Indels

0;

Gaps

0;

QY

252

CAGTGTATTATGTGACACAGGATGAGATGGGAATTGTAGTTATTTCCTCCAGCAACTT

311

Db

625

CGGTGCTCTTGTCTGTAGACGAGGTTCACCTTGGGTGTGTCATGATGGGCACAGGAGTT

566

RESULT 14

US-09-088-651-3/c

; Sequence 3, Application US/09088651

; Patent No. 6165771

; GENERAL INFORMATION:

; APPLICANT: BURGESS, NICOLA A.

; APPLICANT: CLINKENBEARD, HELEN B.

; APPLICANT: SOUTHAN, CHRISTOPHER D.

; TITLE OF INVENTION: NOVEL COMPOUNDS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION NUMBER: US/09/088,651

; FILING DATE: JUNE 1, 1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB9712088.5

; FILING DATE: 10-JUNE-1997

; APPLICATION NUMBER: EP 97308295.1

; FILING DATE: 17-OCT-1997

; APPLICATION NUMBER: GB 9803650.2

; FILING DATE: 20-FEB-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F.

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH30358

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 683 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-09-088-651-3

Query Match

Best Local Similarity

Matches

54;

Conservative

0;

Mismatches

37;

Indels

0;

Gaps

0;

QY

252

CAGTGTATTATGTGACACAGGATGAGATGGGAATTGTAGTTATTTCCTCCAGCAACTT

311

Tue Dec 30 10:20:36 2003

Db 369 CGGTGCTTTTCTGTAGACAGGTTGCACCTTGGGTGTGTGCGATGATGGGCACAGCGAGTT 310  
QY 312 GGTGAGGAGGAGCGGTGTATACAGGAGGCC 342  
Db 309 TCTGCAGGATCCGCGGTTCCGGCAGGAGGTC 279

## RESULT 15

US-09-023-942A-30/C  
; Sequence 30, Application US/09023942A  
; Patent No. 6479274  
; GENERAL INFORMATION:  
; APPLICANT: (US only) ANTALIS Toni Marie and HOOPER John David  
; TITLE OF INVENTION: NOVEL MOLECULES  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
; STREET: 400 GARDEN CITY PLAZA  
; CITY: GARDEN CITY  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,942A  
; FILING DATE: 13-FEB-1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: P05101/97  
; FILING DATE: 13-FEB-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: P04022/97  
; FILING DATE: 18-NOV-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: International PCT Application  
; FILING DATE: 13-FEB-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DIGIGLIO, FRANK S  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 11168  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742 4343  
; TELEFAX: (516) 742 4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 980 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-023-942A-30

Query Match 8.3%; Score 31.8; DB 4; Length 980;  
Best Local Similarity 59.3%; Pred. NO. 1.2;  
Matches 54; Conservative 0; Mismatches 37; Indels 0; Gaps 0;  
QY 252 CAGTGTATTATGGTACACAGGATGAGATGGGAATTGTAGTTATTTCCCGCAACTT 311  
Db 525 CGGTGCTTTTCTGTAGACAGGTTGCACCTTGGGTGTGTGCGATGATGGGCACAGCGAGTT 466  
QY 312 GGTGAAGGAGCAGCGGTGTATACAGGAGGCC 342  
Db 465 TCTGCAGGATCCGCGGTTCCGGCAGGAGGTC 435

Search completed: December 30, 2003, 06:10:40  
Job time : 33.014 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 13.2661 Seconds  
(without alignments)  
927.898 Million cell updates/sec

Title: US-10-019-455A-12

Perfect score: 676

Sequence: 1 MARILILLGLVLCAGH.....RVQEQATKEIPTTIDFFCE 128

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277.5	41.1	131	2	I38019
2	277.5	41.1	844	1	transforming protein
3	91.5	13.5	844	1	transforming prote
4	84.5	13.2	839	1	transforming prote
5	81.5	12.1	1215	2	Gene VAV2 protein
6	79	11.7	722	2	myosin-IA - Acanth
7	78.5	11.6	1589	1	hypothetical prote
8	77	11.4	695	2	cell division cont
9	76.5	11.3	176	2	protein-glutamine
10	76	11.2	259	2	hypothetical prote
11	75	11.1	406	2	hypothetical prote
12	74.5	11.0	1097	2	hypothetical prote
13	74	10.9	332	2	hypothetical prote
14	73	10.8	344	2	hypothetical prote
15	73	10.8	994	2	hypothetical prote
16	72.5	10.7	93	2	hypothetical prote
17	72	10.7	308	2	hypothetical prote
18	72	10.7	344	2	hypothetical prote
19	72	10.7	585	2	copper ABC transpo
20	72	10.7	636	2	ATP-dependent RNA
21	72	10.7	1084	2	receptor kinase ho
22	71.5	10.6	847	1	ribonucleotide red
23	71	10.5	340	2	mixed-lineage prec
24	71	10.5	340	2	yceG protein precu
25	71	10.5	340	2	probable thymidyla
26	71	10.5	373	2	dTMP kinase (EC 2.
27	71	10.5	946	1	VHS domain contain
28	70.5	10.4	333	2	ror-related recept
29	70.5	10.4	505	1	transcription regu
					protein-tyrosine k

protein-tyrosine k  
hypothetical prote  
hypothetical prote  
probable chromomet  
3',5'-cyclic-GMP p  
cell division cycl  
alliin lyase (EC 4  
connexin 45 - mous  
S-receptor kinase  
ribonucleoside-dip  
hypothetical prote  
hypothetical prote  
probable peroxisom  
probable signal tr  
hypothetical prote  
Snf2 family protei

30 70.5 10.4 506 1 S24553  
31 70.5 10.4 718 2 T02310  
32 70.5 10.4 780 2 T29580  
33 70.5 10.4 839 2 G96719  
34 70.5 10.4 859 2 S13030  
35 70 10.4 295 2 F90113  
36 70 10.4 486 2 S29302  
37 69.5 10.3 396 2 S23589  
38 69.5 10.3 413 2 T02893  
39 69.5 10.3 714 2 D65047  
40 69.5 10.3 714 2 B91071  
41 69.5 10.3 714 2 B85915  
42 69 10.2 288 2 T38696  
43 69 10.2 670 2 S67383  
44 69 10.2 816 2 T17257  
45 69 10.2 1032 2 D95177

#### ALIGNMENTS

##### RESULT 1

I38019  
melanoma-derived growth regulatory protein MIA - human  
C:Species: Homo sapiens (man)  
C>Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000  
C:Accession: I38019; S40238  
R:Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hessdoerfer, B.; Schmitt, A.; Jac  
Cancer Res. 54, 5695-5701, 1994  
A:Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA.  
A:Reference number: I38019; MUID:95007612; PMID:7923218  
A:Accession: I38019  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-131 <RES>  
A:Cross-references: EMBL:X75450; NID:9438057; PIDN:CAA53203.1; PID:9438058  
C:Genetics:  
A:Gene: mia  
C:Superfamily: human melanoma-derived growth regulatory protein MIA

Query Match 41.1%; Score 277.5; DB 2; Length 131;  
Best Local Similarity 43.4%; Pred. No. 6.6e-21;  
Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;

QY 1 MARILILLGLVLC---AGHVF---MDKLSSKKLCADSECYVTSIARAQEDYNAPD 54  
DB 1 MARSLVCL--GVIIILSAFSGPGVGRGMPKLAQRKLCADQECSPISMAVALQDYMAPD 58  
QY 55 CRFTDVKKGQOIYVYVSKLVTENGAGE--FWAGSVYGDHQDEMGI--VGYPFSPNLVKEQRYVQ 112  
DB 59 CRFTTIHRGQVYVFSKL---KGRGRLEFGSGVQGDYVGDLAARLGYPFSSIVREDQTLK 115

QY 113 EATKEIPTTIDFFCE 128  
DB 116 PGKVDVKTDKWDFYQ 131

##### RESULT 2

TVMSV  
transforming protein vav - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 03-May-1994 #sequence revision 16-Feb-1996 #text\_change 18-Jun-1999  
C:Accession: A61187; A39576; S36941; S23669  
R:Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M.  
Cell Growth Differ. 2, 95-105, 1991  
A:Title: Mechanism of activation of the vav protooncogene.  
A:Reference number: A61187; MUID:91299578; PMID:2069873  
A:Accession: A61187  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-844 <COP>  
R:Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991



DB 862 GRIGWFPSTVVEEGI 877

RESULT 5

T32734

myosin-IA - Acanthamoeba castellanii

C:Species: Acanthamoeba castellanii

C>Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 08-Sep-2000

C:Accession: T32734

R:Lee, W.L.; Ostap, E.M.; Zot, H.G.; Pollard, T.D.

Submitted to the EMBL Data Library, August 1998

A:Description: Hydrodynamic and ligand binding properties of Acanthamoeba myosin-IA GPa/

A:Reference number: Z21216

A:Accession: T32734

A>Status: preliminary; translated from GB/EMBL/DDBY

A:Molecule type: DNA

A:Residues: 1-1215 <LEE>

A:Cross-references: EMBL:AF085185; NID:G3599477; PID:G3599478; PIDN:AAC35357.1

A:Experimental source: strain Nefi

C:Genetics:

A:Gene: MIA

A:Introns: 1/3; 41/3; 72/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 500/3

C:Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homolo

F:14-674/Domain: myosin motor domain homology <MMO>

Query Match 12.1%; Score 81.5; DB 2; Length 1215;

Best Local Similarity 30.0%; Pred. No. 5.9;

Matches 21; Conservative 13; Mismatches 23; Indels 13; Gaps 2;

QY 38 VYTIISLARAQEDYNAPDCRIDVKKGOIYVYKLVTEGAGFEWAGSVVGDHQDEMGIV 97

DB 1158 VPTVGRCALYDGAQAEELTLREGDVIDIQK-----SGBWEETLNGK-----T 1204

QY 98 GYRPSNLVKE 107

DB 1205 GVFPANVVED 1214

RESULT 6

G86746

hypothetical protein nrDE [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C:Species: Lactococcus lactis subsp. lactis

C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001

C:Accession: G86746

R:Bohlooin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich

Genome Res. 11, 731-753, 2001

A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s

A:Reference number: A86625; MUID:21235186; PMID:11337471

A:Accession: G86746

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-722 <STO>

A:Cross-references: GB:AE005176; PID:g12723918; PIDN:AAK05073.1; GSPDB:GN00146

A:Experimental source: strain IL1403

C:Genetics:

A:Gene: nrDE

C:Superfamily: Salmonella typhimurium ribonucleoside-diphosphate reductase

Query Match 11.7%; Score 79; DB 2; Length 722;

Best Local Similarity 29.0%; Pred. No. 5.9;

Matches 31; Conservative 17; Mismatches 53; Indels 6; Gaps 2;

QY 11 GLVVLCAHGVMFKLSKKLCADEEC-VYTIISLARAQEDYNAPDCRIDVKKGOIYVY 69

DB 249 GVYVLSLPHFDIMBFLSKENADEKIRVKTLSLG-----VTVPDKFVELVKGETWYLF 303

QY 70 SKLVTEGAGFEWAGSVVGDHQDEMGIVGYPFNSLVKEQRYQVQATK 116

DB 304 EPYFVKYKGFPAFVDITABYDKXVANPEIRKTSINARELEQLSK 350

RESULT 7

RGBCYS

cell division control protein CDC25 - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein L2142.6; protein YLR310C

C:Species: Saccharomyces cerevisiae

C>Date: 31-Mar-1988 #sequence\_revision 31-Mar-1993 #text\_change 21-Jul-2000

C:Accession: A26596; S51442; A23444; S43051; S47990

R:Broek, D.; Toda, T.; Michaeli, T.; Levin, L.; Birchmeier, C.; Zoller, M.; Powers, S.

Cell 48, 789-799, 1987

A:Title: The S. cerevisiae CDC25 gene product regulates the RAS/adenylate cyclase path

A:Reference number: A26596; MUID:87131091; PMID:3545497

A:Accession: A26596

A:Molecule type: DNA

A:Residues: 1-1589 <BRO>

A:Cross-references: EMBL:M15458; NID:G171184; PIDN:AAA34478.1; PID:G171185

R:Fauley, A.

Submitted to the EMBL Data Library, November 1994

A:Description: The sequence of S. cerevisiae cosmid L2142.

A:Reference number: S51437

A:Accession: S51442

A:Molecule type: DNA

A:Residues: 1-1589 <PAU>

A:Cross-references: EMBL:U17247; NID:G577216; PIDN:AB67360.1; PID:G577222; GSPDB:GN00

R:Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.

EMBO J. 5, 375-380, 1986

A:Title: Characterization, cloning and sequence analysis of the CDC25 gene which contr

A:Reference number: A23444; MUID:86220116; PMID:3011405

A:Accession: A23444

A:Molecule type: DNA

A:Residues: 1-496, 1-498-953, 'LSVIMNLSR', 964-1589 <CAM>

A:Cross-references: EMBL:X03579; NID:G3483; PIDN:CAA27259.1; PID:G3484

R:Daniel, J.H.

Curr. Genet. 10, 879-885, 1986

A:Title: The CDC25 "start" gene of Saccharomyces cerevisiae: sequencing of the active

A:Reference number: S43051; MUID:88194639; PMID:3329037

A:Accession: S43051

A:Molecule type: DNA

A:Residues: 877-1589 <DAN>

A:Cross-references: EMBL:X03579

C:Genetics:

A:Gene: SGD:CDC25; CTN1; MIPS:YLR310C

A:Cross-references: SGD:S0004301; MIPS:YLR310C

C:Function: 12R

A:Description: positive control of level of cellular CAMP at the stage at which the ce

C:Superfamily: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator h

C:Keywords: cell cycle control; transmembrane protein

F:65-123/Domain: SH3 homology <SH3>

F:1301-1542/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 11.6%; Score 78.5; DB 1; Length 1589;

Best Local Similarity 27.0%; Pred. No. 16;

Matches 24; Conservative 18; Mismatches 36; Indels 11; Gaps 4;

QY 26 LSKKKLCADBECCVYTIISLARAQEDYNAP-----DCRFIDVKKGOIYVYKLVTEGAGE 80

DB 45 LSSSPSTSELTIRPIGIVVAAYDFNPYPIKDDSSQLLSVQQGETIVILNK----NSSG- 99

QY 81 FWAGSVVGDHQDEMGIVGYPFNSLVKEQOR 109

DB 100 WWDGLVIDDSNGKVN-RGWFFQNGRPLR 127

RESULT 8

S66662

protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - red sea bream

N:Alternate names: transglutaminase

C:Species: Chrysophrys major (red sea bream)

C>Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999

C:Accession: S66662

R:Yasueda, H.; Nakanishi, K.; Kumazawa, Y.; Nagase, K.; Motoki, M.; Matsui, H.

Eur. J. Biochem. 232, 411-419, 1995

A:Title: Tissue-type transglutaminase from red sea bream (Pagrus major). Sequence anal;

A:Reference number: S66662; MUID:96035874; PMID:7556189

[illegible]

```

A:Residues: 1-406 <HAL>
A:Cross-references: EMBL:X70810; NID:g415327; PIDN:CAA50139.1; PID:g415795
A:Experimental source: Strain Pringsheim Z
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
C:Genetics:
C:Genome: chloroplast
C:Superfamily: Euglena gracilis chloroplast hypothetical protein 406 (sl6S rRNA 3' region)
C:Keywords: chloroplast

      Query Match      11.1%; Score 75; DB 2; Length 406;
      Best Local Similarity 26.0%; Pred. No. 8;
      Matches 33; Conservative 14; Mismatches 38; Indels 42; Gaps 7;

QY      3  RIILILLGLLVLCAGHGVMFKLSKKLCADCECVTISLARAGEDVNAPCRFDIVKK 62
      ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      220 RVVIFUICLTWVLCAAGGFSCRRHNNK-----KRSNASTTP-----VPD 260

QY      63  GGOIYVYSKLVTEANGAEF-----WAGSVYGDHQDEMGIVGYFNSLVKE--QRVYQ 112
      ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB      261 NVAIF-----NDLGKYKAKVPVEMQNA---HAHSLCIMP-LPPLNLVNMSSSEIK 307

QY      113 EATKEIP 119
      || | | | |
DB      308 EAILEVP 314

RESULT 12
T31504
hypothetical protein Y116A8C.36 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T31504

```

**us-10-019-455a-12.rpr**

A;Accession: C81920  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-344 <PAR>  
A;Cross-references: GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB84045.1; PID:g737399  
A;Experimental source: serogroup A, strain Z2491  
C;Genetics:  
A;Gene: NMA0762

Query Match 10.8%; Score 73; DB 2; Length 344;  
Best Local Similarity 28.1%; Pred.No. 11;  
Matches 27; Conservative 17; Mismatches 46; Indels 6; Gaps 4;

Qy 17 AGHGVFMDKLSKKLCAD--BECVYTISLARAQEDYNAPDCRFIDVKKGQOIYVYVKLV- 73  
Db 170 AGKCVFAYNANYDKLSANHPENCQIGIHFTAAIEGTSLHDNSFIN-NESQVKYVSTRFLD 228  
Qy 74 -TENGAGFWA-GSVYGDHDEMGIYGVFPPSNLVKE 107  
Db 229 WSEGHGHNYSWDSNAPDLNGDGFSDSAYRPNGIIDQ 264

RESULT 15  
T21356  
Hypothetical protein F25H2.13 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T21356; T21540  
R;Wilkinson, J.  
submitted to the EMBL Data Library, September 1996  
A;Reference number: Z19411  
A;Accession: T21356  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-994 <WIL>  
A;Cross-references: EMBL:Z79754; PIDN:CAB02102.1; GSPDB:GN00019; CESP:F25H2.13  
A;Experimental source: clone F25H2  
R;Wilkinson, J.  
submitted to the EMBL Data Library, December 1996  
A;Reference number: Z19437  
A;Accession: T21540  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-994 <W12>  
A;Cross-references: EMBL:Z83224; PIDN:CAB05720.1; GSPDB:GN00019; CESP:F25H2.13  
A;Experimental source: clone F29C6  
C;Genetics:  
A;Gene: CESP:F25H2.13  
A;Map position: 1  
A;Introns: 129/2; 177/1; 206/2; 349/3; 436/3; 506/2; 626/3; 689/3; 772/3; 845/3; 903/3

Query Match 10.8%; Score 73; DB 2; Length 994;  
Best Local Similarity 27.6%; Pred.No. 34;  
Matches 37; Conservative 20; Mismatches 45; Indels 32; Gaps 9;

Qy 23 MDKL-SKKKL-----CADBECVYTISLARAQEDYNAPDCRFIDVKKGQOIYVYVK- 71  
Db 339 MDKLFGSSQLKSVPLPSGRASDGE-ILLETAKAGFDANSVE-RLVDVLRDAISYLLSKN 396  
Qy 72 ---LVTENAG-----EFWAGSVYGDH-QDEMGIYGV- 113  
Db 397 EEVVALTERGDGMEKVADFL-LSYSTHAQDVAAVGEETVKLVDRDPKTVARNCKLIQ 455  
Qy 114 ATKETPTTDDIFFC 127  
Db 456 KKDNEKLTIKYFC 469

Search completed: December 29, 2003, 16:10:39  
Job time : 14.2661 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 5.01961 Seconds  
(without alignments)  
1199.181 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
Sequence: 1 MARTILLILOGVVLVLCAGH.....RVYQATKEIPTTIDDFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676	100.0	128	1	OTOR_MOUSE
2	602	89.1	128	1	OTOR_HUMAN
3	468.5	69.3	132	1	OTOR_CHICK
4	412	60.9	133	1	OTOR_RANCA
5	277.5	41.1	131	1	MIA_HUMAN
6	268	39.6	130	1	MIA_RAT
7	267	39.5	130	1	MIA_BOVIN
8	251	37.1	130	1	MIA_MOUSE
9	91.5	13.5	843	1	VAV_RAT
10	91.5	13.5	845	1	VAV_MOUSE
11	91.5	13.5	847	1	VAV3_MOUSE
12	89.5	13.2	845	1	VAV3_HUMAN
13	89.5	13.2	847	1	VAV2_MOUSE
14	85.5	12.6	868	1	VAV2_HUMAN
15	84.5	12.5	878	1	CC25_YEAST
16	78.5	11.6	1589	1	CC25_YEAST
17	77	11.4	695	1	TGM2_PAGMA
18	77	11.4	2161	1	SHK1_HUMAN
19	76	11.2	259	1	YAZO_METJA
20	75	11.1	406	1	YCX9_EUGGR
21	75	11.1	1696	1	ITN2_HUMAN
22	75	11.1	2167	1	SHK1_RAT
23	74	10.9	1217	1	ITN1_RAT
24	73	10.8	451	1	TBG_ENTHI
25	71	10.5	340	1	YCSG_ECOLI
26	71	10.5	1714	1	ITN1_MOUSE
27	71	10.5	1721	1	ITN1_HUMAN
28	71	10.5	1815	1	SHK3_RAT
29	70.5	10.4	505	1	SRK1_SPOLA
30	70.5	10.4	506	1	SRK4_SPOLA
31	70.5	10.4	858	1	CNRA_MOUSE
32	70	10.4	486	1	ALLN_ALLSA
33	69.5	10.3	396	1	CXA7_MOUSE

ALIGNMENTS

RESULT 1

ID	OTOR_MOUSE	STANDARD;	PRT;	128 AA.
AC	Q9JIE3;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Otoraplin precursor (Melanoma inhibitory activity-like protein).			
GN	OTOR OR MIAL.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=20334619; PubMed=10873378;			
RA	Robertson N.G., Heller S., Lin J.S., Resendes B.L., Werenowicz S.,			
RA	Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;			
RT	"A novel conserved cochlear gene, OTOR: identification, expression			
RT	analysis, and chromosomal mapping.";			
RL	Genomics 66:242-248(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Petal;			
RA	MEDLINE=21100875; PubMed=11161796;			
RA	Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;			
RT	"Identification and characterization of an inner ear-expressed human			
RT	melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent			
RL	polymorphism that abolishes translation.";			
RL	Genomics 71:40-52(2001).			
CC	-!- SUBCELLULAR LOCATION: Secreted (Potential).			
CC	-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.			
CC	-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.			
CC	-!- SIMILARITY: Contains 1 SH3 domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AF233333; AAF82079.1; -			
DR	EMBL; AJ243939; CAC27444.1; -			
DR	HSSP; Q16674; 111J			
DR	MGI; MGI:188678; Otor.			
DR	GO; GO:0001502; P:cartilage condensation; IMP.			
DR	InterPro; IPR001452; SH3.			
DR	Pfam; PF00018; SH3; 1.			
DR	SMART; SM00326; SH3; 1.			
DR	PROSITE; PS50002; SH3; 1.			
DR	Signal; SH3 domain.			
FT	SIGNAL 1 18			POTENTIAL.
FT	CHAIN 19 128			OTORAPLIN.
FT	DOMAIN 39 110			SH3.



FT DISULFID 32 37 BY SIMILARITY.  
 FT DISULFID 55 127 BY SIMILARITY.  
 SQ SEQUENCE 128 AA; 14328 MW; 3DD47D4C77C4A7FD CRC64;  
 Query Match 100.0%; Score 676; DB 1; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-59;  
 Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
 DB 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
 QY 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 DB 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 QY 121 TDIDFCE 128  
 DB 121 TDIDFCE 128

RESULT 2

OTOR HUMAN STANDARD; PRT: 128 AA.  
 ID Q9NRC9;  
 AC 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Otoraplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory  
 DE activity like protein).  
 OS Homo sapiens (Human).  
 GN OTOR OR FDP OR MIAL.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cochlea;  
 RX MEDLINE=20334619; PubMed=10873378;  
 RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,  
 RA Denis C.S., Bell A.M., Rudspeth A.J., Morton C.C.;  
 RT "A novel conserved cochlear gene, OTOR: identification, expression  
 RT analysis, and chromosomal mapping."  
 RL Genomics 66:242-248(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20568254; PubMed=10998416;  
 RA Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;  
 RT "Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an  
 RT in vitro effect on the early differentiation of the inner ear  
 RT mesenchyme."  
 RL J. Biol. Chem. 275:40036-40041(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, and Cochlea;  
 RX MEDLINE=21100875; PubMed=11161796;  
 RA Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;  
 RT "Identification and characterization of an inner ear-expressed human  
 RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent  
 RT polymorphism that abolishes translation."  
 RL Genomics 71:40-52(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21639749; PubMed=11780052;  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavridis G., Almeida J.P., Babbage A.K., Baguley C.L.,  
 RA Bailey J., Barlow K.F., Bead K.N., Beare D.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leivaeslahti M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie I.J., McEay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Symamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tomans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
 CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.

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 CC  
 CC EMBL; AF233261; AAF82078.1; -  
 CC EMBL; AF243505; BAG42356.1; -  
 CC EMBL; AJ242552; CAC27443.1; -  
 CC EMBL; AJ252324; CAC28085.1; -  
 CC EMBL; AJ252325; CAC28085.1; JOINED.  
 CC EMBL; AJ252326; CAC28085.1; JOINED.  
 CC EMBL; AJ252327; CAC28085.1; JOINED.  
 CC EMBL; AJ034428; CAC16848.1; -  
 CC HSP; Q16674; ILLJ.  
 CC Genew; HGNC=8517; OTOR.  
 CC MIM; 606067; -  
 CC GO; GO:0007605; P.hearing; TAS.  
 CC InterPro: IPR001452; SH3.  
 CC Pfam; PF00018; SH3; 1.  
 CC SMART; SM00326; SH3; 1.  
 CC PROSITE; PS50002; SH3; FALSE NEG.  
 CC SIGNAL; 1 18 POTENTIAL.  
 CC CHAIN 19 128 OTORAPLIN.  
 CC DOMAIN 39 110 SH3.  
 CC DISULFID 32 37 BY SIMILARITY.  
 CC DISULFID 55 127 BY SIMILARITY.  
 SQ SEQUENCE 128 AA; 14332 MW; 9BB52C7F5D4FB700 CRC64;

Query Match 89.1%; Score 602; DB 1; Length 128;  
 Best Local Similarity 86.7%; Pred. No. 5.5e-52;  
 Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
 DB 1 MARILLGLLVLCAGHGVFMDKLSKKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60  
 QY 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 DB 61 KKGQIYVYKLVTEGAGFVAGSVYGDHGVFVPSNVLKQRYVQATKEIPT 120  
 QY 121 TDIDFCE 128  
 DB 121 TDIDFCE 128

Tue Dec 30 10:20:38 2003

```
OTOR CHICK STANDARD; PRT; 132 AA.
ID Q918P6;
AC Q918P6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20334619; PubMed=10873378;
RX Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF233518; AAF82727.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain.
FT SIGNAL 1 23
FT CHAIN 24 132
FT DOMAIN 42 114
FT DISULFID 35 40
FT DISULFID 58 131
FT DISULFID 58 131
SQ SEQUENCE 132 AA; 15177 MW; 9D1C807FD353CE1C CRC64;

Query Match 69.3%; Score 468.5; DB 1; Length 132;
Best Local Similarity 71.0%; Pred. No. 6.2e-39;
Matches 88; Conservative 14; Mismatches 15; Indels 7; Gaps 2;

Qy 12 LVLCAG-----HGFMFKLSKKLCADEECVVTISLARAQEDYNAPDCRFIDVKKGQQ 65
Db 9 VFLFCGLMNPFAFGIEMDKLASKLCADEECVVTISLARAQEDYNAPDCRFIDVKKGQQ 68
Qy 66 IYVYSKLVTEGAGFVWAGSVYVGD-HQDEMGIYGVPSNLVKQRYVQEAKEIPTTDD 124
Db 69 IYVYSKLVTEGAGFVWAGSVYVGD-HQDEMGIYGVPSNLVKQRYVQEAKEIPTTDD 128
Qy 125 PFCE 128
Db 129 PFCE 132

RESULT 4
ID OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q918P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20334619; PubMed=10873378;
RX Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF233518; AAF82727.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain.
FT SIGNAL 1 23
FT CHAIN 24 132
FT DOMAIN 42 114
FT DISULFID 35 40
FT DISULFID 58 131
FT DISULFID 58 131
SQ SEQUENCE 132 AA; 15177 MW; 9D1C807FD353CE1C CRC64;

Query Match 69.3%; Score 468.5; DB 1; Length 132;
Best Local Similarity 71.0%; Pred. No. 6.2e-39;
Matches 88; Conservative 14; Mismatches 15; Indels 7; Gaps 2;

Qy 12 LVLCAG-----HGFMFKLSKKLCADEECVVTISLARAQEDYNAPDCRFIDVKKGQQ 65
Db 9 VFLFCGLMNPFAFGIEMDKLASKLCADEECVVTISLARAQEDYNAPDCRFIDVKKGQQ 68
Qy 66 IYVYSKLVTEGAGFVWAGSVYVGD-HQDEMGIYGVPSNLVKQRYVQEAKEIPTTDD 124
Db 69 IYVYSKLVTEGAGFVWAGSVYVGD-HQDEMGIYGVPSNLVKQRYVQEAKEIPTTDD 128
Qy 125 PFCE 128
Db 129 PFCE 132

RESULT 5
MIA_HUMAN
ID MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=95007612; PubMed=7923218;
RX Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
```

```
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=20334619; PubMed=10873378;
RX Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -----
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CC -----
DR EMBL; AF233519; AAF82728.1; -.
DR HSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain.
FT SIGNAL 1 23
FT CHAIN 24 133
FT DOMAIN 48 115
FT DISULFID 35 40
FT DISULFID 58 132
FT DISULFID 58 132
SQ SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;

Query Match 60.9%; Score 412; DB 1; Length 133;
Best Local Similarity 57.6%; Pred. No. 2.1e-33;
Matches 72; Conservative 28; Mismatches 17; Indels 8; Gaps 3;

Qy 12 LVLCAG-----HGFMFKLSKKLCADEECVVTISLARAQEDYNAPDCRFIDVKKGQQ 65
Db 9 VIVLCGLFIHQKAYGVYMQKLSKCLCADDCEIVASFGRAEDDYNAPDCRFVNLKKGEL 68
Qy 66 IYVYSKLVTEGAGFVWAGSVYVGD-HQDEMGIYGVPSNLVKQRYVQEAKEIPTTDD 123
Db 69 VYIVTKLVKENDDAGEFWGSGVYSDQYRDQOGLVGFPSLLVTLTYKDELQELPTTAV 128
Qy 124 DFCE 128
Db 129 DFYCD 133

RESULT 5
MIA_HUMAN
ID MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP MEDLINE=95007612; PubMed=7923218;
RX Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
```

RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;  
 RT "Cloning of a novel malignant melanoma-derived growth-regulatory  
 RL protein, MIA."; Cancer Res. 54:5695-5701(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=96132947; PubMed=8550608;  
 RA Bossert A., Hein R., Bogdahn U., Buettner R.;  
 RT "Structure and promoter analysis of the gene encoding the human  
 RL melanoma-inhibiting protein MIA."; J. Biol. Chem. 271:490-495(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Skin;  
 RX MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RL human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-131.  
 RX MEDLINE=2124635; PubMed=11331761;  
 RA Loughhead J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;  
 RT "Structure of melanoma inhibitory activity protein, a member of a  
 RL recently identified family of secreted proteins"; Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520(2001).  
 CC -!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO  
 CC AS WELL AS SOME NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND  
 CC INFREQUENTLY IN GLIOMA CELL LINES.  
 CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
 CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
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 CC -----  
 DR EMBL; X75450; CAA53203.1; -;  
 DR EMBL; X84707; CAA59195.1; -;  
 DR EMBL; BC005910; AAH05910.1; -;  
 DR PIR; I38019; I38019.  
 DR PDB; 1HJ; 16-MAY-01.  
 DR PDB; 1HJD; 29-JAN-02.  
 DR PDB; 1K0X; 24-JUL-02.  
 DR Genew; HGNC:7076; MIA.  
 DR MIM; 601340; -;  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0008283; P:cell proliferation; TAS.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00018; SH3; 1.

DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS00002; SH3; 1.  
 KW Growth factor; Signal; SH3 domain; 3D-structure.  
 FT FT SIGNAL 1 24  
 FT CHAIN 25 131 MELANOMA DERIVED GROWTH REGULATORY  
 FT PROTEIN.  
 FT SH3.  
 FT DOMAIN 43 113  
 FT DISULFID 36 41  
 FT DISULFID 59 130  
 FT STRAND 33 36  
 FT TURN 39 40  
 FT STRAND 46 50  
 FT STRAND 54 54  
 FT TURN 59 60  
 FT TURN 61 61  
 FT STRAND 64 64  
 FT TURN 66 67  
 FT STRAND 69 76  
 FT STRAND 78 80  
 FT HELIX 81 82  
 FT TURN 83 89  
 FT STRAND 93 94  
 FT TURN 96 96  
 FT STRAND 101 104  
 FT HELIX 105 107  
 FT STRAND 108 113  
 FT STRAND 119 122  
 FT HELIX 126 128  
 SQ SEQUENCE 131 AA; 14509 MW; 4D3BB30BD6008BDC CRC64;  
 Query Match 41.1%; Score 277.5; DB 1; Length 131;  
 Best Local Similarity 43.4%; Pred. No. 2.8e-20;  
 Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;  
 QY 1 MARILILLGLIVLC---AGHVF---MDKLSSKKLCADSECVYVITSLARAQEDYNAPD 54  
 Db 1 MARSIVCL--GVIIILSAFSGVGGVGGPMPLADKLCADQECSPISNAVALQDYMAPD 58  
 QY 55 CRFTIUVKKGQIYVYVSKLVTENGAGE-FWAGSVYGDHDEMGI-VGYFPPSNLVKEQRYVQ 112  
 Db 59 CRFTIHRGQVYVFSKL---KGRGLFWGSGVQGDYVGDLAARLGYPFSSIVREDQTLK 115  
 QY 113 BATKEIPTTDIDFFCE 128  
 Db 116 PGKVDVTKDWDVFCQ 131  
 RESULT 6  
 MIA RAT STANDARD; PRT; 130 AA.  
 AC Q62946; P97591;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Melanoma derived growth regulatory protein precursor (Melanoma  
 DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive  
 DE protein) (CD-RAP).  
 GN MIA OR CD-RAP.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Mammary gland;  
 RA Lu J.X.;  
 RT "Gene expression changes associated with chemically-induced rat  
 RL mammary carcinogenesis";  
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 34-124 FROM N.A.  
 RC TISSUE=Cartilage;  
 RX MEDLINE=96216414; PubMed=8621736;



RA Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hoesdörfer B.,  
RA Schmitt A., Jachimczak P., Lottspeich F., Büttner R., Bogdahn U.,  
RT "Cloning of a novel malignant melanoma-derived growth-regulatory  
RT protein, MIA."; 5695-5701(1994).  
RL Cancer Res. 54:5695-5701(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SV;  
RX MEDLINE=97251341; PubMed=9097023;  
RA Bosserhoff A.K., Kondo S., Moser M., Dietz U., Copeland N.G.,  
RA Gilbert D.J., Jenkins N.A., Büttner R., Sandell L.J.;  
RT "Mouse CD-RAP/MIA gene: structure, chromosomal localization, and  
RT expression in cartilage and chondrosarcoma.";  
RL Dev. Dyn. 208:516-525(1997).  
CC -!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AS  
CC WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY  
CC SIMILARITY). LOCATION: Secreted.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND  
CC INFREQUENTLY IN GLIOMA CELL LINES.  
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
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CC -----  
CC EMBL; X94322; CAA63983.1; -;  
CC EMBL; U85612; AAB42082.1; -;  
CC EMBL; X97965; CAA66608.1; -;  
CC HSSP; Q16674; 11LJ.  
CC MGD; MGI:109615; MIA.  
CC GO; GO:0007160; P:cell-matrix adhesion; IMP.  
CC GO; GO:0030198; P:extracellular matrix organization and bioge. .; IMP.  
CC InterPro; IPR001452; SH3.  
CC Pfam; PF00018; SH3; 1.  
CC SMART; SM00326; SH3; 1.  
CC PROSITE; PS50002; SH3; FALSE NEG.  
CC Growth factor; Signal; SH3 domain.  
CC SIGNAL 1 22 POTENTIAL.  
CC CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY  
CC PROTEIN.  
CC DOMAIN 42 112 SH3.  
CC FT DISULFID 35 40 BY SIMILARITY.  
CC FT DISULFID 58 129 BY SIMILARITY.  
CC FT CONFLICT 112 113 TL -> NS (IN REF. 1).  
CC SQ SEQUENCE 130 AA; 14593 MW; 16C957459C5B5F9 CRC64;  
CC  
CC Query Match 37.1%; Score 251; DB 1; Length 130;  
CC Best Local Similarity 43.0%; Pred. No. 1.1e-17;  
CC Matches 55; Conservative 23; Mismatches 40; Indels 10; Gaps 4;  
CC  
CC QY 8 LLGLVLCAGHV-----FMKLSKKLCADEECVVTISLARAQEDYNAPDCRFIDVK 62  
CC Db :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 65  
CC 6 VLLGIIVLVSVFGSPSRADRAMPKLADKWLKCADEECVVTISLARAQEDYNAPDCRF 65  
CC QY 63 GQIIVYVSKLVTEGAGE-FWAGSVYGDHDEMGI-VGYFPNVLVKQVYVQEAATKEIPT 120  
CC Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 122  
CC 66 GQVIVFSKL---KGRGLFWGSGVQGGYGGDIAARLGYFPSSIVREDLTLKPKIDMK 122  
CC  
CC QY 121 TDIDFFCE 128  
CC Db |||:|:  
CC 123 DQWDFYCQ 130  
CC  
CC RESULT 9  
CC VAV\_RAT  
CC ID\_VAV\_RAT STANDARD; PRT; 843 AA.  
CC  
CC AC P54100;  
CC DT 01-OCT-1996 (Rel. 34, Created)  
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)  
CC DT 15-SEP-2003 (Rel. 42, Last annotation update)  
CC DE Vav proto-oncogene (p95).  
CC GN VAVI OR VAV.  
CC OS Rattus norvegicus (Rat).  
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
CC OX NCBI\_TaxID=10116;  
CC RN [1]  
CC RP SEQUENCE FROM N.A.  
CC RX MEDLINE=99323974; PubMed=10395673;  
CC RA Song J.S., Haleem-Smith H., Arudchandran R., Gomez J., Scott P.M.,  
CC RA Mill J.F., Fan T.-H., Rivera J.;  
CC RT "Tyrosine phosphorylation of Vav stimulates IL-6 production in mast  
CC cells by a Rac/c-Jun N-terminal kinase-dependent pathway.";  
CC RL J. Immunol. 163:802-810(1999).  
CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of  
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or  
CC proliferation.  
CC -!- SUBUNIT: Interacts with SLA (By similarity).  
CC -!- PTM: Phosphorylated on tyrosine residues.  
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC -!- SIMILARITY: Contains 1 PH domain.  
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
CC binding domain.  
CC -!- SIMILARITY: Contains 1 SH2 domain.  
CC -!- SIMILARITY: Contains 2 SH3 domains.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL; U39476; AAA98606.1; -;  
CC HSSP; P29354; IGRI.  
CC InterPro; IPR001715; Calponin-like.  
CC InterPro; IPR003247; CH type.  
CC InterPro; IPR002219; DAG\_PE-bind.  
CC InterPro; IPR001331; GDS\_CDC24.  
CC InterPro; IPR001849; PH.  
CC InterPro; IPR000219; RHOGEF.  
CC InterPro; IPR000980; SH2.  
CC InterPro; IPR001452; SH3.  
CC InterPro; IPR003096; SM22\_calponin.  
CC Pfam; PF00307; CH; 1.  
CC Pfam; PF00130; DAG\_PE-bind; 1.  
CC Pfam; PF00169; PH; 1.  
CC Pfam; PF00621; RHOGEF; 1.  
CC Pfam; PF00017; SH2; 1.  
CC Pfam; PF00018; SH3; 2.  
CC PRINTS; PR00401; SH2DOMAIN.  
CC PRINTS; PR00452; SH3DOMAIN.  
CC PRINTS; PR00888; SM22CALPONIN.  
CC ProDom; PD001527; CH type; 1.  
CC ProDom; PD000093; SH2; 1.  
CC ProDom; PD000066; SH3; 1.  
CC SMART; SM00109; C1; 1.  
CC SMART; SM00033; CH; 1.  
CC SMART; SM00233; PH; 1.  
CC SMART; SM00325; RHOGEF; 1.  
CC SMART; SM00252; SH2; 1.  
CC SMART; SM00326; SH3; 2.  
CC PROSITE; PS50021; CH; 1.  
CC PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
CC PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
CC PROSITE; PS50010; DH\_2; 1.  
CC PROSITE; PS00741; DH\_1; 1.

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DR PROSITE; PSS0003; PH_DOMAIN; 1.
DR PROSITE; PSS0001; SH2; 1.
DR PROSITE; PSS0002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
FT DOMAIN 1 119
FT DOMAIN 194 373
FT DOMAIN 402 504
FT DOMAIN 516 564
FT DOMAIN 615 658
FT DOMAIN 669 763
FT DOMAIN 780 840
SQ SEQUENCE 843 AA; 97953 MW; C4A5ACAD45FCB80E CRC64;

Query Match 13.5%; Score 91.5; DB 1; Length 843;
Best Local Similarity 32.9%; Pred. No. 0.28;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

Qy 44 ARAQEDYNAPCRIDVKKGOIIVYSKLVTEGAGFEWAGSVVGDHDEMGIVGYPPSN 103
Db 785 AKARYDFCARDSELSLEKGDII----KILNKGQGGWWRGEIYGR-----IGWFFPSN 833

Qy 104 LVKEQVYQVE 113
Db 834 YVEED--YSE 841

RESULT 10
VAV_MOUSE STANDARD; PRT; 845 AA.
AC P27670;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DR Vav proto-oncogene.
GN VAV1 OR VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228488; PubMed=1565462;
RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization.";
RL Oncogene 7:611-618(1992).
RN [2]
RP SEQUENCE OF 1-93 FROM N.A.
RX MEDLINE=91172176; PubMed=2005887;
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RT oncogene activates its transforming potential.";
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [3]
RP INTERACTION WITH SLA.
RX MEDLINE=20130290; PubMed=10662792;
RA Sosinowski T., Pandey A., Dixit V.M., Weiss A.;
RT "Src-like adaptor protein (SLAP) is a negative regulator of T cell
RT receptor signaling.";
RL J. Exp. Med. 191:463-474(2000).
CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
CC proliferation.
CC -!- SUBUNIT: Interacts with SLA.
CC -!- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but
CC not in other cell types.
CC -!- PTM: Phosphorylated on tyrosine residues (By similarity).
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG

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CC binding domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X64361; CAA45713.1; -.
DR EMBL; M59833; AAA63402.1; -.
DR PIR; A61187; TVMSV.
DR PDB; 1F5X; 15-SEP-00.
DR PDB; 1GCP; 28-JAN-03.
DR PDB; 1GCQ; 28-JAN-03.
DR PDB; 1K1Z; 18-DEC-02.
DR TRANSFAC; T01230; -.
DR MGI; MGI:98923; Vav1. Calponin-like.
DR InterPro; IPR001715; CH type.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_CDC24.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH_type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;
KW 3D-structure.
FT DOMAIN 1 119
FT DOMAIN 194 373
FT DOMAIN 402 504
FT DOMAIN 516 564
FT DOMAIN 617 660
FT DOMAIN 671 765
FT DOMAIN 782 842
FT DOMAIN 845 AA; 98136 MW; 3666DCCD1C5229DA CRC64;
SQ SEQUENCE 845 AA; 98136 MW; 3666DCCD1C5229DA CRC64;

Query Match 13.5%; Score 91.5; DB 1; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.28;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

```



RT oncogene activates its transforming potential."; Mol. Cell. Biol. 11:1912-1920(1991). [4].

RN SEQUENCE OF 299-837 FROM N.A.

RA Romero F.; Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases. [5].

RP SEQUENCE OF 299-334 FROM N.A.

RQ MEDLINE=96038895; PubMed=7478592;

RX Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J., RA Tortolero M., Fischer S.; "The proline-rich region of Vav binds to Grb2 and Grb3-3."; Oncogene 11:1665-1669(1995). [6].

RP SIMILARITY TO CDC24 FAMILY.

RQ MEDLINE=92228488; PubMed=1565462;

RX Adams J.M., Houston H., Allen J., Lints T., Harvey R.; "The hematopoietically expressed vav proto-oncogene shares homology with the db1 GDP-GTP exchange factor, the bcr gene and a yeast gene (CDC24) involved in cytoskeletal organization."; Oncogene 7:611-618(1992).

RT CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of the Rho/Rac GTPases, thus leading to cell differentiation and/or proliferation.

CC -!- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2 and Grb3.

CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT NOT IN OTHER CELL TYPES.

CC -!- PTM: Phosphorylated on tyrosine residues.

CC -!- MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew alphabet.

CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.

CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.

CC -!- SIMILARITY: Contains 1 PH domain.

CC -!- SIMILARITY: Contains 1 zinc-dependent phosphol-ester and DAG binding domain.

CC -!- SIMILARITY: Contains 1 SH2 domain.

CC -!- SIMILARITY: Contains 2 SH3 domains.

CC -!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts in position 322 and 355.

CC

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CC

DR EMBL; AF030227; AAC25011.1; JOINED.

DR EMBL; AF030201; AAC25011.1; JOINED.

DR EMBL; AF030202; AAC25011.1; JOINED.

DR EMBL; AF030203; AAC25011.1; JOINED.

DR EMBL; AF030204; AAC25011.1; JOINED.

DR EMBL; AF030205; AAC25011.1; JOINED.

DR EMBL; AF030206; AAC25011.1; JOINED.

DR EMBL; AF030207; AAC25011.1; JOINED.

DR EMBL; AF030208; AAC25011.1; JOINED.

DR EMBL; AF030209; AAC25011.1; JOINED.

DR EMBL; AF030210; AAC25011.1; JOINED.

DR EMBL; AF030211; AAC25011.1; JOINED.

DR EMBL; AF030212; AAC25011.1; JOINED.

DR EMBL; AF030213; AAC25011.1; JOINED.

DR EMBL; AF030214; AAC25011.1; JOINED.

DR EMBL; AF030215; AAC25011.1; JOINED.

DR EMBL; AF030216; AAC25011.1; JOINED.

DR EMBL; AF030217; AAC25011.1; JOINED.

DR EMBL; AF030218; AAC25011.1; JOINED.

DR EMBL; AF030219; AAC25011.1; JOINED.

DR EMBL; AF030220; AAC25011.1; JOINED.

DR EMBL; AF030221; AAC25011.1; JOINED.

DR EMBL; AF030222; AAC25011.1; JOINED.

DR EMBL; AF030223; AAC25011.1; JOINED.

DR EMBL; AF030224; AAC25011.1; JOINED.

DR EMBL; AF030225; AAC25011.1; JOINED.

DR EMBL; AF030226; AAC25011.1; JOINED.

DR EMBL; X16316; CAA34383.1; ALT\_FRAME.

DR EMBL; M59834; AAA63267.1; -.

DR EMBL; X83931; CAA58783.1; -.

DR PIR; B39576; TVHUVV.

DR HSSP; P29354; IGRI.

DR TRANSFAC; T00880; -.

DR Genew; HGNC:12857; VAV1.

DR MIM; 164875; -.

DR GO; GO:0003700; F:transcription factor activity; TAS.

DR GO; GO:0007048; P:oncogenesis; TAS.

DR InterPro; IPR001715; Calponin-like.

DR InterPro; IPR003247; CH type.

DR InterPro; IPR002219; DAG\_PE-bind.

DR InterPro; IPR001331; GDS\_CDC24.

DR InterPro; IPR001849; PH.

DR InterPro; IPR000219; RhoGEF.

DR InterPro; IPR000980; SH2.

DR InterPro; IPR001452; SH3.

DR InterPro; IPR003096; SM22\_calponin.

DR Pfam; PF00307; CH; 1.

DR Pfam; PF00130; DAG\_PE-bind; 1.

DR Pfam; PF00169; PH; 1.

DR Pfam; PF00621; RhoGEF; 1.

DR Pfam; PF00017; SH2; 1.

DR Pfam; PF00018; SH3; 2.

DR PRINTS; PR00401; SH2DOMAIN.

DR PRINTS; PR00452; SH3DOMAIN.

DR PRINTS; PR00888; SM22CALPONIN.

DR ProDom; PD001527; CH type; 1.

DR ProDom; PD000093; SH2; 1.

DR ProDom; PD000066; SH3; 1.

DR SMART; SM00109; C1; 1.

DR SMART; SM00033; CH; 1.

DR SMART; SM00325; RhoGEF; 1.

DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 2.

DR PROSITE; PS00021; CH; 1.

DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.

DR PROSITE; PS00081; DAG\_PE\_BIND\_DOM\_2; 1.

DR PROSITE; PS0010; DH 2; 1.

DR PROSITE; PS00741; DH 1; 1.

DR PROSITE; PS00003; PH\_DOMAIN; 1.

DR PROSITE; PS00001; SH2; 1.

DR PROSITE; PS00002; SH3; 2.

KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Guanine-nucleotide releasing factor; Repeat; Phosphorylation.

KW

FT DOMAIN 1 119

FT DOMAIN 194 373

FT DOMAIN 402 504

FT DOMAIN 516 564

FT DOMAIN 617 660

FT DOMAIN 671 765

FT DOMAIN 782 842

FT DOMAIN 264 264

FT CONFLICT 718 718 I -> TV (IN REF. 2).

FT CONFLICT 718 718 I -> TV (IN REF. 2).

SQ SEQUENCE 845 AA; 98313 MW; AC3BC9736FD2F138 CRC64;

Query Match 13.2%; Score 89.5; DB 1; Length 845;

Best Local Similarity 32.9%; Pred. No. 0.44;

Matches 23; Conservative 14; Mismatches 13; Gaps 3;

QY 44 ARAQSDYNAPCRFDIVKKGQOIVYVSKLVTENGAGEFWAGSVYGDHDEMGIVGFFSN 103

Db 787 AKARYDFCARDSELSLKEGDII-----KILNKKGQGGWRRGEIYGR-----VGWFFAN 835

QY 104 LVKEQRTVQE 113

Db 836 YVEED--YSE 843



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RESULT 13
ID VAV3 HUMAN STANDARD; PRT; 847 AA.
AC Q9UKW4; O95230; Q9Y5X8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vav-3 protein.
GN VAV3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RP MEDLINE=99455043; PubMed=10523675;
RX Movilla N., Bustelo X.R.;
RT "Biological and regulatory properties of Vav-3, a new member of the
RT Vav family of oncoproteins.";
RN [2]
SEQUENCE FROM N.A.
RP TISSUE=Breast, and Colon carcinoma;
RX MEDLINE=98371222; PubMed=9705494;
RT Trenkle T., Welsh J., Jung B., Mathieu-Daude F., McClelland M.;
RT "Non-stoichiometric reduced complexity probes for cDNA arrays.";
RL Nucleic Acids Res. 26:3883-3891(1998).
CC -!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
CC TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
CC STATES OF THOSE GTPASES.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9UKW4-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9UKW4-2; Sequence=VSP_001820;
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DBP-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phosphatase and DAG
CC binding domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
CC
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CC
CC EMBL; AF118887; AAD20349.1; -.
CC EMBL; AF118886; AAD20348.1; -.
CC EMBL; AF067817; AAC79695.1; -.
CC HSP; P29355; 13EM.
CC Genew; HGNC:12659; VAV3.
CC MIM; 605541; -.
CC GO; GO:0005096; F:GTPase activator activity; TAS.
CC GO; GO:0005070; F:SH3/SH2 adaptor protein activity; TAS.
CC GO; GO:0007264; P:small GTPase mediated signal transduction; TAS.
CC InterPro; IPR001715; Calponin-like.
CC InterPro; IPR003247; CH type.
CC InterPro; IPR002219; DAG PE-bind.
CC InterPro; IPR001331; GPS_CDC24.
CC InterPro; IPR001849; PH.
CC InterPro; IPR000219; RhoGEF.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR001452; SH3.
CC InterPro; IPR003096; SM22_calponin.
CC Pfam; PF00307; CH_1.
CC Pfam; PF00130; DAG_PE-bind; 1.

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DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
KW Guanine-nucleotide releasing
FT DOMAIN 1 119
FT DOMAIN 192 371
FT DOMAIN 400 502
FT DOMAIN 514 562
FT DOMAIN 592 660
FT DOMAIN 672 766
FT DOMAIN 788 847
FT VARSPLIC 1 107
FT FT
FT FT
FT FT
FT FT
FT CONFLICT 107 107
FT CONFLICT 217 217
FT CONFLICT 298 298
FT CONFLICT 429 429
FT CONFLICT 847 AA; 97775 MW; CIE29F0B094CB721 CRC64;
SQ SEQUENCE 847 AA; 97775 MW; CIE29F0B094CB721 CRC64;

Query Match 13.2%; Score 89.5; DB 1; Length 847;
Best Local Similarity 32.8%; Pred. No. 0.44;
Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;

QY 41 ISLARAQEDYNAPDCRFIDVKKGOIYVYVKLVTEGAGFEWAGSVYGDHQDEMGIVGYF 100
Db LGIATARYDFCARDNRELSLKGDVVKIYTKM-----SANGWWRGEVNGR-----VGNP 838

QY 101 PSNLVKE 107
Db 839 PSTYVEE 845

RESULT 14
ID VAV2 MOUSE STANDARD; PRT; 868 AA.
AC Q60992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vav-2 protein.
GN VAV2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;

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Tue Dec 30 10:20:38 2003

RE MEDLINE=96313271; PubMed=9710375;  
RA Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,  
RT "Isolation and characterization of murine vav2, a member of the vav  
family of proto-oncogenes";  
RL Oncogene 13:363-371(1996).  
CC -!- FUNCTION: Guanine nucleotide exchange factor for the Rho family  
of Ras-related GTPases (By similarity).  
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC -!- SIMILARITY: Contains 1 PH domain.  
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
binding domain.  
CC -!- SIMILARITY: Contains 1 SH2 domain.  
CC -!- SIMILARITY: Contains 2 SH3 domains.  
CC -!- SIMILARITY: Contains 2 SH3 domains.  
CC -----  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U37017; AAC52761.1; -.  
DR HSSP; Q60631; IGBQ.  
DR MGP; MG1:102718; Vav2.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR003247; CH type.  
DR InterPro; IPR002219; DAG PE-bind.  
DR InterPro; IPR001331; GDS\_CDC24.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR000219; RhogEF.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00307; CH; 1.  
DR Pfam; PF00130; DAG PE-bind; 1.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhogEF; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 2.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR PRODOM; PD001527; CH type; 1.  
DR PRODOM; PD000093; SH2; 1.  
DR PRODOM; PD000066; SH3; 2.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00033; CH; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhogEF; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS00021; CH; 1.  
DR PROSITE; PS00479; DAG PE BIND DOM\_1; 1.  
DR PROSITE; PS00081; DAG PE BIND DOM\_2; 1.  
DR PROSITE; PS00010; DH\_2; 1.  
DR PROSITE; PS00741; DH\_1; 1.  
DR PROSITE; PS00043; PH DOMAIN; 1.  
DR PROSITE; PS00001; SH2; 1.  
DR PROSITE; PS00002; SH3; 2.  
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;  
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.  
FT DOMAIN 1 119  
FT DOMAIN 193 371  
FT DOMAIN 400 502  
FT DOMAIN 514 562  
FT DOMAIN 576 642  
FT DOMAIN 663 757  
FT DOMAIN 806 867  
FT MOD\_RES 142 142  
FT MOD\_RES 159 159  
FT MOD\_RES 159 159  
FT PHOSPHORYLATION (BY EGFR) (BY  
FT PHOSPHORYLATION (BY EGFR) (BY  
FT SIMILARITY).

FT MOD\_RES 172 172 PHOSPHORYLATION (BY EGFR) (BY  
FT SIMILARITY).  
SQ SEQUENCE 868 AA; 99915 MW; D18581E7EB2DBC2 CRC64;  
Query Match 12.6%; Score 85.5; DB 1; Length 868;  
Best Local Similarity 28.9%; Pred.No.1.1;  
Matches 22; Conservative 19; Mismatches 22; Indels 13; Gaps 3;  
QY 38 VYT---ISLARAQEDYNAPCRFDVKKGOQIVVYSLVTENGAGFEWAGSVYGDHDEM 94  
DB 802 VFTPRVIGTAVRYNFAARDMRELSRGDGVVKIYSRIGGDQ---WWKG-----ETN 851  
QY 95 GIVGYPPSNLVKEQV 110  
DB 852 GRIGWFFSTVVEEGV 867  
RESULT 15  
VAV2 HUMAN  
ID VAV2\_HUMAN STANDARD; PRT; 878 AA.  
AC P52735;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vav-2 protein.  
GN VAV2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain.  
RX MEDLINE=95283235; PubMed=7762982;  
RA Henske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramlakhan S.,  
RA Haines J.L., Kwiatkowski D.J.;  
RT "Identification of VAV2 on 9q34 and its exclusion as the tuberous  
sclerosis gene TSC1";  
RL Ann. Hum. Genet. 59:25-37(1995).  
RN [2]  
RP PHOSPHORYLATION OF TYR-142; TYR-159 AND TYR-172.  
RX MEDLINE=22464432; PubMed=12454019;  
RA Tamás P., Solti Z., Bauer P., Illés A., Sipke S., Bauer A.,  
RA Farago A., Downward J., Buday L.;  
RT "Mechanism of epidermal growth factor regulation of Vav2, a guanine  
nucleotide exchange factor for Rac";  
RL J. Biol. Chem. 278:5163-5171(2003).  
CC -!- FUNCTION: Guanine nucleotide exchange factor for the Rho family  
of Ras-related GTPases.  
CC -!- TISSUE SPECIFICITY: Widely expressed.  
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC -!- SIMILARITY: Contains 1 PH domain.  
CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
binding domain.  
CC -!- SIMILARITY: Contains 1 SH2 domain.  
CC -!- SIMILARITY: Contains 2 SH3 domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; S76992; AAB34377.1; -.  
DR PIR; I51940; I51940.  
DR HSSP; P08631; IBU1.  
DR Genew; HGNC:12658; VAV2.  
DR MIM; 600428; -.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR003247; CH\_type.

```

DR InterPro; IPR002219; DAG PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 2.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG PE BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG PE BIND_DOM_2; 1.
DR PROSITE; PS00010; DH; 2; 1.
DR PROSITE; PS00741; DH; 1; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing CH.
FT DOMAIN 1 119
FT DOMAIN 198 376
FT DOMAIN 405 512
FT DOMAIN 524 572
FT DOMAIN 586 652
FT DOMAIN 673 767
FT DOMAIN 816 877
FT MOD RES 142 142
FT MOD RES 159 159
FT MOD RES 172 172
SQ SEQUENCE 878 AA; 101256 MW; C8FF7681032146B4 CRC64;

Query Match      12.5%; Score 84.5; DB 1; Length 878;
Best Local Similarity 27.6%; Pred. No. 1.4;
Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;

QY 38 VYT---ISLARAQEDYNAPDCRFIDVKKGQIYVYKLVTEGAGREFWAGSVYGDHDEM 94
Db 812 VFTPRVIGTAVARYNFAARDMKELSLREGDVVRIYSRIGGDQG---WKKG-----ETN 861
QY 95 GIVGYFSPNLVKEQRV 110
Db 862 GRIGWFPSTVVEEGI 877

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Search completed: December 29, 2003, 16:04:13  
 Job time : 6.01961 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 19.7199 Seconds  
(without alignments)  
1674.996 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
Sequence: 1 MARILLLLGLVLCAGH.....RVYQEAATKEIPTTIDRFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 23:\*  
1: sp archaea:\*  
2: sp bacteria:\*  
3: sp fungi:\*  
4: sp human:\*  
5: sp invertebrate:\*  
6: sp mammal:\*  
7: sp mhc:\*  
8: sp organelle:\*  
9: sp phage:\*  
10: sp plant:\*  
11: sp rodent:\*  
12: sp virus:\*  
13: sp vertebrate:\*  
14: sp unclassified:\*  
15: sp virus:\*  
16: sp bacteriap:\*  
17: sp archaeap:\*

ALIGNMENTS																					
RESULT 1																					
17	86.5	12.8	839	13	Q8UUX5	Q8UUX5 gallus gall															
18	82.5	12.2	259	10	Q8RZZ8	Q8RZZ8 oryza sativ															
19	82	12.1	827	13	Q8UWE6	Q8UWE6 tetraodon n															
20	81.5	12.1	1196	4	Q9H0H2	Q9H0H2 homo sapien															
21	81.5	12.1	1196	4	Q8N157	Q8N157 homo sapien															
22	81.5	12.1	1215	5	O77202	O77202 acanthamoeb															
23	81	12.0	615	10	Q94E30	Q94E30 oryza sativ															
24	80.5	11.9	636	10	Q9FTZ8	Q9FTZ8 oryza sativ															
25	80	11.8	344	10	Q9FU07	Q9FU07 oryza sativ															
26	80	11.8	643	10	Q9FU04	Q9FU04 oryza sativ															
27	80	11.8	655	10	Q9AVH5	Q9AVH5 oryza sativ															
28	79	11.7	569	6	Q28616	Q28616 oryctolagus															
29	79	11.7	638	10	Q9ATQ5	Q9ATQ5 triticum ae															
30	79	11.7	722	16	Q9CGW7	Q9CGW7 lactococcus															
31	78	11.5	630	10	Q9ARM8	Q9ARM8 oryza sativ															
32	77.5	11.5	635	10	Q9FU01	Q9FU01 oryza sativ															
33	76.5	11.3	176	5	Q17629	Q17629 caenorhabdi															
34	76	11.2	352	10	Q94EK2	Q94EK2 allium asca															
35	76	11.2	352	10	Q94EK5	Q94EK5 allium wake															
36	76	11.2	479	10	Q43366	Q43366 allium cepa															
37	76	11.2	479	10	Q9SVV1	Q9SVV1 allium cepa															
38	76	11.2	641	10	Q9ATQ6	Q9ATQ6 triticum ae															
39	75.5	11.2	353	12	Q67711	Q67711 human adeno															
40	75.5	11.2	498	4	Q9H803	Q9H803 homo sapien															
41	75.5	11.2	514	10	Q8S003	Q8S003 oryza sativ															
42	75	11.1	707	16	Q9XD63	Q9XD63 corynebacte															
43	74.5	11.0	346	3	Q9HDZ9	Q9HDZ9 schizosacch															
44	74.5	11.0	839	10	Q94F88	Q94F88 arabidopsis															
45	74.5	11.0	1097	5	Q9U2T9	Q9U2T9 caenorhabdi															
ALIGNMENTS																					
RESULT 1																					
Q9J109	ID	Q9J109	PRELIMINARY;	PRT;	96 AA.																
AC	Q9J109																				
DT	01-OCT-2000	(TREMBLrel. 15, Created)																			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)																			
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)																			
DE	Melanoma inhibitory activity protein (fragment).																				
OS	Mesocricetus auratus (Golden hamster).																				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;																				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;																				
OC	Mesocricetus.																				
OX	NCBI_taxid=10036;																				
RN	[1]																				
RP	SEQUENCE FROM N.A.																				
RA	Guba M., Bossertsoff A.K., Steinbauer M., Anthuber M., Buettner R.,																				
RA	Jauch K.W.;																				
RT	"Overexpression of MIA enhances extravasation and metastasis of A-mel3																				
RT	melanoma cells.";																				
CC	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.																				
CC	-I- SIMILARITY: CONTAINS 1 SH3 DOMAIN.																				
DR	EMBL;	AF271694;	AAF76220.1;																		
DR	HSSP;	Q16674;	111J.																		
DR	InterPro;	IPR001452;	SH3.																		
DR	Pfam;	PF00018;	SH3; 1.																		
DR	SMART;	SM00326;	SH3; 1.																		
DR	PROSITE;	PS00002;	SH3; 1.																		
KW	SH3 domain.																				
FT	NON_TER	1	1																		
FT	NON_TER	96	96																		
SQ	SEQUENCE	96 AA;	10756 MW;	E7B466C3B5505BFB	CRC64;																
Query Match 34.2%; Score 231.5; DB 11; Length 96;																					
Best Local Similarity 45.4%; Pred. No. 8.3e-17;																					
Matches 44; Conservative 22; Mismatches 26; Indels 5; Gaps 3;																					
QY	26 LSSKKLCADBECCVYITSLARAQEDYNAPDCRFIDVKKGQOIYVYKSLVTENGAGE-FWAG 84																				
Db	1 LADRLKCAQECQSHPI SMAVALQDWPDCRFITLHRGQVYVFSKL---KGRGLFWGG 57																				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	231.5	34.2	96	11	Q9J109 mesocricetu
2	218	32.2	288	11	Q8BJE9 mus musculu
3	218	32.2	1239	11	Q8B184 mus musculu
4	196	29.0	68	11	Q8C899 mus musculu
5	187.5	27.7	137	11	Q921X3 mus musculu
6	179.5	26.6	88	13	Q90XF1 tetraodon n
7	165	24.4	119	4	Q96PC5 homo sapien
8	156	23.1	119	11	Q91ZV0 mus musculu
9	91.5	13.5	166	11	O08526 mus musculu
10	91.5	13.5	287	11	Q8R076 mus musculu
11	91.5	13.5	806	11	Q8VDU4 mus musculu
12	91.5	13.5	845	11	Q8BTV7 mus musculu
13	91.5	13.5	846	13	Q8UUX6 gallus gall
14	90	13.3	1257	5	Q9VMA8 drosophila
15	90	13.3	1430	5	Q9VMA7 drosophila
16	89.5	13.2	719	4	Q96D37 homo sapien

QY 85 SVYGDHDEMGI-VGYFESNLVKEORVYQEAATKEIPT 120  
 Db 58 SVQGDYDGLAARLGIFPSSIVREDQTLKPGKVDYKT 94

RESULT 2  
 Q8BJE9 PRELIMINARY; PRT; 268 AA.

AC Q8BJE9; TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Weakly similar to NP1P-like protein (Fragment).  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Eye;  
 RA MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK084344; BAC39164.1; -.  
 FT NON TER 268  
 SQ SEQUENCE 268 AA; 29722 MW; 67339C562F684402 CRC64;

Query Match 32.2%; Score 218; DB 11; Length 268;  
 Best Local Similarity 42.2%; Pred. No. 7.6e-15;  
 Matches 46; Conservative 13; Mismatches 38; Indels 12; Gaps 4;  
 QY 19 HGVFMDKLSKKLCADEECVYVTSILARAQEDYNAPDCRFIDVKKQGIYVYVKLVTENGA 78  
 Db 28 HG---RRFSDLKVCDECSMLMYRGALEDFTPGDCRFVNFKKGGDDVYVYKLA--GGS 82  
 QY 79 GEFWAGSVGDHDEMGI-VGYFESNLVKEORVYQEAATKEIPTTDDIDFFC 127  
 Db 83 LELWAGSV--EHS-----FGYFPKDLIKVLKHYTEELHIPADETDFVC 124

RESULT 3  
 Q8BI84 PRELIMINARY; PRT; 1239 AA.

AC Q8BI84; TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Weakly similar to NP1P-like protein.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Retina;  
 RA MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK044749; BAC32064.1; -.  
 SQ SEQUENCE 1239 AA; 136350 MW; 6E16F9D42ECCFF05 CRC64;

Query Match 32.2%; Score 218; DB 11; Length 1239;  
 Best Local Similarity 42.2%; Pred. No. 4.8e-14;  
 Matches 46; Conservative 13; Mismatches 38; Indels 12; Gaps 4;  
 QY 19 HGVFMDKLSKKLCADEECVYVTSILARAQEDYNAPDCRFIDVKKQGIYVYVKLVTENGA 78

Db 28 HG---RRFSDLKVCDECSMLMYRGALEDFTPGDCRFVNFKKGGDDVYVYKLA--GGS 82  
 QY 79 GEFWAGSVGDHDEMGI-VGYFESNLVKEORVYQEAATKEIPTTDDIDFFC 127  
 Db 83 LELWAGSV--EHS-----FGYFPKDLIKVLKHYTEELHIPADETDFVC 124

RESULT 4  
 Q8C899 PRELIMINARY; PRT; 68 AA.

AC Q8C899; TREMBLrel. 23, Created)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
 DE Otoraplin.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RA MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium;  
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs."  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK047965; BAC33202.1; -.  
 SQ SEQUENCE 68 AA; 7431 MW; 3CBE75527D3CBF7F CRC64;

Query Match 29.0%; Score 196; DB 11; Length 68;  
 Best Local Similarity 64.6%; Pred. No. 3.1e-13;  
 Matches 42; Conservative 5; Mismatches 8; Indels 10; Gaps 2;  
 QY 1 MARILLLLGGLVLCAGHGVFMDKLSKKLCADEECV-----YTISLARAQEDYNA 52  
 Db 1 MARILLLLGGLVLCAGHGVFMDKLSKKLCADEECVCKALLTVNFSLSFYHMGNLISG 60  
 QY 53 --PDC 55  
 Db 61 KQPDG 65

RESULT 5  
 Q921X3 PRELIMINARY; PRT; 137 AA.

AC Q921X3; TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 23, Last annotation update)  
 DE Similar to cartilage derived retinoic acid sensitive protein.  
 GN CDRA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC009815; AAH09815.1; -.  
 DR MGI; MGI:109615; Cdrap.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00018; SH3; 1.  
 DR SMART; SM00326; SH3; 1.  
 SQ SEQUENCE 137 AA; 15441 MW; 971415552E6FD536 CRC64;

Query Match 27.7%; Score 187.5; DB 11; Length 137;  
 Best Local Similarity 50.6%; Pred. No. 5.7e-12;  
 Matches 43; Conservative 11; Mismatches 22; Indels 9; Gaps 3;

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QY 8 LLGLVVLKAGHV-----FMDKLSKKLCADBEVCYVTTISLARAQEDYNAPDCRFIDVKK 62
Db 6 VLLGIVVLSVFGSPSRADRAKPLADKLCADBECHPISMAVALQDYVAPDCRFITYYR 65
QY 63 GQOIYVYKLVTEGAGE-FWAGSV 86
Db 66 GQVYVFSKL-----KGRGLFWGGSV 87

RESULT 6
Q90XF1 PRELIMINARY; PRT; 88 AA.
ID Q90XF1
AC Q90XF1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma inhibitory activity protein (Fragment).
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Telostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP SEQUENCE FROM N.A.
RA Bosserhoff A.K., Buettner R.;
RT "Characterization of the MIA gene family.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF390176; AAL26991.1; -.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1
DR SMART; SM00326; SH3; 1
DR NON TER 1
FT SEQUENCE 88 AA; 10080 MW; C355C1FE04DA22EA CRC64;

Query Match 26.6%; Score 179.5; DB 13; Length 88;
Best Local Similarity 42.4%; Pred. No. 2.3e-11;
Matches 39; Conservative 17; Mismatches 25; Indels 11; Gaps 4;

QY 41 ISLARAQEDYNAPDCRFIDVKKQOIYVYKLVTEGAG-FWAGSV-----YGDHQDEMG 95
Db 3 IMIARALQDYVPADCCXFPPIRQGLIYVYAML---KGRSQFWAGSVQDSYVGQOEAR-- 57
QY 96 IVGFPNSLVKEQRYQEAATKPIPTDIDFFC 127
Db 58 -IGHFPPIVEETHPLMAAQTEVTSNMDFYC 88

RESULT 7
Q96PC5 PRELIMINARY; PRT; 119 AA.
ID Q96PC5
AC Q96PC5
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma inhibitory activity protein 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bosserhoff A.K., Buettner R.;
RT "Characterization of the MIA gene family.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF390175; AAL26990.1; -.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
SQ SEQUENCE 119 AA; 13535 MW; AEF529762D880AC5 CRC64;

Query Match 24.4%; Score 165; DB 4; Length 119;
Best Local Similarity 33.6%; Pred. No. 1.1e-09;

Matches 43; Conservative 16; Mismatches 45; Indels 24; Gaps 4;

QY 6 ILLGLVVLKAGHVFMKLSKKL-----CADBEVCYVTTISLARAQEDYNAPDCRFID 59
Db 9 ILLLAISLTKC-----LESTKLADLKCGDLECEALINRVSAMRDYRGDPDCRYLN 59
QY 60 VKRQGOIYVYKLVTEGAGFWAGSVYGDHQDEMGIVGFPNSLVKEQRYQEAATKEIP 119
Db 60 FTGGEISVYVVKLAGER--EDLWAGSKGKE-----FGYFPRDAVQIEEVFISEIQMS 110
QY 120 TTDIDFFC 127
Db 111 TKESDFLC 118

RESULT 8
Q91ZV0 PRELIMINARY; PRT; 119 AA.
ID Q91ZV0
AC Q91ZV0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Melanoma inhibitory activity protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Embryo;
RA Bosserhoff A.K., Buettner R.;
RT "Characterization of the MIA gene family.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF390177; AAL26992.1; -.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
SQ SEQUENCE 119 AA; 13397 MW; 589F390C0B49D1C7 CRC64;

Query Match 23.1%; Score 156; DB 11; Length 119;
Best Local Similarity 33.6%; Pred. No. 1e-08;
Matches 42; Conservative 20; Mismatches 49; Indels 14; Gaps 5;

QY 3 RILILLGLVVLKAGHVFMKLSKKLCADBEVCYVTTISLARAQEDYNAPDCRFIDVKK 62
Db 8 RILLVVS--LAKCL-EGTKL--LAHLKKCGDLECEALISRVIALRDYTGDPDCRYLNFTT 62
QY 63 GQOIYVYKLVTEGAGFWAGSVYGDHQDEMGIVGFPNSLVKEQRYQEAATKEIPTD 122
Db 63 GGEISVYVVKLGDDR--EDLWAGSKGKD-----FGYFPRDAVQIEEVFISEIQMSTKE 113
QY 123 IDFFC 127
Db 114 SDFLC 118

RESULT 9
O08526 PRELIMINARY; PRT; 166 AA.
ID O08526
AC O08526
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vav-T.
GN VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ddy; TISSUE=Testis;
RX MEDLINE=97190224; PubMed=9038379;
RA Okumura K., Kaneko Y., Nonoguchi K., Nishiyama H., Yokoi H.,
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RA Higuchi T., Itoh K., Yoshida O., Miki T., Fujita J.;  
 RT "Expression of a novel isoform of Vav, Vav-T, containing a single  
 RL Strchomology 3 domain in murine testicular germ cells.";  
 CC Oncogene 14:713-720(1997).  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 DR EMBL; D83266; BAA18950.1; --  
 DR HSSP; Q60631; 1GBQ.  
 DR MGD; MGI:98923; Vav.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW SH3 domain.  
 SQ SEQUENCE 166 AA; 19434 MW; 2C3AF1FF07A5018F CRC64;  
 Query Match 13.5%; Score 91.5; DB 11; Length 166;  
 Best Local Similarity 32.9%; Pred. No. 0.099;  
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;  
 QY 44 ARAQEDYNAPDCRFIDVKKQQIYVYVSKLVTEGAGFEWAGSVYGDHDEMGIYGVFPN 103  
 DB 108 AKARYDFCARDSELSLKEGDI-----KILNKKQQQGWGRGEIYGR-----IGWFPN 156  
 QY 104 LVKEQRTVQOE 113  
 DB 157 VYEDD--YSE 164  
 RESULT 10  
 ID Q8R076 PRELIMINARY; PRT; 287 AA.  
 AC Q8R076;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Hypothetical 32.7 kDa protein.  
 GN VAV3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBSJ databases.  
 DR EMBL; BC027242; AAH27242.1; --  
 DR MGD; MGI:188518; Vav3.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;  
 Query Match 13.5%; Score 91.5; DB 11; Length 287;  
 Best Local Similarity 32.8%; Pred. No. 0.19;  
 Matches 22; Conservative 13; Mismatches 21; Indels 11; Gaps 2;  
 QY 41 ISLARAQEDYNAPDCRFIDVKKQQIYVYVSKLVTEGAGFEWAGSVYGDHDEMGIYGVF 100  
 DB 230 LGIAIARYDFCARDRELSLLKGMVKIYTKM-----SANGWWRGEVNGR-----VGWF 278

QY 101 PSNLVKE 107  
 DB 279 PSTYVEE 285  
 RESULT 11  
 ID Q8VDU4 PRELIMINARY; PRT; 806 AA.  
 AC Q8VDU4;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Similar to vav oncogene.  
 GN VAV.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 PH DOMAIN.  
 DR EMBL; BC020487; AAH20487.1; --  
 DR MGD; MGI:98923; Vav.  
 DR InterPro; IPR005613; AIP3.  
 DR InterPro; IPR001715; Calponin-like.  
 DR InterPro; IPR003247; CH type.  
 DR InterPro; IPR002219; DAG PE-bind.  
 DR InterPro; IPR001331; GDS\_CDC24.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR000219; RhoGEF.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR003096; SM22\_calponin.  
 DR Pfam; PF03915; AIP3; 1.  
 DR Pfam; PF00307; CH; 1.  
 DR Pfam; PF00130; DAG\_PE-bind; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RhoGEF; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00888; SM22CALPONIN.  
 DR ProDom; PD001527; CH type; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00109; CL; 1.  
 DR SMART; SM00033; CH; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RhoGEF; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50021; CH; 1.  
 DR PROSITE; PS00479; DAG PE BIND\_DOM\_1; 1.  
 DR PROSITE; PS50081; DAG PE BIND\_DOM\_2; 1.  
 DR PROSITE; PS00741; DH\_1; 1.  
 DR PROSITE; PS50010; DH\_2; 1.  
 DR PROSITE; PS50003; PH\_DOMAIN; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 SQ SEQUENCE 806 AA; 93868 MW; F4368CD13A62D695 CRC64;  
 Query Match 13.5%; Score 91.5; DB 11; Length 806;  
 Best Local Similarity 32.9%; Pred. No. 0.66;  
 Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;  
 QY 44 ARAQEDYNAPDCRFIDVKKQQIYVYVSKLVTEGAGFEWAGSVYGDHDEMGIYGVFPN 103  
 DB 748 AKARYDFCARDSELSLKEGDI-----KILNKKQQQGWGRGEIYGR-----IGWFPN 796  
 QY 104 LVKEQRTVQOE 113

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Db          797 YVEED--YSE 804

RESULT 12
QBTV7      PRELIMINARY;      PRT;      845 AA.
ID Q8TV7
AC Q8TV7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE VAV proto-oncogene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus; PubMed=12466851;
RX MEDLINE=22354683;
RA The FANTOM Consortium,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK08586; BAC40436.1; -. 5D0DE0D93111DFB8B CRC64;
SQ SEQUENCE 845 AA; 98093 MW; 5D0DE0D93111DFB8B CRC64;

Query Match      13.5%; Score 91.5; DB 11; Length 845;
Best Local Similarity 32.9%; Pred. No. 0.7;
Matches 23; Conservative 14; Mismatches 20; Indels 13; Gaps 3;

QY          44 ARAQEDYNAPDCRFIDVKKGQIYVYVSKLVTEGAGFEWAGSVYGDHDEMGIVGYFPSN 103
Db          487 AKARYDFPCARDRSELSLKEGDII-----KILNKKGGQGWGRGIYGR-----IGWFPSPN 835
QY          104 LVKEQRYQE 113
Db          836 YVEED--YSE 843

RESULT 13
Q8UUX6      PRELIMINARY;      PRT;      846 AA.
ID Q8UUX6
AC Q8UUX6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE GDF/GTP exchange factor VAV3.
GN VAV3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
RX PubMed=11805146;
RA Inabe K., Ishiai M., Scharenberg A.M., Freshney N., Downward J.,
RA Kurosaki T.;
RT "Vav3 Modulates B Cell Receptor Responses by Regulating
RT Phosphoinositide 3-Kinase Activation.";
RL J. Exp. Med. 195:189-200 (2002).
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AV046915; AAL06249.1; -.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH_type.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.

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DR          InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH_type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS0021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS00010; DH_2; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
DR PROSITE; PS00002; SH3; 2.
KW SH3 domain.
SQ SEQUENCE 846 AA; 97815 MW; C47BE949D873821B CRC64;

Query Match      13.5%; Score 91.5; DB 13; Length 846;
Best Local Similarity 34.3%; Pred. No. 0.7;
Matches 23; Conservative 12; Mismatches 21; Indels 11; Gaps 2;

QY          41 ISLARAQEDYNAPDCRFIDVKKGQIYVYVSKLVTEGAGFEWAGSVYGDHDEMGIVGYF 100
Db          789 IGIAIARYDFCARDRELKLGVDVKIYTKM-----SANGWWRGEVNGR-----VGWF 837
QY          101 PSNLVKE 107
Db          838 PSTYVEE 844

RESULT 14
Q9VMA8      PRELIMINARY;      PRT;      1257 AA.
ID Q9VMA8
AC Q9VMA8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG11098 protein.
GN CG11635 OR CG13768 OR CG13769.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Scheeler F.,  
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,  
 RA Stapleton M., Strong R., Swirskas R., Tector C., Tyler D.,  
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;  
 RT "Sequencing of Drosophila melanogaster genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]  
 RN SEQUENCE FROM N.A.  
 RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,  
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,  
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,  
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,  
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,  
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;  
 RT "Annotation of Drosophila melanogaster genome."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]  
 RN SEQUENCE FROM N.A.  
 RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]  
 RN SEQUENCE FROM N.A.

RA FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003614; AAF52414.2; -.  
 DR FlyBase; FBgn0031842; CG11098.  
 SQ SEQUENCE 1430 AA; 159051 MW; FCF9988A95979349 CRC64;

Query Match 13.3%; Score 90; DB 5; Length 1430;  
 Best Local Similarity 25.6%; Pred. No. 1.9; Indels 12; Gaps 3;  
 Matches 30; Conservative 19; Mismatches 56;

QY	6	ILLGLGLVLCAGHGVFMDKLSKKLCADBEVCYVTISLARQAQDYDAPDCRFIDVKKGQQ	65
Db	17	LALVGLLICLPITLWATLSOKRLCADPKCEQLISMGIAKITTYAIGGEGLSFKINSP	76
QY	66	IYVYSKLVTEGAGFEWAGSVYGDHQMGIQVGFPSNLVKEQVY---QEATKEIP	119
Db	77	IRVLKSGAGSN--MQLWGVDINGRR-----GYANKDFIMEKKILVRDKDLLYEVP	124

Search completed: December 29, 2003, 16:06:25  
 Job time : 20.7199 secs

GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 25.098 Seconds  
(without alignments)  
809.506 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	676	100.0	128	22	Mouse MLP protein
2	655	96.9	128	22	Rat MLP protein se
3	602	89.1	128	22	Human growth regul
4	602	89.1	128	22	Human MLP protein
5	602	89.1	128	23	Human angiogenesis
6	602	89.1	128	23	Human PRO9873 prot
7	602	89.1	128	23	Human PRO protein,
8	602	89.1	128	23	Novel human secret
9	591	87.4	110	22	Mouse MLP protein

10	574	84.9	110	22	AAB69131	Rat MLP protein se
11	547	80.9	110	22	AAB69126	Human MLP protein
12	519	76.8	105	22	AAB82672	Human growth regul
13	449	66.4	87	22	AAB69129	Rat MLP protein se
14	277.5	41.1	131	16	AAR69811	Melanoma inhibitor
15	277.5	41.1	131	22	AAG65614	Human MIA protein
16	275.5	40.8	137	22	AAG65615	Recombinant human
17	247	36.5	130	16	AAR69812	Melanoma inhibitor
18	218	32.2	125	23	ABB82119	Mouse TANGO 130 MI
19	218	32.2	303	22	AAU29304	Human PRO polypept
20	218	32.2	303	22	AAB87608	Human PRO19670. H
21	218	32.2	303	23	ABG93933	Human secreted/tra
22	218	32.2	303	23	ABB84994	Human angiogenesis
23	218	32.2	303	23	ABB84994	Human PRO19670 pro
24	218	32.2	303	24	ABU71392	Human secreted pol
25	218	32.2	303	24	ABU71588	Novel human secret
26	218	32.2	303	24	ABU72034	Human PRO polypept
27	218	32.2	303	24	ABU72191	Human secreted/tra
28	218	32.2	303	24	ABU65849	Novel human secret
29	218	32.2	303	24	ABU66182	Human secreted/tra
30	218	32.2	303	24	ABU67686	Human PRO polypept
31	218	32.2	303	24	ABU65544	Human PRO polypept
32	218	32.2	303	24	ABU58680	Human secreted/tra
33	218	32.2	303	24	ABU56216	Human PRO polypept
34	218	32.2	303	24	ABU57211	Human secreted/tra
35	218	32.2	303	24	ABU10790	Human secreted/tra
36	218	32.2	714	21	AAU70209	Murine TANGO 130 p
37	218	32.2	714	23	ABB82117	Mouse TANGO 130 po
38	209.5	31.0	138	22	AAU25834	Human protein sequ
39	208.5	30.8	125	23	ABB82120	Human TANGO 130 MI
40	208.5	30.8	410	21	AAU70210	Human TANGO 130 pr
41	208.5	30.8	410	23	ABB82118	Human TANGO 130 pa
42	208.5	30.8	1907	23	ABB82127	Human TANGO 130 po
43	200	29.6	499	22	AAU29319	Human PRO polypept
44	200	29.6	499	24	ABU71407	Human PRO20088 pro
45	200	29.6	499	24	ABU65864	Human secreted/tra

ALIGNMENTS

RESULT 1

AAB69125  
ID AAB69125 standard; Protein; 128 AA.

XX AAB69125;

AC AAB69125;

DT 23-APR-2001 (first entry)

XX Mouse MLP protein sequence SEQ ID NO:12.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX cardiant; gene therapy; secretory cell function regulator; promoter;  
XX inhibitor.

OS Mus musculus.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;

DR WPI; 2001-159271/16.

DR N-PSDB; AAF59068.

```

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing e.g. bone and joint
PT diseases
XX
XX Claim 4; Page 93-94; 11lpp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
XX SQ Sequence 128 AA;
Query Match 100.0%; Score 676; DB 22; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.8e-74;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARILILLGLLVLCAGHGVFMDKLSKKLCADEECVYTIISLARAQEDYNAPDCRFIDV 60
Db 1 MARILILLGLLVLCAGHGVFMDKLSKKLCADEECVYTIISLARAQEDYNAPDCRFIDV 60
Qy 61 KKGQIIVYVSKLVTENGAGFEWAGSVYGDHQMGIYGFPSNLVKEQRYQVQATKEIPT 120
Db 61 KKGQIIVYVSKLVTENGAGFEWAGSVYGDHQMGIYGFPSNLVKEQRYQVQATKEIPT 120
Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128
RESULT 2
AAB69130
ID AAB69130 standard; Protein; 128 AA.
AC AAB69130;
XX
XX 23-APR-2001 (first entry)
XX
XX Rat MLP protein sequence SEQ ID NO:47.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW Joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor.
XX
XX Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX N-PSDB; AAF59098.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing e.g. bone and joint
PT diseases
XX
XX Claim 6; Page 106; 11lpp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
XX SQ Sequence 128 AA;
Query Match 96.9%; Score 655; DB 22; Length 128;
Best Local Similarity 96.1%; Pred. No. 6.7e-72;
Matches 123; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MARILILLGLLVLCAGHGVFMDKLSKKLCADEECVYTIISLARAQEDYNAPDCRFIDV 60
Db 1 MARILILLGLLVLCAGHGVFMDKLSKKLCADEECVYTIISLARAQEDYNAPDCRFIDV 60
Qy 61 KKGQIIVYVSKLVTENGAGFEWAGSVYGDHQMGIYGFPSNLVKEQRYQVQATKEIPT 120
Db 61 KKGQIIVYVSKLVTENGAGFEWAGSVYGDHQMGIYGFPSNLVKEQRYQVQATKEIPT 120
Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128
RESULT 3
AAB82671
ID AAB82671 standard; Protein; 128 AA.
AC AAB82671;
XX
XX 02-OCT-2001 (first entry)
XX
XX Human growth regulatory-like polypeptide.
XX
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Peptide 1..23 /label= Signal_peptide
FT Protein 24..128 /label= Mature_protein
FT /note= "separately claimed in Claim 10"
XX
XX WO200155332-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02455.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX 02-MAY-2000; 2000US-0563786.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX
XX WPI; 2001-483233/52.
XX
XX N-ESDB; AAH26343.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
PT hyperproliferative disorders, coagulation disorders, and nervous system
PT

```





## RESULT 7

[illegible]



XX DE Human MLP protein sequence SEQ ID NO:24.  
XX DE MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW Joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX OS Homo sapiens.  
XX PN WO200102564-A1.  
XX PD 11-JAN-2001.  
XX PF 29-JUN-2000; 2000WO-JP04278.  
XX PR 30-JUN-1999; 99JP-0186718.  
XX PA (TAKE ) TAKEDA CHEM IND LTD.  
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX WPI; 2001-159271/16.  
DR N-PSDB; AAF59079.  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX Claim 1; Page 97-98; 111pp; Japanese.  
XX CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX SQ Sequence 110 AA;  
Query Match 80.9%; Score 547; DB 22; Length 110;  
Best Local Similarity 90.0%; Pred. No. 9e-59; Mismatches 0; Gaps 0;  
Matches 99; Conservative 7; Indels 4;  
Qy 19 HGVFMDKLSKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 78  
Db 1 HGIFMDRLASKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 60  
Qy 79 GEFWAGSVYGDHDEMIGVGFPSNLVKEQRYQVQATKEIPTTIDPFCE 128  
Db 61 GEFWAGSVYGDHDEMIGVGFPSNLVKEQRYQVQATKEIPTTIDPFCE 110  
RESULT 12  
AAB82672  
ID AAB82672 standard; Protein; 105 AA.  
XX AAB82672;  
XX AC AC  
XX DT 02-OCT-2001 (first entry)  
XX Human growth regulatory-like polypeptide (mature protein).  
XX DE Growth regulatory-like polypeptide; human; cartilage; melanoma;  
KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.  
XX OS Homo sapiens.  
XX PN WO200155332-A2.

XX DE Human MLP protein sequence SEQ ID NO:49.  
XX DE MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW Joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX OS Rattus sp.  
XX PN WO200102564-A1.  
XX PD 11-JAN-2001.  
XX PF 29-JUN-2000; 2000WO-JP04278.  
XX PR 30-JUN-1999; 99JP-0186718.  
XX PA (TAKE ) TAKEDA CHEM IND LTD.  
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX WPI; 2001-159271/16.  
DR N-PSDB; AAF59099.  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX Claim 5; Page 107; 111pp; Japanese.  
XX CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX SQ Sequence 110 AA;  
Query Match 84.9%; Score 574; DB 22; Length 110;  
Best Local Similarity 96.4%; Pred. No. 4.5e-62;  
Matches 106; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
Qy 19 HGVFMDKLSKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 78  
Db 1 HGVFMDKLSKKLCADDECVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVYSKLVTEGA 60  
Qy 79 GEFWAGSVYGDHDEMIGVGFPSNLVKEQRYQVQATKEIPTTIDPFCE 128  
Db 61 GAFWAGSVYGDHDEMIGVGFPSNLVKEQRYQVQATKEIPTTIDPFCE 110  
RESULT 11  
AAB69126  
ID AAB69126 standard; Protein; 110 AA.  
XX AAB69126;  
XX AC AC  
XX DT 23-APR-2001 (first entry)

XX MIP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX Rattus sp.  
XX WO200102564-A1.  
XX 11-JAN-2001.  
XX 29-JUN-2000; 2000WO-JP04278.  
XX 30-JUN-1999; 99JP-0186718.  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
XX WPI; 2001-159271/16.  
XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX Example 9; Page 103; 111pp; Japanese.  
XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX Sequence 87 AA;  
SQ Query Match 66.4%; Score 449; DB 22; Length 87;  
Best Local Similarity 96.6%; Pred. No. 6.5e-47;  
Matches 84; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 24 DKLSKKLCADDEECVYTTISLARAQEDYNAPDCRFIDVKKQQIYYVSKLVTEGAGFWA 83  
Db 1 DKLSKKLCADDEECVYTTISLARAQEDYNAPDCRFIDVKKQQIYYVSKLVTEGAGFWA 60  
QY 84 GSVYGDHODEMGIVGFPSNLVKEQV 110  
Db 61 GSVYGDHODEMGIVGFPSNLVKEQV 87  
RESULT 14  
AAB69811  
ID AAB69811 standard; Protein; 131 AA.  
XX AAB69811;  
XX 25-MAR-2003 (updated)  
DT 26-OCT-1995 (first entry)  
XX Melanoma inhibiting protein (human).  
XX Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;  
KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;  
KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;  
KW probe; fusion protein.  
XX Homo sapiens.  
XX W09503328-A2.  
PN

XX 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-US02455.  
XX 25-JAN-2000; 2000US-0491404.  
XX 02-MAY-2000; 2000US-0563786.  
XX (HYSE-) HYSEQ INC.  
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
PI Drmanac RT;  
XX WPI; 2001-483233/52.  
XX N-PSDB; AAB26343.  
XX Isolated human growth regulatory-like polypeptide useful for treating  
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
PT hyperproliferative disorders, coagulation disorders, and nervous system  
PT disorders -  
XX Claim 10; Page 117; 119pp; English.  
XX The present sequence is that of a novel human growth regulatory-like  
CC polypeptide (GRLP) mature protein. The sequence is predicted from  
CC a novel assembled cDNA (see AAB26343) based on Hyseq clone number  
CC 16372272. The protein has a mol.wt. of 14 kDa and glycosylated. GRLP  
CC belongs to the same protein family as growth regulatory proteins,  
CC growth factors, human melanoma derived growth regulatory protein  
CC precursor (64% similarity and 45% identity over 111 amino acids)  
CC or melanoma inhibitory protein (CD-RAP, 44% identity and 64%  
CC retinoic acid sensitive protein) and other retinoic acid-sensitive  
CC proteins. GRLP polypeptides and polynucleotides of the invention  
CC can be used in the prophylaxis, treatment (including gene therapy)  
CC and diagnosis of disorders and diseases caused by, or involving,  
CC cartilage development and maintenance, inhibition of melanoma cell  
CC growth and tumours, including neuroectodermal tumours such as  
CC gliomas. The polypeptides, which include the GRLP mature protein,  
CC may also have nutritional uses, cytokine and cell proliferation  
CC or differentiation activity, stem cell growth factor activity,  
CC haematopoiesis regulating activity, tissue growth activity,  
CC immunosuppressive or immunostimulant activity, activin/inhibin  
CC activity, chemotactic/chemokinetic activity, haemostatic and  
CC thrombolytic activity, use in cancer diagnosis and therapy,  
CC drug screening, receptor/ligand activity, antiinflammatory  
CC activity, and treatment of leukaemia, nervous system disorders,  
CC arthritis and inflammation.  
XX Sequence 105 AA;  
SQ Query Match 76.8%; Score 519; DB 22; Length 105;  
Best Local Similarity 90.5%; Pred. No. 2.3e-55;  
Matches 95; Conservative 6; Mismatches 4; Indels 0; Gaps 0;  
QY 24 DKLSKKLCADDEECVYTTISLARAQEDYNAPDCRFIDVKKQQIYYVSKLVTEGAGFWA 83  
Db 1 DRLASKKLCADDEECVYTTISLARAQEDYNAPDCRFIDVKKQQIYYVSKLVTEGAGFWA 60  
QY 84 GSVYGDHODEMGIVGFPSNLVKEQVQATKEIPTTIDDFCE 128  
Db 61 GSVYGDHODEMGIVGFPSNLVKEQVQATKEIPTTIDDFCE 105  
RESULT 13  
AAB69129  
ID AAB69129 standard; Protein; 87 AA.  
XX AAB69129;  
XX 23-APR-2001 (first entry)  
DT Rat MLP protein sequence SEQ ID NO:39.  
DE

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XX PD 02-FEB-1995.
XX PF 19-JUL-1994; 94WO-EP02369.
XX PR 20-JUL-1993; 93DE-4324247.
XX PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX PI Bogdahn U, Buettner R, Kaluza B;
XX WPI; 1995-075191/10.
DR N-PSDB; AAQ84050, AAQ84051.
XX New melanoma inhibiting protein and related nucleic acid -
PT vectors, transformed cells, antibodies etc., useful for treating
PT tumours and as immunosuppressant e.g. by gene therapy
XX Claim 1; Page 54; 85pp; German.
XX This protein has melanoma-inhibiting activity and can be used to
CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell
CC lung cancer, neuroectodermal tumours) or as an immunosuppressant
CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of
CC peripheral blood lymphocytes). Antibodies raised against the
CC protein can be used to detect cell producing the protein and also
CC for protein purification. Probes derived from DNA encoding the
CC protein (AAQ84050, AAQ84051) can be used to detect sequences encoding
CC the protein or related proteins. The protein may be expressed as
CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 131 AA;
Query Match 41.1%; Score 277.5; DB 16; Length 131;
Best Local Similarity 43.4%; Pred. No. 1.1e-25;
Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;
Qy 1 MARILILLGLLVLC---AGHGVF---MDKLSKKLCADCECVYTISLARAQEDYNAPD 54
Db 1 MARSLVCL--GVILLSAFSGPGVGGPMPKLDRLKLCADQECSPISMAVALQDYMAPD 58
Qy 55 CRFIDVKKGOIYVYVSKLVTENGAGE-FWAGSVYGDHDEMG1-VGYFPPSNLVKEQRYVQ 112
Db 59 CRFTIHRGQVYVFSKL---KGRGLFWGSGVQGDYGLAARLGYFPSPSIVREDQTLK 115
Qy 113 EATKEIPTDIDFCE 128
Db 116 PGKVDVTKDKWDFYCQ 131
RESULT 15
ID AAG65614
AC AAG65614 standard; Protein; 131 AA.
DT 07-JAN-2002 (first entry)
DE Human MIA protein sequence.
KW MIA: melanoma inhibiting activity protein; antiinflammatory; human;
KW antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;
KW immunosuppressive; ophthalmological; dermatological; antidiabetic;
KW neuroprotective; immune tolerance; T-cell tolerance.
OS Homo sapiens.
PN WO200170253-A1.
XX 27-SEP-2001.
XX PD 15-MAR-2001; 2001WO-EP02991.
XX

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XX PR 23-MAR-2000; 2000EP-0201063.
XX PA (ALKU ) AKZO NOBEL NV.
XX PI Nelissen RLH, Verheijden GFM;
XX WPI; 2001-611446/70.
DR N-PSDB; AAH47783.
XX Use of melanoma inhibiting activity protein or its derivatives as
PT immune modulatory agents for the treatment of inflammatory diseases,
PT specifically rheumatoid arthritis -
XX Example 4; Page 34; 41pp; English.
XX The invention relates to the use of melanoma inhibiting activity (MIA)
CC protein and/or its fragments that have anti-inflammatory effects and
CC induce systemic immune tolerance or specific T-cell tolerance to MIA
CC antigen, for manufacturing a preparation against inflammatory diseases
CC and for induction of systemic immune tolerance or specific T-cell
CC tolerance in patients suffering from or susceptible to inflammatory
CC diseases. A fragment of MIA is useful as a therapeutic substance and is
CC useful for manufacture of pharmaceutical preparations against
CC inflammatory diseases such as an immune-cell mediated cartilage
CC destruction disease, specifically rheumatoid arthritis, autoimmune
CC diseases like Graves' disease, juvenile arthritis, primary
CC glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,
CC myasthenia gravis, Addison's disease, primary biliary sclerosis,
CC uveitis, systemic lupus erythematosus, inflammatory bowel disease,
CC multiple sclerosis or diabetes. The MIA polypeptides have specific
CC effect on the autoreactive T-cells thus leaving the other components of
CC the immune system intact as compared to the non-specific suppressive
CC effect of immunosuppressive drugs. The present sequence represents a
CC human MIA protein.
XX SQ Sequence 131 AA;
Query Match 41.1%; Score 277.5; DB 22; Length 131;
Best Local Similarity 43.4%; Pred. No. 1.1e-25;
Matches 59; Conservative 29; Mismatches 35; Indels 13; Gaps 6;
Qy 1 MARILILLGLLVLC---AGHGVF---MDKLSKKLCADCECVYTISLARAQEDYNAPD 54
Db 1 MARSLVCL--GVILLSAFSGPGVGGPMPKLDRLKLCADQECSPISMAVALQDYMAPD 58
Qy 55 CRFIDVKKGOIYVYVSKLVTENGAGE-FWAGSVYGDHDEMG1-VGYFPPSNLVKEQRYVQ 112
Db 59 CRFTIHRGQVYVFSKL---KGRGLFWGSGVQGDYGLAARLGYFPSPSIVREDQTLK 115
Qy 113 EATKEIPTDIDFCE 128
Db 116 PGKVDVTKDKWDFYCQ 131
Search completed: December 29, 2003, 16:09:02
Job time : 25.098 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:09:08 ; Search time 17.5686 Seconds  
(without alignments)  
1449.984 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
Sequence: 1 MARILLILGLVLCAGHG.....RVQKATKIPITDIDFFCE 128

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 724715 seqs, 199017464 residues 724715  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

1:	/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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7:	/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	602	89.1	128	12	US-10-216-163-72
2	602	89.1	128	12	US-10-218-765-72
3	602	89.1	128	12	US-10-219-063-72
4	602	89.1	128	12	US-10-219-066-72
5	602	89.1	128	12	US-10-219-067-72
6	602	89.1	128	12	US-10-219-068-72
7	602	89.1	128	12	US-10-219-069-72
8	602	89.1	128	12	US-10-219-073-72
9	602	89.1	128	12	US-10-219-475-72
10	602	89.1	128	12	US-10-219-480-72
11	602	89.1	128	12	US-10-219-483-72
12	602	89.1	128	12	US-10-219-525-72
13	602	89.1	128	12	US-10-219-526-72
14	602	89.1	128	12	US-10-219-530-72
15	602	89.1	128	12	US-10-219-531-72

16	602	89.1	128	12	US-10-219-532-72
17	602	89.1	128	12	US-10-219-533-72
18	602	89.1	128	12	US-10-223-081-360
19	602	89.1	128	12	US-10-230-437-72
20	602	89.1	128	12	US-10-232-228-72
21	602	89.1	128	12	US-10-223-082-360
22	602	89.1	128	15	US-10-227-884-72
23	602	89.1	128	15	US-10-230-163-72
24	602	89.1	128	15	US-10-230-338-72
25	602	89.1	128	15	US-10-218-631-72
26	602	89.1	128	15	US-10-230-414-72
27	602	89.1	128	15	US-10-216-159A-72
28	602	89.1	128	15	US-10-218-849-72
29	602	89.1	128	15	US-10-227-873-72
30	602	89.1	128	15	US-10-227-883-72
31	602	89.1	128	15	US-10-219-076-72
32	602	89.1	128	15	US-10-230-434-72
33	602	89.1	128	15	US-10-219-003-72
34	602	89.1	128	15	US-10-219-075-72
35	602	89.1	128	15	US-10-219-464-72
36	602	89.1	128	15	US-10-219-466-72
37	602	89.1	128	15	US-10-219-479-72
38	602	89.1	128	15	US-10-219-481-72
39	602	89.1	128	15	US-10-230-260-72
40	602	89.1	128	15	US-10-232-231-72
41	602	89.1	128	15	US-10-232-233-72
42	602	89.1	128	15	US-10-216-165-72
43	602	89.1	128	15	US-10-218-956-72
44	602	89.1	128	15	US-10-219-468-72
45	602	89.1	128	15	US-10-219-478-72

ALIGNMENTS

RESULT 1

US-10-216-163-72  
; Sequence 72, Application US/10216163  
; Publication No. US20030149239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530F1C3  
; CURRENT APPLICATION NUMBER: US/10/216,163  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656

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us-10-019-455a-12.rapb

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-216-163-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLLLGLVLCAGHGFMDKLSKKLCADDECVYTISLARAOEDYNAPDCRFIDV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MARILLLPGLVAVCAVHGIFMDRLASKKLCADDECVYTISLASAQEDYNAPCRFINV 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 KKGQIYVYSKLVTENGAGFEWAGSVYGDHDEMGIVGYFSPNIVKGRVYQEAATKEIPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 KKGQIYVYSKLVENGAGFEWAGSVYGDGDENGVGVPFRNLVKEQRVYQEAATKEVPT 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 TDIDFFCE 128
   |||||:|||||
Db 121 TDIDFFCE 128
   |||||:|||||

RESULT 2
US-10-218-765-72
; Sequence 72, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095916
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/096146
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/096791
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: 60/097986
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: 60/098544
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 60/099596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101786
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: 60/101916
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Db 61 KRGGQIYVYVSKLVKENGAGFWAGSVYGDGDGVGVPFRNLVKEQRVYQEAATKEVPT 120  
QY 121 TDIDFFCE 128  
Db 121 TDIDFFCE 128

RESULT 6  
US-10-219-068-72  
; Sequence 72, Application US/10219068  
; Publication No. US20030187205A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C31  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR FILING DATE: 10/119,480  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-068-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MARILLLLGLVLCAGHGVFMDKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILLFLPLGVAVCAVHGIFMDRLASKKLCADDECVYTISLARAQEDYNAPDCRFIN 60  
61 KRGGQIYVYVSKLVKENGAGFWAGSVYGDGDGVGVPFRNLVKEQRVYQEAATKEIPT 120  
61 KRGGQIYVYVSKLVKENGAGFWAGSVYGDGDGVGVPFRNLVKEQRVYQEAATKEVPT 120  
121 TDIDFFCE 128  
121 TDIDFFCE 128

RESULT 7  
US-10-219-069-72  
; Sequence 72, Application US/10219069  
; Publication No. US20030187206A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C40  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR FILING DATE: 10/119,480  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-069-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
QY 1 MARILLLLGLVLCAGHGVFMDKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILLFLPLGVAVCAVHGIFMDRLASKKLCADDECVYTISLARAQEDYNAPDCRFIN 60  
61 KRGGQIYVYVSKLVKENGAGFWAGSVYGDGDGVGVPFRNLVKEQRVYQEAATKEIPT 120  
61 KRGGQIYVYVSKLVKENGAGFWAGSVYGDGDGVGVPFRNLVKEQRVYQEAATKEVPT 120  
121 TDIDFFCE 128  
121 TDIDFFCE 128  
RESULT 8  
US-10-219-073-72  
; Sequence 72, Application US/10219073  
; Publication No. US20030187207A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.



APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC52  
CURRENT APPLICATION NUMBER: US/10/219,073  
CURRENT FILING DATE: 2002-08-14  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 72  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-219-073-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 MARILLGLVLCAGHGVFMDKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILLFLPLVAVCAVHGIFMDRLASKKLCADDECVYTISLARAQEDYNAPDCRFIN 60  
Qy 61 KKGQIYVYVKLVKENGAGFVWAGSVYGDHDEMGIYGFPSNLVKEQVYQEAATKEIPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVWAGSVYGDHDEMGIYGFPSNLVKEQVYQEAATKEIPT 120  
Qy 121 TDIDFCE 128  
Db 121 TDIDFCE 128

RESULT 9  
US-10-219-475-72  
Sequence 72, Application US/10219475  
Publication No. US20030187208A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria

APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC49  
CURRENT APPLICATION NUMBER: US/10/219,475  
CURRENT FILING DATE: 2002-08-13  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 72  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-219-475-72

Query Match 89.1%; Score 602; DB 12; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2.7e-64;  
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;  
Qy 1 MARILLGLVLCAGHGVFMDKLSKKLCADDECVYTISLARAQEDYNAPDCRFIDV 60  
Db 1 MARILLFLPLVAVCAVHGIFMDRLASKKLCADDECVYTISLARAQEDYNAPDCRFIN 60  
Qy 61 KKGQIYVYVKLVKENGAGFVWAGSVYGDHDEMGIYGFPSNLVKEQVYQEAATKEIPT 120  
Db 61 KKGQIYVYVKLVKENGAGFVWAGSVYGDHDEMGIYGFPSNLVKEQVYQEAATKEIPT 120  
Qy 121 TDIDFCE 128  
Db 121 TDIDFCE 128

RESULT 10  
US-10-219-480-72  
Sequence 72, Application US/10219480  
Publication No. US20030187209A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC38  
CURRENT APPLICATION NUMBER: US/10/219,480

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; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-483-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 KKGQIYVYVKLVTEGAGFVAGSVYGDHGDGEMGIVGYFPFNSLVKQRYVQEAATKEIPT 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 KKGQIYVYVKLVTEGAGFVAGSVYGDHGDGEMGIVGYFPFNSLVKQRYVQEAATKEIPT 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 12
US-10-219-525-72
; Sequence 72, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910

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; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-480-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MARILLGLGVLCAGHGVFMDKLSKKLCADEECVYTISLARAQEDYNAPDCRFIDV 60
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 61 KKGQIYVYVKLVTEGAGFVAGSVYGDHGDGEMGIVGYFPFNSLVKQRYVQEAATKEIPT 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 KKGQIYVYVKLVTEGAGFVAGSVYGDHGDGEMGIVGYFPFNSLVKQRYVQEAATKEIPT 120
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Qy 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 11
US-10-219-483-72
; Sequence 72, Application US/10219483
; Publication No. US20030187210A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC43
; CURRENT APPLICATION NUMBER: US/10/219,483
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-526-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILILLGLVVLVLCAGHGVFMDKLSKKLCADECEVYTISLARAQEDYNAPDCRFIDV 60
Db 1 MARILILLFLPGLVAVCAVHGIFMDRLASKKLCADECEVYTISLARAQEDYNAPDCRFIN 60
QY 61 KKGQIIVYVSKLVKENGAGFVAGSVYGDQDGVGVGFFRNVLVKEQRYVQEAATKEIPT 120
Db 61 KKGQIIVYVSKLVKENGAGFVAGSVYGDQDGVGVGFFRNVLVKEQRYVQEAATKEVPT 120
QY 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 14
US-10-219-530-72
; Sequence 72, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P35301C54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-530-72
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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-525-72

Query Match      89.1%; Score 602; DB 12; Length 128;
Best Local Similarity 86.7%; Pred. No. 2.7e-64;
Matches 111; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARILILLGLVVLVLCAGHGVFMDKLSKKLCADECEVYTISLARAQEDYNAPDCRFIDV 60
Db 1 MARILILLFLPGLVAVCAVHGIFMDRLASKKLCADECEVYTISLARAQEDYNAPDCRFIN 60
QY 61 KKGQIIVYVSKLVKENGAGFVAGSVYGDQDGVGVGFFRNVLVKEQRYVQEAATKEIPT 120
Db 61 KKGQIIVYVSKLVKENGAGFVAGSVYGDQDGVGVGFFRNVLVKEQRYVQEAATKEVPT 120
QY 121 TDIDFFCE 128
Db 121 TDIDFFCE 128

RESULT 13
US-10-219-526-72
; Sequence 72, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P35301C41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
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		Query Match	89.1%; Score 602; DB 12; Length 128;	
		Best Local Similarity	86.7%; Pred.No. 2.7e-64;	
		Matches 111; Conservative	9; Mismatches 8; Indels 0; Gaps 0;	
Qy	1	MARILLILLLGGVLVLCAGHGVMFDKLSKKLCADEECVYIISLARAOEDYNAPCRFIDV	60	
		:           :           :           :           :		
Dd	1	MARILLFLPLGVAVCAVHGLFMDFLRASKKLCADECVYIISLASAEDYNAPCRFINV	60	
		:           :           :           :           :		
Qy	61	KKGQOIIVYSKLVTEENGAGEFFWAGSVYGDHDEMGIYGYFPFNNLVKEQRVVYQEATKEIPT	120	
		:           :           :           :           :		
Dd	61	KKGQOIIIVYSKLVKENGAGEFFWAGSVYGDGDENGVVGYPFRNLVKEQRVVYQEATKEVPT	120	
		:           :           :           :           :		
Qy	121	TDIDFFCE	128	
Dd	121	TDIDFFCE	128	

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RESULT 15
US-10-219-531-72
  Sequence 72, Application US/10219531
  Publication No. US20030187214A1
  GENERAL INFORMATION:
  APPLICANT: Baker, Kevin P.
  APPLICANT: Desnoyers, Luc
  APPLICANT: Gerritsen, Mary
  APPLICANT: Goddard, Audrey
  APPLICANT: Godowski, Paul J.
  APPLICANT: Grimaldi, J. Christopher
  APPLICANT: Gurney, Austin L.
  APPLICANT: Smith, Victoria
  APPLICANT: Stephan, Jean-Philippe F.
  APPLICANT: Watanabe, Colin L.
  APPLICANT: Wood, William I.
  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
  TITLE OF INVENTION: ACIDS ENCODING THE SAME
  FILE REFERENCE: P3530P1C66
  CURRENT APPLICATION NUMBER: US/10/219,531
  CURRENT FILING DATE: 2002-08-14
  PRIOR APPLICATION NUMBER: 10/119,480
  PRIOR FILING DATE: 2002-04-09
  PRIOR APPLICATION NUMBER: 60/059113
  PRIOR FILING DATE: 1997-09-17
  PRIOR APPLICATION NUMBER: 60/062287
  PRIOR FILING DATE: 1997-10-17
  PRIOR APPLICATION NUMBER: 60/063549
  PRIOR FILING DATE: 1997-10-28
  PRIOR APPLICATION NUMBER: 60/064103
  PRIOR FILING DATE: 1997-10-31
  PRIOR APPLICATION NUMBER: 60/069873
  PRIOR FILING DATE: 1997-12-17
  PRIOR APPLICATION NUMBER: 60/078910
  PRIOR FILING DATE: 1998-03-20
  PRIOR APPLICATION NUMBER: 60/079294
  PRIOR FILING DATE: 1998-03-25
  PRIOR APPLICATION NUMBER: 60/079656
  PRIOR FILING DATE: 1998-03-26
  PRIOR APPLICATION NUMBER: 60/079728
  PRIOR FILING DATE: 1998-03-27
  Remaining Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 246
  SEQ ID NO 72
  LENGTH: 128
  TYPE: PRT
  ORGANISM: Homo Sapien
US-10-219-531-72

```

```

Db      1  MARILLFLPGLVAVCAVHGIFMDRELASKKLCADDECYVTTISLASAQEDYNAPDCREFINV  60
Qy      61  KKGQQTIVYVSKLVTEKGAGFWAGSVYGDHODMGIVGYFPSPNLVKQQRVYQEAATKEIPT  120
Db      61  KKGQQTIVYVSKLVKENGAGFWAGSVYGDGDGMGVGYFPFNLVKQQRVYQEAATKEVPT  120
Qy     121  TDIDFFCE 128
         |||||
Db     121  TDIDFFCE 128

Search completed: December 29, 2003, 16:26:15
Job time : 18.5686 secs

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Result No.	§			ID	Description
	Score	Query Match	Length DB		
1	277.5	41.1	131	1	US-08-578-649-2
2	247	36.5	130	1	US-08-578-649-5
3	91.5	13.5	844	1	US-07-646-5379-2
4	82.5	12.2	54	3	US-09-346-510B-21
5	78.5	11.6	1589	3	US-09-356-952-4
6	77	11.4	694	1	US-08-164-839-4
7	77	11.4	694	1	US-08-583-799-4
8	77	11.4	695	1	US-08-164-839-6
9	77	11.4	695	1	US-08-583-799-6
10	75	11.1	509	4	US-08-630-915A-194
11	74.5	11.0	1326	4	US-09-328-352-4886
12	73.5	10.9	48	3	US-09-346-510B-24
13	71.5	10.6	248	4	US-08-630-915A-40
14	71.5	10.6	687	1	US-08-164-839-31
15	71.5	10.6	687	1	US-08-164-839-33
16	71.5	10.6	687	1	US-08-583-799-31
17	71.5	10.6	687	1	US-08-583-799-33
18	71.5	10.6	688	1	US-08-164-839-70
19	71.5	10.6	688	1	US-08-164-839-72
20	71.5	10.6	688	1	US-08-583-799-70
21	71.5	10.6	688	1	US-08-583-799-72
22	71	10.5	462	4	US-08-630-915A-38
23	71	10.5	946	5	PCT-US95-08493-13
24	69.5	10.3	182	2	US-08-467-603-89
25	69.5	10.3	182	2	US-08-466-793-89
26	69.5	10.3	182	2	US-08-491-861A-89
27	69.5	10.3	182	4	US-09-374-671A-89





; FILING DATE: 14-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5607849man F.  
; REGISTRATION NUMBER: 24,618  
; TELEPHONE: (703)412-3000  
; TELEFAX: (703)413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 694 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-583-799-4

Query Match 11.4%; Score 77; DB 1; Length 694;  
Best Local Similarity 27.5%; Pred. No. 0.69;  
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHDEMGIYGVFPSNLV 105  
Db 392 EVNADTIYVQKQGR-----RKITEDHASVGKNISTKSVYGNHREDVTILHYKYPEGSQ 446

Qy 106 KEQVYQBATKEI--PTTDD 123  
Db 447 KEREYKKGAGRRVTEPSNEI 466

US-08-583-799-6

Query Match 11.4%; Score 77; DB 1; Length 695;  
Best Local Similarity 27.5%; Pred. No. 0.69;  
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHDEMGIYGVFPSNLV 105  
Db 393 EVNADTIYVQKQGR-----RKITEDHASVGKNISTKSVYGNHREDVTILHYKYPEGSQ 447

Qy 106 KEQVYQBATKEI--PTTDD 123  
Db 448 KEREYKKGAGRRVTEPSNEI 467

US-08-583-799-6

RESULT 9

US-08-583-799-6  
; Sequence 6, Application US/08583799  
; Patent No. 5607849  
; GENERAL INFORMATION:  
; APPLICANT: YASUEDA, HISASHI  
; APPLICANT: NAKANISHI, KAZUO  
; APPLICANT: MOTOKI, MASAO  
; APPLICANT: NAGASE, KAZUO  
; APPLICANT: MATSUI, HIROSHI  
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED  
; FROM FISH  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/583,799  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/004,729  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5607849man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-599-0  
TELEPHONE: (703)412-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 695 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-583-799-6

Query Match 11.4%; Score 77; DB 1; Length 695;  
Best Local Similarity 27.5%; Pred. No. 0.69;  
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHDEMGIYGVFPSNLV 105

; FILING DATE: 14-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oblon, No. 5607849man F.  
; REGISTRATION NUMBER: 24,618  
; TELEPHONE: (703)412-3000  
; TELEFAX: (703)413-2220  
; TELEX: 248855 OPAT UR  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 694 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-583-799-4

Query Match 11.4%; Score 77; DB 1; Length 694;  
Best Local Similarity 27.5%; Pred. No. 0.69;  
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHDEMGIYGVFPSNLV 105  
Db 392 EVNADTIYVQKQGR-----RKITEDHASVGKNISTKSVYGNHREDVTILHYKYPEGSQ 446

Qy 106 KEQVYQBATKEI--PTTDD 123  
Db 447 KEREYKKGAGRRVTEPSNEI 466

US-08-583-799-6

Query Match 11.4%; Score 77; DB 1; Length 694;  
Best Local Similarity 27.5%; Pred. No. 0.69;  
Matches 22; Conservative 20; Mismatches 28; Indels 10; Gaps 3;

Qy 49 DYNAPDCRFIDVKKGQOIYVYKLVTEGAG---EFWAGSVYGDHDEMGIYGVFPSNLV 105  
Db 392 EVNADTIYVQKQGR-----RKITEDHASVGKNISTKSVYGNHREDVTILHYKYPEGSQ 446

Qy 106 KEQVYQBATKEI--PTTDD 123  
Db 447 KEREYKKGAGRRVTEPSNEI 466

US-08-583-799-6

RESULT 8

US-08-164-839-6  
; Sequence 6, Application US/08164839  
; Patent No. 5514573  
; GENERAL INFORMATION:  
; APPLICANT: YASUEDA, HISASHI  
; APPLICANT: NAKANISHI, KAZUO  
; APPLICANT: MOTOKI, MASAO  
; APPLICANT: NAGASE, KAZUO  
; APPLICANT: MATSUI, HIROSHI  
; TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED  
; FROM FISH  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
; STREET: 1755 Jefferson Davis Highway, Fourth Floor  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/164,839  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/004,729  
FILING DATE: 14-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Oblon, No. 5514573man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 10-599-0  
TELEPHONE: (703)412-3000  
TELEFAX: (703)413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:



Db 393 EVNADTYIVQXGQR-----RKTFEDHASVGKNISTKSVYGNHREDVTLHKYKPSGQ 447  
QY 106 KEORVYQEATKEI--PTTDI 123  
Db 448 KEREVYKAGRRVTEFSNEI 467

RESULT 10  
US-08-630-915A-194  
; Sequence 194, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:  
; APPLICANT: SPARKS, Andrew B.  
; APPLICANT: HOFFMAN, No. 6309820h  
; APPLICANT: KAY, Brian K.  
; APPLICANT: FOWLKES, Dana M.  
; APPLICANT: MCCONNELL, Stephen J.  
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL  
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND  
; TITLE OF INVENTION: USING SAME  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/630,915A  
; FILING DATE: 03-APR-1996  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mistrock, S. Leslie  
; REGISTRATION NUMBER: 18,872  
; REFERENCE/DOCKET NUMBER: 1101-174  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 194:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 509 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-915A-194

Query Match 11.1%; Score 75; DB 4; Length 509;  
Best Local Similarity 22.1%; Pred. No. 0.8;  
Matches 36; Conservative 22; Mismatches 33; Indels 72; Gaps 10;

QY 18 GHGVFMDKLSKKKLCA-----DEECVYT-----ISLARAQEDY----- 50  
Db 210 GQGQVVENLKAQALCSWTAKXNDHNLNFKSHDIITVLEQQENWNWFGVHGGRGWFPKSYVK 269

QY 51 -----NAPDCRFIDVKK-----GQQ-----IYVYSK-----LYTE 75  
Db 270 IIPGSEVKREPEALYAAVNKPTSAAYSVGEEITALYPYSPVEPGDLTFTGEHILVTQ 329

QY 76 NGAGFFWAGSYVDHQDENGIVGYPFNSLV--KEORVYQEATK 116  
Db 330 KD-GEWWTGSI-GDRS-----GIFPSNVYKPKQDESFGSASK 364

RESULT 11

US-09-328-352-4886  
; Sequence 4886, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 4886  
; LENGTH: 1326  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-4886

Query Match 11.0%; Score 74.5; DB 4; Length 1326;  
Best Local Similarity 26.3%; Pred. No. 3.7;  
Matches 36; Conservative 17; Mismatches 47; Indels 37; Gaps 9;

QY 11 GLVVLGAGHGVFMDKLSKKKLCADEECVYTI-----SLARAQEDYNAPDCRFIDV 60  
Db 739 GLTALCGEA--LDTILAELKLLGKVGCLMNVYGTPTETVWSSAR-----ITDAKCIDL 790

QY 61 KK--GQOIYV--YSKLVTENGAGFEWAGSVVGD-----HQDEMGIVGY--FPSNLV 105  
Db 791 GEPLANTQLVLDDEQQRLVPPGVMGELWIG--GDGLAVDYWHRPELTDAQFRTLPS-LP 846

QY 106 KEORVYQEATKEIPTTD 122  
Db 847 NAGRLYRTGDKVCLRTD 863

RESULT 12  
US-09-346-510B-24  
; Sequence 24, Application US/09346510B  
; Patent No. 6281014  
; GENERAL INFORMATION:  
; APPLICANT: O'Brien, Timothy J.  
; APPLICANT: Wang, Yinxiang  
; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof  
; FILE REFERENCE: D6221CIP  
; CURRENT APPLICATION NUMBER: US/09/346,510B  
; CURRENT FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: 08/871,732  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 32  
; SEQ ID NO 24  
; LENGTH: 48  
; TYPE: PRT  
; ORGANISM: unknown  
; FEATURE:  
; NAME/KEY: Domain  
; LOCATION: 2...49  
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain at position 2  
; OTHER INFORMATION: through position 49 of SEQ ID NO. 6281014 21  
US-09-346-510B-24

Query Match 10.9%; Score 73.5; DB 3; Length 48;  
Best Local Similarity 31.6%; Pred. No. 0.041;  
Matches 18; Conservative 11; Mismatches 17; Indels 11; Gaps 2;

QY 49 DYNAPDCRFIDVKKQOIYVYSLVTEENGAGFEWAGSVVGDHQDEMGIVGYPFNSLV 105  
Db 3 DFCARDRSELKSGDII-----KIILKKGGQGGWRGEIYGR-----VGWFPANYV 48

RESULT 13  
US-08-630-915A-40  
; Sequence 40, Application US/08630915A  
; Patent No. 6309820  
; GENERAL INFORMATION:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Opolon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)412-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-164-839-31

Query Match 10.6% Score 71.5; DB 1; Length 687;
Best Local Similarity 26.08; Pred. No. 3.4;
Matches 27; Conservative 19; Mismatches 45; Indels 13; Gaps 4;

QY 25 KLSKKKLCADECVYTISLARAQEDYNAPRCRFIDVKKGQIYV-----SKL-VTE 75
DB 356 ELSDEGYCCGCPVTAIKEGNLSVKYDAP---FIFAENVADIIYMWAGPGGERKKIDVDQ 412

QY 76 NGAGE-FWASGVGDHODEMGIVGFPSNLVKEQRYVQEATKEI 118
DB 413 SGVGKNTSTKSLYGDYEDVTLHYKYBEGSKKEREVIQKAGHRI 456

RESULT 15
US-08-164-839-33
Sequence 33, Application US/08164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,839
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993

```

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APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: McCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSES: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-40

Query Match          10.6%; Score 71.5; DB 4; Length 248;
Best Local Similarity 36.8%; Pred.No.0.78;
Matches      21; Conservative    13; Indels     15; Gaps       4;

Qy   62 KGQQIYVYSKLVTENGAGEFWAGSVGYGHODMGIVGVFPNSLV--KEQRYYQEATK 116
Db   60 EGEEILYTQK-----DGEWWTGSI-GDRS-----GIFFSNYVKPKDDSEFGSGASK 103

RESULT 14
US-08-164-939-31
Sequence 31, Application US/09164839
Patent No. 5514573
GENERAL INFORMATION:
APPLICANT: YASUEDA, HISASHI
APPLICANT: NAKANISHI, KAZUO
APPLICANT: MOTOKI, MASAO
APPLICANT: NAGASE, KAZUO
APPLICANT: MATSUJI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSRE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSRE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
```

Tue Dec 30 10:20:37 2003

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-164-839-33

Query Match      10.6%; Score 71.5; DB 1; Length 687;
Best Local Similarity 26.0%; Pred. No. 3.4;
Matches 27; Conservative 19; Mismatches 45; Indels 13; Gaps 4;

Qy      25 KLSSKKLCADBEQVYTTISLARAQEDYNAPDCRFIDVKKGQOIYVY-----SKL-VTE 75
Db      356 ELSGGEYCCGCPVTAIKEGNLSVKYDAP---FIFAEVNADIIYWMAGPGGERKKIDVDQ 412

Qy      76 NGAGE-FWAGSVYGDHODEMGIVGFPSNLVKEQRYQEAATKEI 118
Db      413 SGVGKNISTKSLYGDYREDVTLHYKYPEGSKKEREVIQKAGHRI 456
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Job time : 10.3221 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: December 29, 2003, 16:11:59 ; Search time 2106.98 Seconds  
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Title: US-10-019-455A-12  
Perfect score: 676  
Sequence: 1 MARILLILGLVLCAGH.....RVQBATKEIPTTIDIFFCE 128

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Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb.htg:\*  
3: gb.in:\*  
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7: gb.ph:\*  
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9: gb.pr:\*  
10: gb.ro:\*  
11: gb.sts:\*  
12: gb.sy:\*  
13: gb.un:\*  
14: gb.vi:\*  
15: em.ba:\*  
16: em.fun:\*  
17: em.hum:\*  
18: em.in:\*  
19: em.mu:\*  
20: em.om:\*  
21: em.or:\*  
22: em.ov:\*  
23: em.pat:\*  
24: em.ph:\*  
25: em.pl:\*  
26: em.ro:\*  
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29: em.vi:\*  
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31: em.htg.inv:\*  
32: em.htg.other:\*  
33: em.htg.mus:\*  
34: em.htg.pln:\*  
35: em.htg.rod:\*  
36: em.htg.mam:\*  
37: em.htg.vrt:\*  
38: em.sy:\*  
39: em.htgo.hum:\*  
40: em.htgo.mus:\*  
41: em.htgo.other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	676	100.0	384	6	BD010805 Novel pol
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3	676	100.0	929	10	AF243504 Mus muscu
4	676	100.0	947	6	BD010821 Novel pol
5	676	100.0	947	6	BD093122 Novel pol
6	676	100.0	958	10	AJ243939 Mus muscu
7	676	100.0	1054	10	AF233333 Mus muscu
8	655	96.9	384	6	BD010835 Novel pol
9	655	96.9	384	6	BD093136 Novel pol
10	602	89.1	384	6	BD010802 Novel pol
11	602	89.1	384	6	BD093103 Novel pol
12	602	89.1	521	6	AX358818 Sequence
13	602	89.1	521	6	AX362311 Sequence
14	602	89.1	521	6	AX454774 Sequence
15	602	89.1	521	6	AX491252 Sequence
16	602	89.1	846	9	AF233261 Homo sapi
17	602	89.1	865	9	AF243505 Homo sapi
18	602	89.1	923	6	BD010820 Novel pol
19	602	89.1	923	6	BD093121 Novel pol
20	602	89.1	1422	9	AJ242552 Homo sapi
21	591	87.4	330	6	BD010817 Novel pol
22	591	87.4	330	6	BD093118 Novel pol
23	574	84.9	330	6	BD010836 Novel pol
24	574	84.9	330	6	BD093137 Novel pol
25	547	80.9	330	6	BD010816 Novel pol
26	547	80.9	330	6	BD093117 Novel pol
27	515	76.2	307	6	BD010830 Novel pol
28	515	76.2	307	6	BD093131 Novel pol
29	468.5	69.3	484	5	AF233518 Gallus ga
30	445	65.8	261	6	BD010829 Novel pol
31	445	65.8	261	6	BD093130 Novel pol
32	412	60.9	466	5	AF233519 Rana cate
33	379.5	56.1	215581	2	AC106161 Rattus no
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35	294	43.5	121151	9	HS705D16 Human DNA
36	277.5	41.1	396	9	BT007044 Homo sapi
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41	277.5	41.1	459	6	AX287209 Sequence
42	277.5	41.1	459	9	HSNGRPM A
43	277.5	41.1	518	9	BC005910 Homo sapi
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45	268	39.6	545	10	U67884 Rattus norv

ALIGNMENTS

[illegible]

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QY	101	ProSerAsnLeuVallyysGluGlnArgValTyrGlnGluAlaThrlyysGluIleProThr	120
Db	301	CCCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCCACCAAGGAGATCCCAACC	360
QY	121	ThrAspIleAspPheCysGlu	128
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DEFINITION	Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.		
ACCESSION	AF243504		
VERSION	AF243504.1	GI:11991841	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1	(bases 1 to 929)	
AUTHORS	Cohen-Salmon, M., Frensz, D., Liu, W., Verpy, E., Voegelings, S. and Petit, C.		
TITLE	Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme		
JOURNAL	J. Biol. Chem.	275 (51), 40036-40041	(2000)
MEDLINE	20568254		
PUBMED	10998416		
REFERENCE	2	(bases 1 to 929)	
AUTHORS	Cohen-Salmon, M., Frensz, D., Verpy, E., Voegelings, S. and Petit, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue du Dr. Roux, Paris 75015, France		
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	/db_xref="GI:11991842"		
	/translation="MARILILLGLVLCAGHGVFMDKLSKKLCADEECVYTISLA		
	RAQEDNAPDCRFIDVKKGQOIYVYSLVTENGAEVFWAGSVYGDHQEMGVGVFPS		
	NLVKEQRYQEAATKEIPTDIDFCE"		
BASE COUNT	260 a 156 c 220 g 293 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	1..4e-71	Length:	929
Score:	676.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0
US-10-019-455A-12 (1-128) x AF243504 (1-929)			
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QY	21	ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluCysValTyrThr	40
Db	69	GTATTATTGATTAACCTTCTTCTAAGAGCTTGTGCGGATGAGGAGTGTGCTATACT	128
QY	41	IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal	60
Db	129	ATTTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCCAGACTGTAGGTTTCATGATGTC	188
QY	61	LysIleGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
Db	189	AAGAAAGGGCAGCAGATCTATGTTTACTCCAAAGCTGGTAAACAGAAACGGAGCTGGAGAG	248
QY	81	PheTriaAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
Db	249	TTTTGGCTGGCAGTGTATTGATGGTACCACAGGATGAGATGGGAATTGTAGGTTATTTC	308
QY	101	ProSerAsnLeuVallyysGluGlnArgValTyrGlnGluAlaThrlyysGluIleProThr	120
Db	309	CCCAGCAACTTGGTGAAGGACGCGGTGTATACAGAGGCCACCAAGGAGATCCCAACC	368
QY	121	ThrAspIleAspPheCysGlu	128
Db	369	ACGGATATTGACTTCTCTGTGAA	392
RESULT 4			
LOCUS	BD010821	947 bp DNA linear	PAT 31-JAN-2002
DEFINITION	Novel polypeptide and DNA thereof.		
ACCESSION	BD010821		
VERSION	BD010821.1	GI:18639194	
KEYWORDS	JP 2001069994-A/22.		
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	1	(bases 1 to 947)	
AUTHORS	Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.		
TITLE	Novel polypeptide and DNA thereof		
JOURNAL	Patent: JP 2001069994-A 22 21-MAR-2001;		
COMMENT	TAKEDA CHEMICAL INDUSTRIES LTD		
	OS Mus sp. (mouse)		
	PN JP 2001069994-A/22		
	PD 21-MAR-2001		
	PF 29-JUN-2000 JP 2000195911		
	PR		
	PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,		
	PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA		
	PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,		
	PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//		
	PC C12P21/08, C12N15/00, A61K37/02, C12N5/00		
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Alignment Scores:			
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Score:	676.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-019-455A-12 (1-128) x BD010821 (1-947)

Qy	1	MetAlaArgIleLeuIleLeuLeuLeuLenglyGlyLeuValValLeuCysAlaGlyHisGly	20
Db	11	ATGCAAGGATATTGATTCTTTTGGCTGGGGCCCTTGGTCTATATGCGCGGATGGT	70
Qy	21	ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr	40
Db	71	GTATTTATGGATAAATCTTCTTAAGAAGTTGTGTGCGGATGAGAGTGTCTATACT	130
Qy	41	IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal	60
Db	131	ATTCTCTGGCAAGAGCACAGGAAGATTACAATGCCCAGACTGTAGGTTCATCGATGTC	190
Qy	61	LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
Db	191	AAGAAAGGCGACGACATCTATCTTTACTCCAAAGCTGGTAACAGAAACGGAGCTGGAGAG	250
Qy	81	PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe	100
Db	251	TTTTGGGCTGGCGAGTGTATGGTGACCAACCAAGGATGAGATGGGAATTTGAGGTATTTC	310
Qy	101	ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr	120
Db	311	CCCAGCACTTGGTGAAGGAGCAGCGTGTATTACAGGAGGCCACCAAGAGATCCCAACC	370
Qy	121	ThrAspIleAspPheCysGlu	128
Db	371	ACGGATATTGACTTCTTCTGTGAA	394

RESULT 5			
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LOCUS	BD093122	947 bp	DNA linear PAT 27-AUG-2002
BD093122 plasmectid and its DNA			

BD0931422  
 ED0931422.1 GI:22638710  
 VERSION  
 WO 0102564-A/22.  
 KEYWORDS  
 Mus sp.  
 SOURCE  
 ORGANISM  
 Mus sp.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1. (bases 1 to 947)  
 Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
 Yoshimura, K. and Tanaka, H.  
 Novel polypeptide and its DNA  
 Patent: WO 0102564-A 22 11-JAN-2001;  
 TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO  
 OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,  
 HIDEYUKI TANAKA

OS	Mus sp. (mouse)	COMMENT
FN	WO 0102564-A/22	
PD	11-JAN-2001	
PF	29-JUN-2000 WO 2000JP004278	
PR	30-JUN-1999 JP 99P 186718	
PI	YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,	
PI	MOGI,	
PI	YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA	
PC	C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17,	
PC	A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/02, C12R1:19)	

CC	FH	Key	Location/Qualifiers.

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BASE COUNT      279 a 158 c 221 g 289 t
ORIGIN

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Alignment Scores:	1.43e-71	Length:	947
Pred. No.:	676.00	Matches:	128
Score:	676.00	Conservative:	0
Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%	Indels:	0
Query Match:	100.00%	Gaps:	0
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US-10-019-455A-12 (1-128) x BD093122 (1-947)

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Dd		11	ATGCACAAGGATAATTGATTCITTTGGCTGGGGCCCTTGTGGTTCTATGTGCCGGGCGATGGT	70
Qy		21	ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyThr	40
Dd		71	GTAATTTATGGATAAACTTCTTCTTAAGAAGTTGTGTGCGGATGAGGAGTGtGTCTATACT	130
Qy		41	IleSerLeuAlaArgAlaGlnGluAspTyrrAsnAlaProAspCysArgPheIleAspVal	60
Dd		131	ATTTCTCTGGCAAGAGCACAGGAAGATTACAAATGCCCCAGACTGTAGGTTCATCGATGTC	190
Qy		61	LysLysGlyGlnGlnIleTyrrValTyrrSerLysLeuValThrGluAsnGlyAlaGlyGlu	80
Dd		191	AAGAAAGGGCAGCAGCATCTATGTCTTTACTCCAAGCTGGTAACAGAAACCGAGCTGGAGAG	250
Qy		81	PheTrpAlaGlySerValTyrrGlyVasPhisGlnAspGluMetGlyIleValGlyTyrrPhe	100
Dd		251	TTTTTGGGCTGGCAGTGTTTATGGTGCACCACAGGATGAGATCGGAATTCGTAGGTATTTC	310
Qy		101	ProSerAsnLeuValLysGluGlnArgValTyrrGlnGluAlaThrLysGluIleProThr	120
Dd		311	CCCACAACTTGGTAGAGGAGCAGCGTGATACCGAGGAGCCACCAGAGAGATCCCAAACC	370
Qy		121	ThrAspIleAspPheCysGlu	128
Dd		371	ATGGATATTGACTCTTCTGTGAA	394

## RESULT 6

MMU243939

LOCUS

## DEFINITION

ACCESSION  
NUMBER

VERSION  
REVISED

KEYWORDS  
SOURCES

ORGANISM

## REFERENCE

## AUTHORS

TTT.F

TTTT

**JOURNAL**

MEDLINE

PUBMED

## REFERENCE

## AUTHORS

THE JOURNAL

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COMMENT

## FEATURES

**Source**

[illegible]



Db 361 ACGATATTGACCTCTCTCTGTGAA 384

RESULT 9  
BD0931136  
LOCUS  
DEFINITION Novel polypeptide and its DNA.  
ACCESSION BD0931136  
VERSION BD0931136.1 GI:22638724  
KEYWORDS WO 0102564-A/36.  
SOURCE Rattus sp.  
ORGANISM Rattus sp.  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 384)  
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.  
Novel polypeptide and its DNA  
Patent: WO 0102564-A 36 11-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,  
HIDEYUKI TANAKA  
COMMENT  
OS Rattus sp. (rat)  
PN WO 0102564-A/36  
PD 11-JAN-2001  
PF 29-JUN-2000 WO 2000JP004278  
PR 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI,  
YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, P01A61K38/17,  
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/02, C12R1:19)  
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Score: 655.00 Matches: 123  
Percent Similarity: 98.44% Conservative: 3  
Best local Similarity: 96.09% Mismatches: 2  
Query Match: 96.89% Indels: 0  
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US-10-019-455A-12 (1-128) x BD093136 (1-384)

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Db 1 ATGGCAAGAAATATGATTTCTTTTGGCTTGGGGGCTTGTGGCTCTCTGTGCCGGGCATGGC 60  
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Qy 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40  
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Db 61 ATGTTTATGGATAAACTTTCTCTTAAGAAGTTGTGTGCATCAGGAGTGTGTCTATACC 120  
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Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
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Db 121 ATTTCCTGCGAAGACGACGAGTCTATGTTATTCCAACTGTAACAAATGGAGCTGGGCA 180  
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Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
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Db 181 AAGAAGGGCAGCAGATCTATGTTATTCCAACTGTAACAAATGGAGCTGGGCA 240  
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Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
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Db      241 TTCTGGCTGGCAGTGTATGGTGACCAACGATGAGATGGGAATTGTGGGTATTTC 300
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Db      301 CCCAGCAACTGGTTAGAGACACAGAGTGTACCAAGAGGCCACCAAGGAGATTCCAAAC 360
Qy      121 ThrAspIleAspPheCysGlu 128
Db      361 ACGGATATTGACTTCTCTGTGGAA 384

RESULT 10
LOCUS   BD010802                                384 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010802
VERSION   BD010802.1 GI:18639175
KEYWORDS  JP 2001069994-A/3.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 3 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Homo sapiens (human)
PN JP 2001069994-A/3
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
CC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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FT Location/Qualifiers
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/db_xref="taxon:9606"
BASE COUNT 99 a 70 c 106 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 3.97e-63 Length: 384
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
Gaps: 0
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Qy      1 MetAlaArgIleLeuIleLeuLeuLeuGlyLeuValValLeuCysAlaGlyHisGly 20
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Qy      21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValTyrThr 40
Db      61 ATATTATGGACCGTCTAGCTTCCAAAGAGCTCTGTGCAGATGATGATGCTATATCTACT 120
Qy      41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
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Qy      61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAenGlyAlaGlyGlu 80
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Qy      101 ProSerAsnLeuValLysGluInArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db      301 CCCAGCAACTGGTTAGAGACACAGAGTGTACCAAGAGGCCACCAAGGAGATTCCCAAC 360
Qy      121 ThrAspIleAspPheCysGlu 128
Db      361 ACGGATATTGACTTCTCTGTGGAG 384

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DEFINITION Novel polypeptide and its DNA..
ACCESSION BD093103
VERSION   BD093103.1 GI:22638691
KEYWORDS  WO 0102564-A/3.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 384)
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and its DNA
Patent: WO 0102564-A 3 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
OS Homo sapiens (human)
PN WO 0102564-A/3
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PR 30-JUN-1999 JP 99P 186718
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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BASE COUNT 99 a 70 c 106 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 3.97e-63 Length: 384
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
Gaps: 0
US-10-019-455A-12 (1-128) x BD093103 (1-384)
Qy      1 MetAlaArgIleLeuIleLeuLeuLeuGlyLeuValValLeuCysAlaGlyHisGly 20
Db      1 ATGGCAAGAAATATTGTACTTTCTCCCGGGCTTTGTGGCTGTATGCTGTGTCATGGA 60

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Job time : 2108.98 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:23:14 ; Search time 1324.28 Seconds  
(without alignments)  
2349.180 Million cell updates/sec

Title: US-10-019-455A-12  
Perfect score: 676  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: gb\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
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25: em\_gss\_rod:\*  
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27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	676	100.0	514	13	BQ568498	BQ568498 gi109c02..
4	676	100.0	534	13	BQ564134	BQ564134 gi114d01.y
5	676	100.0	560	13	BQ569741	BQ569741 gi135f01..
6	676	100.0	608	13	BQ564944	BQ564944 gi27909.y
7	676	100.0	630	13	BQ568471	BQ568471 gi108g04..
8	676	100.0	696	10	BB611549	BB611549 BB611549
9	671	99.3	474	13	BQ565637	BQ565637 gi142g03.y
10	669	99.0	684	13	BQ563768	BQ563768 gi06c09.y
11	646	95.6	409	13	BQ566932	BQ566932 gi173g09.y
12	611	90.4	490	13	BQ565411	BQ565411 gi137b12.y
13	585	86.5	365	13	BY232622	BY232622 BY232622
14	539	79.7	604	13	BQ567343	BQ567343 gi188d08.y
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16	447	66.1	280	13	BQ568785	BQ568785 gi114f04..
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20	378.5	56.0	677	13	BQ563227	BQ563227 gi01a05.y
21	375.5	55.5	533	9	AL925854	AL925854 AL925854
22	366	54.1	588	13	BQ566776	BQ566776 gi69b07.y
23	359.5	53.2	678	10	BB647928	BB647928 BB647928
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25	277.5	41.1	480	12	BM715936	BM715936 UI-E-EJO-
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ALIGNMENTS

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LOCUS gi143b10.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus CDNA  
DEFINITION clone gi143b10 5', mRNA sequence.  
ACCESSION BQ570035.1 GI:21473352  
VERSION BQ570035  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 398)



**FEATURES**

source

Location/Qualifiers

1..488

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="g119h02"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and the Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-Rt) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTCATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 143 A 83 C 135 G 127 T

ORIGIN

Alignment Scores:

Pred. No.:	2,02e-81	Length:	488
Score:	676.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0



from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp , respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXASist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watlham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN

Alignment Scores:  
Pred. No.: 2.18e-81 Length: 514  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x BQ568498 (1-514)

QY 1 MetAlaArgIleLeuLeuLeuGlyLeuValValLeuCysAlaGlyHisGly 20  
DB 5 ATGGCAAGGATATGATCTTTTGGTCTGGGGCCCTTGCTTCTATGTCGGGATGCT 64  
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluCysValTyThr 40  
DB 65 GTATTTATGGATAAACTTTCTTCTAAGAAAGTTGTGTGGGATGAGGAGTGTCTATACT 124

QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
DB 125 ATTTCTCTGGCAAGAGCAGAGAGATTACAACTGCCCCAGACTGTAGGTTTCATCGATGTC 184  
QY 61 LysLysGlyGlnGlnIleTyValTySerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
DB 185 AAGAAGAGGCGACACATCTATGTTTACTTCCAAAGCTGGTAACAGAAAACCGAGCTGGAGAG 244  
QY 81 PheTTPAlaGlySerValTyGlyAspHisGlnAspGluMetGlyTleValGlyTyPhe 100  
DB 245 TTTTGGCGCTGGCAGGTGTTTATGTCACACAGGATGAGATGGAAATTGTAGTTATTTC 304  
QY 101 ProSerAsnLeuValLysGluGlnArgValTyGlnGlnAlaThrLysGluIleProThr 120  
DB 305 CCCGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATCCCAACC 364  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 365 ACGGATATTGACTTCTTCTGTGAA 388

RESULT 4  
BQ564134

LOCUS  
DEFINITION

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

BQ564134 534 bp mRNA linear EST 19-JUN-2002  
gillid01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gillid01 5', mRNA sequence.  
BQ564134  
BQ564134.1 GI:21467451  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar, B.  
EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 11 row: d column: 01  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1..534  
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/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.  
Total RNA was extracted using the micro Fasttrack kit  
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
to manufacturer's instructions. Reverse transcription and  
library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both



columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on M13 Tetrad thermal cyclers (MJ Research, Watham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 160 a 92 c 154 g 153 t 1 others  
ORIGIN

Alignment Scores:  
Pred. No.: 2,478-81 Length: 560  
Score: 676.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x BQ564941 (1-560)

QY 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
DB 6 ATGGCAAGGATATTGATCTTTTGTCTGGGGCCCTTGTTGTTCTATGTCGGGGCATGGT 65  
QY 21 ValPheMetAspLysIleuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40  
DB 66 GTATTATTGGATAAACTTCTTCTAAGAAAGTTGTGTGGGATGAGAGGTGTCTATACT 125  
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
DB 126 ATTTCTTGGCAAGAGCAGACAGATACATGCCCCAGACTGTAGTTTCATCGATGTC 185  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
DB 186 AAGAAGGGCGACAGCATCTATCTTTACTCCAGCTGGTAACAGAAAACGAGCTCGAGAG 245  
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
DB 246 TTTTGGCTGGCAGGTATTATGGTGACCACCGAGATGAGATGGGAATTTGTAGTTATTTC 305  
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
DB 306 CCCACCACTTGGTGAAGAGCAGCGGTGTATACAGGAGGCCACCAAGAGATCCCAACC 365  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 366 ACGGATATTGACTTCTCTGTGAA 389

RESULT 6  
LOCUS BQ564944 608 bp mRNA linear EST 19-JUN-2002  
DEFINITION G127g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone g127g09 5', mRNA sequence.

ACCESSION BQ564944  
VERSION BQ564944.1  
KEYWORDS GI:21468261  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 608)  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 27 row: g column: 09  
Seq primer: M13RP1 reverse primer (ABI).

FEATURES  
source

1..608  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="BALB/c"  
/db\_xref="taxon:10090"  
/clone="g127g09"  
/sex="male and female"  
/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapak III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen,



12% are uncharacterized ESTs and 20% are unidentified.  
 BASE COUNT 178 a 111 c 167 g 174 t  
 ORIGIN

Alignment Scores: 2,92e-81 Length: 630  
 Pred. No.: 676.00 Matches: 128  
 Score: 100.00% Conservativeness: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 13 Gaps: 0  
 DB:

US-10-019-455a-12 (1-128) x BQ568471 (1-630)

QY 1 MetAlaArgLeuLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 Db 13 ATGCACAGGATTAATGATCTTTCTTGGGGGCTTGTGGTTCTATGTCGGCGCATGGT 72  
 QY 21 ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysValThr 40  
 Db 73 GTATTTATGATAAATCTTCTTCTAGAGAGTGTGTGGCATGAGGAGTGTGTCTATCT 132  
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 Db 133 ATTTCTCTGGCAGACAGCAGGAGAGATTCAATGCCCCAGACTGTAGGTTTCATCGAGTC 192  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 193 AAGAAAGGGCAGCAGATCTATGTTTCTCAAGCTGTGTAACAGAAAACGAGCTGGAGAG 252  
 QY 81 PheTrpAlaGlySerValTyrGlyAspHisGluAspGluMetGlyIleValGlyTyrPhe 100  
 Db 253 TTTTGGGCTGGCAGTGTATTATGGTACACACAGATGAGATGGAATGTAGGTTATTTTC 312  
 QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 Db 313 CCCAGCACTTGGTGAAGGACGCGGTATACCCAGGAGGCCACCAAGGAGATCCCAACC 372  
 QY 121 ThrAspIleAspPheCysGlu 128  
 Db 373 ACGGATATTGACTTCTTCTGTGAA 396

RESULT 8  
 LOCUS BB611549 696 bp mRNA linear EST 31-AUG-2001  
 DEFINITION BB611549 RIKEN full-length enriched, 13 days embryo head Mus  
 musculus cDNA clone 3110083012 5', mRNA sequence.  
 ACCESSION BB611549  
 VERSION BB611549.1 GI:15393547  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 696)  
 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,  
 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda,  
 M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,  
 Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki,  
 D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,  
 Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toyota, T.,  
 Muramatsu, M., and Hayashizaki, Y.  
 RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
 Unpublished

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 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suenho-cho, Tsukuba, Ibaraki, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@gsc.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh,  
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura,  
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
 Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10  
 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara,  
 Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa,  
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,  
 Ishii, Y. and Hayashizaki, Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
 Funct. Genomics 2 pre, 172-186 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
 further details.  
 e mouse tissues.

#### FEATURES

Location/Qualifiers  
 1..696  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:10090"  
 /clone="3110083012"  
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 head"  
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 prepared and sequenced in Mouse Genome Encyclopedia  
 Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in  
 RIKEN. Division of Experimental Animal Research in Riken  
 contributed to prepare mouse tissues. 1st strand cDNA was  
 primed with a primer [5'  
 GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTNN 3'], cDNA was  
 prepared by using trehalose thermo-activated reverse  
 transcriptase and subsequently enriched for full-length by  
 cap-trapper. cDNA went through one round of normalization  
 to Rot = 10.0 and subtraction to Rot = 50.0. Second strand  
 cDNA was prepared with the primer adapter of sequence [5'  
 GAGAGAGAGATTCGAGTTAATTAATTAATCCGCCCCCCCCC 3']. cDNA  
 was cleaved with XhoI and SstI."

BASE COUNT 204 a 122 c 176 g 194 t

#### ORIGIN

#### Alignment Scores:

Pred. No.: 3,37e-81 Length: 696  
 Score: 676.00 Matches: 128  
 Percent Similarity: 100.00% Conservativeness: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-10-019-455a-12 (1-128) x BB611549 (1-696)

QY 1 MetAlaArgLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 Db 24 ATGCACAGGATTAATGATCTTTTGGGGGCTTGTGGTTCTATGTCGGCGCATGGT 83  
 QY 21 ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysValThr 40  
 Db 84 GTATTTATGATAAATCTTCTTCTAGAGAGTGTGTGGCATGAGGAGTGTGTCTATCT 143  
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60

Db 144 ATTCTCTGCGAAGACACAGAGATATCAATGCCAGACTGAGGTTTCATGATGTC 203  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 204 AAGAAAGGCGAGCAGATCTATGTTACTCAAGCTGGTAACAGAAACGAGCTGGAGAG 263  
 Qy 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 Db 264 TTTTGGGCTGGCAGTGTATTGATGACCAACAGGATGAGATGGGAATTTGATGTTATTTTC 323  
 Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 Db 324 CCCAGCAACTTGGTGAAGGAGCAGCGTGTATACAGGAGGCCACCAAGAGATCCCAACC 383  
 Qy 121 ThrAspIleAspPhePheCysGlu 128  
 Db 384 ACGGATATTGACTTCTCTGTGAA 407

RESULT 9  
 B0565637  
 LOCUS  
 DEFINITION g142903.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 clone g142903 5', mRNA sequence.

ACCESSION  
 B0565637  
 VERSION  
 B0565637.1 GI:21468954  
 KEYWORDS  
 EST.

SOURCE  
 Mus musculus (house mouse)

ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
 Unpublished  
 Contact: Kachar, B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599

Fax: 301-402-1765  
 Email: kachar@nidcd.nih.gov  
 Plate: 42 row: 9 column: 03  
 Seq primer: M13RPI reverse primer (AB1).  
 Location/Qualifiers

FEATURES  
 source

1..474  
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 /clone="g142903"  
 /sex="male and female"  
 /dev\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was

reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 145 a 78 c 131 g 120 t  
 ORIGIN

Alignment Scores:

Pred. No.: 9,27e-81 Length: 474  
 Score: 671.00 Matches: 127  
 Percent Similarity: 99.22% Conservative: 0  
 Best Local Similarity: 99.22% Mismatches: 1  
 Query Match: 99.26% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x B0565637 (1-474)

Qy 1 MetaAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 Db 14 ATGGCAGGATATGATTCTTTTGGTGGGGCCTTGCTGTTCTATGTCGGGCGATGCT 73  
 Qy 21 ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40  
 Db 74 GTATTTATGATAAATCTTCTTCTTAATAAGTTGTTGTCGGGATGAGGAGTGTCTATACT 133  
 Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 Db 134 ATTCTCTGCGACAGACACAGAGGAGATTACATGCCAGACTGTAGGTTCTCGATGTC 193  
 Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 194 AAGAAAGGCGAGCAGATCTATGTTACTCAAGCTGGTAACAGAAACGAGCTGGAGAG 253  
 Qy 81 PheTTPAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 Db 254 TTTTGGGCTGGCAGTGTATTGATGACCAACAGGATGAGATGGGAATTTGATGTTATTTTC 313  
 Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120















```
Db      ||||| 215 AAAAAAGGACAGTGGATCTATGTTTACTCAAAGCTG----- 250
Qy      81 PheTIPAlaGlySerValTyrGlyAspHis--GlnAspGluMetGlyIleValGlyTyr 99
Db      ||||| 251 -----GTCATGGCAATCAGTCTGAGGATGAAATGGGAACCGTGGGTAT 295
Qy      100 PheProSerAsnLeuVallysGluGlnArgValTyrGlnGluAlaThrIysGluIlePro 119
Db      ||||| 296 TTTCAGCAACTTGGTCCAGGAACAACATGTGTACCAAGAAGCCACCAAGGAAGTCTCT 355
Qy      120 ThrThrAspIleAspPhePheCysGlu 128
Db      ||||| 356 ACCACGGATATGACTTTTCTGCGAG 382
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Search completed: December 29, 2003, 22:00:46  
Job time : 1326.28 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 154.353 Seconds  
(without alignments)  
2238.558 Million cell updates/sec

Title: US-10-019-455A-12

Perfect score: 676

Sequence: 1 MARIILLGLGIVLCAGH.....RVYQATKPTTIDIFFCE 128

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DRV=xlh  
-O=/cgn2\_1/USPTO.spool/US10019455/runat\_29122003\_160347\_230/app\_query.fasta\_1.1770  
-DB=N Geneseq 19Jun03 -QFMT=fasta -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10019455 @CGN\_1\_1\_0@runat\_29122003\_160347\_230 -NCPUS=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 19Jun03:\*

- 1: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1980.DAT:\*
- 2: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1981.DAT:\*
- 3: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1982.DAT:\*
- 4: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1983.DAT:\*
- 5: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1984.DAT:\*
- 6: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1985.DAT:\*
- 7: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1986.DAT:\*
- 8: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1987.DAT:\*
- 9: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1988.DAT:\*
- 10: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1989.DAT:\*
- 11: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1990.DAT:\*
- 12: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1991.DAT:\*
- 13: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1992.DAT:\*
- 14: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1993.DAT:\*
- 15: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1994.DAT:\*
- 16: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1995.DAT:\*
- 17: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1996.DAT:\*
- 18: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1997.DAT:\*
- 19: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1998.DAT:\*
- 20: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA1999.DAT:\*
- 21: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA2000.DAT:\*
- 22: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA2001A.DAT:\*
- 23: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA2001B.DAT:\*
- 24: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA2002.DAT:\*
- 25: /SIDSI/gcgdataa/geneseq/geneseq-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	676	100.0	384	22	AAF59068	Mouse MLP nucleoti
2	676	100.0	947	22	AAF59084	Mouse MLP nucleoti
3	655	96.9	384	22	AAF59098	Rat MLP nucleotide
4	602	89.1	384	22	AAF59065	Human MLP nucleoti
5	602	89.1	387	24	AAH17583	DNA encoding novel
6	602	89.1	426	22	AAH26341	Human growth regul
7	602	89.1	521	24	ABL95740	Human angiogenesis
8	602	89.1	521	24	ABL88251	Human PRO9873 cDNA
9	602	89.1	521	24	ABK33571	CDNA encoding huma
10	602	89.1	891	22	AAH98228	Human EST-derived
11	602	89.1	891	22	AAH26342	Human growth regul
12	602	89.1	923	22	AAF59083	Human MLP nucleoti
13	602	89.1	1201	22	AAH26343	Human growth regul
14	591	87.4	330	22	AAF59080	Mouse MLP nucleoti
15	574	84.9	330	22	AAF59099	Human MLP nucleoti
16	547	80.9	330	22	AAF59079	Human MLP nucleoti
17	515	76.2	307	22	AAF59093	Rat MLP nucleotide
18	445	65.8	261	22	AAF59092	Rat MLP nucleotide
19	277.5	41.1	459	16	AAQ84050	Sequence encoding
20	277.5	41.1	459	22	AAI70083	Melanoma inhibitor
21	277.5	41.1	459	22	AAI18732	Human antitense ol
22	275.5	40.8	433	22	AAH47783	Recombinant human
23	263	38.9	442	24	ABL63602	Breast cancer rela
24	263	38.9	442	24	ABL64012	Breast cancer rela
25	261.5	38.7	330	16	AAQ84061	Sequence encoding
26	261.5	38.7	555	23	ABV59229	Human prostate exp
27	247	36.5	581	16	AAQ84052	Sequence encoding
28	219.5	32.5	305	16	AAQ84055	Amplified fragment
29	218	32.2	1060	22	AAF92140	Human PRO19670 cDN
30	218	32.2	1060	24	ABT74460	Human cDNA encodin
31	218	32.2	1060	24	ABT95738	Human angiogenesis
32	218	32.2	1060	24	ABL88249	Human PRO19670 cDN
33	218	32.2	1060	25	ACA57963	Human PRO19670 cDN
34	218	32.2	1060	25	ACA58892	CDNA encoding huma
35	218	32.2	1060	25	ACA60445	Novel human secret
36	218	32.2	1060	25	ACA63455	CDNA encoding huma
37	218	32.2	1060	25	ABX98433	Human cDNA encodin
38	218	32.2	1060	25	ABX98935	Novel human secret
39	218	32.2	1060	25	ACA05980	Human secreted/tra
40	218	32.2	1060	25	ABX98024	Human PRO polynucl
41	218	32.2	1060	25	ABX78808	Human PRO polynucl
42	218	32.2	1060	25	ABX75821	Human cDNA encodin
43	218	32.2	1060	25	ABX77026	Human PRO polynucl
44	218	32.2	1060	25	ABX16866	Human cDNA encodin
45	218	32.2	1061	22	AA546205	Human DNA encoding

# ALIGNMENTS

## RESULT 1

AAF59068

ID AAF59068 standard; DNA; 384 BP.

AC AAF59068;

XX 23-APR-2001 (first entry)

DT Mouse MLP nucleotide sequence SEQ ID NO:10.

DE MIP; MIA; melanoma inhibitory activity; cancer; bone disease;

KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KW cardiant; gene therapy; secretory cell function regulator; promoter;

KW inhibitor; ds.

XX Mus musculus.

OS

XX





CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.

XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,79e-74 Length: 384  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-12 (1-128) x AAF59065 (1-384)

Qy 1 MetAlaArgIleLeuLeuLeuLeuLeuGlyGlyValValLeuValLeuCysAlaGlyHisGly 20  
 Db 1 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTGTGCTGTATGCTGTGCTGATGGA 60  
 Qy 21 ValPheMetAspLysLeuSerLysLeuValLeuValLeuValLeuValLeuValLeuVal 40  
 Db 61 ATATTATGACCGCTGAGCTTCAAGAAGCTCTGTCAGATGATGAGTGTCTATGCTACT 120  
 Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 Db 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTTATATGTCCTCCCGAGCTGTAGATTCAACGTT 180  
 Qy 61 LysIleGlyGlnGlnIleValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 Db 181 AAAAAGGGCAGCAGATCTATGTTACTCAAGCTGTATAAAGAAATGAGCTGGAGAA 240  
 Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspMetGlyLeuValGlyTyrPhe 100  
 Db 241 TTTTGGCTGGCAGTGTATTGTTGATGGCCAGCAGATGGAGTGTGGTATTTC 300  
 Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluLeuProThr 120  
 Db 301 CCCAGGAACCTGGTCAAGGACAGCGGTGTACAGAGAGCTACCAAGGAAGTTCCTCCACC 360  
 Qy 121 ThrAspIleAspPheCysGlu 128  
 Db 361 ACCGATATTGACTTCTTCTGGAG 384

RESULT 5

AA517583

ID AA517583 standard; cDNA; 387 BP.

XX AC AA517583;

XX DT 26-FEB-2002 (first entry)

XX DE DNA encoding novel secreted protein #12.

XX KW Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine;  
 XX KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
 XX KW human; cancer; autoimmune disease; wound healing disorder; infection;  
 KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX CDS 1..387

XX FT /\*tag= a

XX FT /product= "Human secreted protein"

XX WO200179454-A1.

XX PD 25-OCT-2001.

XX

PF 11-APR-2001; 2001WO-US11797.

XX 13-APR-2000; 2000US-196603P.

PR 24-APR-2000; 2000US-199417P.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;

XX WPI; 2002-061975/08.

DR P-PSDB; AAU09871.

XX

PT New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, cancer -

XX Claim 2; Page 44; 92pp; English.

XX The invention relates to an isolated novel secreted polypeptide (I) and  
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,  
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic  
 CC disorders, inflammatory disorders, infertility, neurological and  
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,  
 CC renal diseases, or gastrointestinal diseases. These may also be used to  
 CC treat diseases, abnormalities and disorders caused by abnormal  
 CC expression, production, function and/or metabolism of the genes, as  
 CC vaccines for inducing immunological response in a mammal, and in  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and polypeptide in cells. The polypeptides can be used  
 CC as immunogens to produce antibodies immunospecific for the polypeptides,  
 CC and to identify membrane-bound or soluble receptors. The polynucleotides  
 CC may be used as diagnostic reagents, in chromosome localisation studies,  
 CC and in tissue expression studies. The present sequence represents the  
 CC coding sequence of novel human secreted protein #12.

XX Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;

Alignment Scores:

Pred. No.: 3,83e-74 Length: 387  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9  
 Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 24 Gaps: 0

US-10-019-455A-12 (1-128) x AAS17583 (1-387)

Qy 1 MetAlaArgIleLeuLeuLeuLeuGlyGlyValValLeuValLeuCysAlaGlyHisGly 20

Db 1 ATGGCAAGAATATTGTTACTTTCTCCCGGGTCTTGTGCTGTATGCTGTGCTGATGGA 60

Qy 21 ValPheMetAspLysLeuSerLysLysLeuValLeuValLeuValLeuValLeuVal 40

Db 61 ATATTATGACCGCTGAGCTTCAAGAAGCTCTGTGACAGATGATGAGTGTCTTACT 120

Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60

Db 121 ATTTCTCTGGCTAGTGTCTCAAGAAGATTTATATGCCCGAGCTGTAGATTCAACGTT 180

Qy 61 LysIleGlyGlnGlnIleValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80

Db 181 AAAAAGGGCAGCAGATCTATGTTACTCAAAAGCTGGTAAAGAAATGGAGCTGGAGAA 240

Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100

Db 241 TTTTGGCTGGCAGTGTATTGTTGATGGCCAGGACGAGATGGAGTGTGGTATTTC 300

Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120

Db 301 CCCAGGAACCTGGTCAAGGAACAGCGTGTGTACCAGAGAGCTTACCAGGAAGTTCCTCCACC 360



QY 121 ThrAspIleAspPheCysGlu 128  
 DB 361 ACGGATATTGACTTCTCTGCGAG 384

## RESULT 6

AAH26341  
 ID AAH26341 standard; cDNA; 426 BP.

AC AAH26341;

XX 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide clone 16372272.

KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.

OS Homo sapiens.

XX WO200155332-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX Mize NK, Boyle BJ, Ford JB, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;

XX MPI; 2001-483233/52.

XX Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -

XX Example 1; Page 114; 119pp; English.

XX The present sequence is that of Hyseq clone identification number  
 CC 16372272, which was obtained from a human thymus cDNA library  
 CC using standard PCR with primers specific for vector sequences  
 CC flanking the inserts, sequencing by hybridisation sequence  
 CC signature analysis, and Sanger sequencing techniques. This  
 CC expressed sequence tag was used in the assembly of a full-length  
 CC cDNA sequence (see AAH26341) encoding a novel human growth  
 CC regulatory-like polypeptide (GRLP, see AAH2671). The GRLP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein, (CD-RAP, 44% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRLP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.

XX Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

## Alignment Scores:

Pred. No.: 4 39e-74 Length: 426  
 Score: 602.00 Matches: 111  
 Percent Similarity: 93.75% Conservative: 9

Best Local Similarity: 86.72% Mismatches: 8  
 Query Match: 89.05% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-12 (1-128) x AAH26341 (1-426)

QY 1 MetAlaArgIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
 DB 19 ATGGCAAGAATATTGTACTTTCTCCCGGTCTGTGGTGTATGTGTGTCATGA 78  
 QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40  
 DB 79 ATATTATGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTTACT 138  
 QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
 DB 139 ATTCTCTGGCTAGTGTCTCAAGAGATTATATGCTCCCGGACTGTAGATTATTACGTT 198  
 QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80  
 DB 199 AAAAAAGGCGCAGACATCTATGTACTCAAAGCTGGTAAAGAAATATGGAGCTGGAGAA 258  
 QY 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
 DB 259 TTTTGGCTGGCAGTGTATTGTGTATGTCGCCAGCAGATGGAGTCTGGGTATTTC 318  
 QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 DB 319 CCCAGGAACCTTGGTCAAGGAAACAGCGTGTGTACCAAGGAAGCTACCAAGAAAGTCCCACC 378  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 379 ACGGATATTGACTTCTCTGCGAG 402

## RESULT 7

ABL95740

ID ABL95740 standard; cDNA; 521 BP.

XX ABL95740;

XX 19-JUL-2002 (first entry)

XX Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
 KW antiarteriosclerotic; gene; ss.

XX Homo sapiens.

XX WO200208284-A2.

XX 31-JAN-2002.

XX 09-JUL-2001; 2001WO-US21735.

XX 20-JUL-2000; 2000US-219556P.

XX 25-JUL-2000; 2000US-220624P.

XX 25-JUL-2000; 2000US-220664P.

XX 28-JUL-2000; 2000WO-US20710.

XX 02-AUG-2000; 2000US-222695P.

XX 17-AUG-2000; 2000US-0643657.

XX 23-AUG-2000; 2000WO-US23522.

XX 24-AUG-2000; 2000US-230978P.

XX 07-SEP-2000; 2000US-000000P.

XX 15-SEP-2000; 2000US-064610.

XX 18-SEP-2000; 2000US-0665350.

XX 24-OCT-2000; 2000US-242922P.

XX 08-NOV-2000; 2000US-0709238.

XX 08-NOV-2000; 2000WO-US30952.

XX 10-NOV-2000; 2000WO-US30873.



```

PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796499.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 20-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
XX WPI; 2002-090516/12.
DR P-PSDB; ABB84996.
DR
XX
XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
XX Claim 2; Fig 359; 565pp; English.
XX
XX ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiac, cytostatic,
CC antiangiogenic, hypotensive and polynucleotides have cardiac, cytostatic,
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
XX Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;
SQ
Alignment Scores:
Pred. No.: 5.85e-74 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 24 Gaps: 0
US-10-019-455A-12 (1-128) x ABL88251 (1-521)
QY 1 MetAlaArgIleLeuLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTTGTGGCTGTGTGTGTCATGGA 97
QY 21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValThr 40
Db 98 ATATTATGACCGCTAGCTTCCAGAGAGCTGTGTCAGATGATGATGTCCTACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 158 ATTCTCTGCTAGTGTCTCAGAGAGATTATTAATGCCCGGACGTGATATTCATACGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80

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Db 218 AAAAAGGGCAGCAGATCTATGTGTCTCAAGCTGGTAAAGAAATGGAGCTGGAGAA 277
QY 81 PheTrpAlaGlySerValTyrGlyAspHieGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGGCTGGCAGCTTTTATGTTGATGGCCAGGACGAGATGGGAGTCGTGGTTATTTC 337
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACCTTGGTCAAGGACACGCTGTGTACCCAGGAAGCTACCAAGGAAGTTCACCAC 397
QY 121 ThrAspIleAspPhePheCysGlu 128
Db 398 ACGGATATTGACTTCTCTCGGAG 421
RESULT 9
ABK33571
ID ABK33571 standard; cDNA; 521 BP.
XX
XX AC ABK33571;
XX
XX DT 08-MAY-2002 (first entry)
XX
XX DE cDNA encoding human PRO protein, Seq ID No 71.
XX
XX KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200208288-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 29-JUN-2001; 2001WO-US21066.
XX
XX PR 20-JUL-2000; 2000US-219556P.
XX PR 25-JUL-2000; 2000US-220585P.
XX PR 25-JUL-2000; 2000US-220605P.
XX PR 25-JUL-2000; 2000US-220607P.
XX PR 25-JUL-2000; 2000US-220624P.
XX PR 25-JUL-2000; 2000US-220636P.
XX PR 25-JUL-2000; 2000US-220664P.
XX PR 25-JUL-2000; 2000US-220666P.
XX PR 26-JUL-2000; 2000US-220893P.
XX PR 28-JUL-2000; 2000WO-US20710.
XX PR 23-AUG-2000; 2000WO-US23522.
XX PR 24-AUG-2000; 2000WO-US23328.
XX PR 15-SEP-2000; 2000US-000000P.
XX PR 10-NOV-2000; 2000WO-US30873.
XX PR 28-NOV-2000; 2000US-253646P.
XX PR 01-DEC-2000; 2000WO-US32678.
XX PR 20-DEC-2000; 2000US-0747259.
XX PR 20-DEC-2000; 2000WO-US34956.
XX PR 28-FEB-2001; 2001WO-US06520.
XX PR 10-MAY-2001; 2001US-0854280.
XX PR 25-MAY-2001; 2001WO-US17092.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
XX WPI; 2002-172001/22.
DR P-PSDB; AAU83627.
XX
XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumours
PT such as lung cancer, colon cancer, breast cancer, prostate tumour, rectal
PT tumour or liver tumour -
XX

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PS Claim 2; Figure 71; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. ABK33536-ABK33657 represent human
CC PRO protein coding sequences of the invention.
XX
SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:
Pred. No.: 5.85e-74 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 24 Gaps: 0

US-10-019-455A-12 (1-128) x ABK33571 (1-521)
QY 1 MetAlaArgIleLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
DB 38 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTTTGGCTGTATGTGCTGTGCATGGA 97
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
DB 98 ATATTATTGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGCTGTACTACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
DB 158 ATTCTCTGGCTAGTGCTCAAGAGATATTATATGCCCGGAGCTGTAGATTCAATTAACGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
DB 218 AAAAAGGCGCAGACAGATCTATGTGTACTCAAAAGCTGTTAAAGAGAAATGGAGCTGAGAA 277
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 278 TTTTGGCTGGCAGGTATTATGGTATGGCCAGGACGAGATGGAGTCTGGGTATTTC 337
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 338 CCCAGGAACCTTGGTCAAGGACAGCGTGTGTACCAAGGAGCTTACCAAGGAGTCCACC 397
QY 121 ThrAspIleAspPheCysGlu 128
DB 398 ACGGATATTGACTTCTTCTGCGAG 421

RESULT 10
AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX
AC AAH98228;
XX
CC Human EST-derived coding sequence SEQ ID NO: 85.
DE 12-OCT-2001 (first entry)
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.

XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX P-PSDB; AAM23569.
DR WPI; 2001-476164/51.
DR P-PSDB; AAM23569.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 236; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Alignment Scores:
Pred. No.: 1.25e-73 Length: 891
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-12 (1-128) x AAH98228 (1-891)
QY 1 MetAlaArgIleLeuLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
DB 19 ATGGCAAGATATTGTTACTTTCTCCCGGCTCTTTGGCTGTATGTGCTGTGCATGGA 78
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThr 40
DB 79 ATATTATTGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTCTACTACT 138
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
DB 139 ATTTCTTGGCTAGTGCTCAAGAGATATTATATGCCCGGAGCTGTAGATTCAATTAACGTT 198
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
DB 199 AAAAAGGCGCAGACAGATCTATGTGTACTCAAAAGCTGTTAAAGAGAAATGGAGCTGAGAA 258
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 259 TTTTGGCTGGCAGGTATTATGGTATGGCCAGGACGAGATGGAGTCTGGGTATTTC 318
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 319 CCCAGGAACCTTGGTCAAGGACAGCGTGTGTACCAAGGAGCTTACCAAGGAGTCCACC 378
QY 121 ThrAspIleAspPheCysGlu 128
```

```

DB: 22 Gaps: 0
US-10-019-455A-12 (1-128) x AAH26342 (1-891)
QY 1 MetAlaAArgIleLeuLeuLeuLeuGlyGlyLeuValLeuCysAlaGlyHisGly 20
DB 19 ATGGCAAGAATATTGTTACTTTTCCCTCCCGGGTCTTGGCTGTATGCTGTGTCATGGA 78
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40
DB 79 ATATTATTATGACCGCTAGCTTCCAAGAAGCTCTGTCAGATGATGAGTGTGTCTATACT 138
QY 41 IleSerLeuAlaAargAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
DB 139 ATTTCCTGGCTAGTCTCAAGAAGATTATATATGCCCGGACTGTAGATTCAATACGTT 198
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAenglyAlaGlyGlu 80
DB 199 AAAAAGGGCAGCAGATCTATGTACTCAAGCTGTAAAGAAATAAGAGCTGGAGAA 258
QY 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
DB 259 TTTTGGCTGGCAGTGTATGCTGATGCCAGCAGAGATGGAGTGGGTATTATTC 318
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
DB 319 CCCAGGAACCTTGGTCAGGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTCCACC 378
QY 121 ThrAspIleAspPhePheCysGlu 128
DB 379 ACGGATATTGACTTCTTCGCGAG 402

RESULT 12
AAH26342
ID AAF59083 standard; DNA; 923 BP.
AC AAF59083;
XX
XX
XX 23-APR-2001 (first entry)
DE Human MLP nucleotide sequence SEQ ID NO:29.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
XX Homo sapiens.
XX
XX W0200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 1; Page 99-100; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX

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Tue Dec 30 10:20:37 2003

Db 93 ATATTATGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGATGTGTCTACT 152  
Qy 41 ILeSerLeuAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
Db 153 ATTTCCTGCTAGTCTCAGAGAGATTAATGAGCCCGGACTGTAGATTCATTAAGTT 212  
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAenGlyAlaGlyGlu 80  
Db 213 AAAAAAGGCGAGAGATCTATGTCTACTCAAGCTGGTAAAGAAAATGGAGCTGGAGAA 272  
Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
Db 273 TTTTGGGCTGCGAGTGTATGCTGATGGCGAGACGAGATGGGAGTCGTGGGTATTTC 332  
Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
Db 333 CCCAGGAACTTGGTCAAGGAACACGGTGTGTACCAAGAGTACCAAGGAAGTCCCAACC 392  
Qy 121 ThrAspIleAspPheCysGlu 128  
Db 393 ACGGATATTGACTTCTTCTGCGAG 416  
RESULT 14  
ID AAF59080 standard; DNA; 330 BP.  
XX AAF59080;  
XX AC AAF59080;  
XX DT 23-APR-2001 (first entry)  
XX DE Mouse MLP nucleotide sequence SEQ ID NO:25.  
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;  
XX KW inhibitor; ds.  
XX OS Mus musculus.  
XX PN WO200102564-A1.  
XX PD 11-JAN-2001.  
XX PF 29-JUN-2000; 2000WO-JP04278.  
XX PR 30-JUN-1999; 99JP-0186718.  
XX PA (TAKE ) TAKEDA CHEM IND LTD.  
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
XX PI Tanaka H;  
XX DR WPI; 2001-159271/16.  
XX DR P-PSDB; AAB69127.  
XX XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX PS Claim 10; Page 98; 111pp; Japanese.  
XX CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
XX in the exemplification of the present invention.  
XX SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

Alignment Scores: 1.03e-72 Length: 330  
Pred. No.: 591.00 Matches: 110  
Score: 591.00 Conservatives: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 87.43% Gaps: 0  
DB: 22  
US-10-019-455A-12 (1-128) x AAF59080 (1-330)  
Qy 19 HisGlyValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysVal 38  
Db 1 CATGCTGCTATTATGGATAAACITTCCTTAAGAAGTTGTGCGGATGAGGAGTGTCTC 60  
Qy 39 TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 58  
Db 61 TATACTATTTCTCTGGCAAGAGCACAGCAAGATTACAAATGCCCAGACTGTAGGTTTCATC 120  
Qy 59 AspValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla 78  
Db 121 GATGTCAAGAAAGGCGAGCATCTATGTTTCTCCAGCTGCTTAACAGAAACGAGCT 180  
Qy 79 GlyGluPheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly 98  
Db 181 GGAGAGTTTGGGCTGGCAGTGTATGTTGTCACCCAGGATGAGATGGGAATTGTAGGT 240  
Qy 99 TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIle 118  
Db 241 TATTTCCCAACAACTTGGTGAAGGAGCAGCGTGTATACCAAGAGGCCCAAGAGATC 300  
Qy 119 ProThrThrAspIleAspPheCysGlu 128  
Db 301 CCAACCCAGGATATTGACTTCTTCTGTGAA 330  
RESULT 15  
ID AAF59099 standard; DNA; 330 BP.  
XX AAF59099;  
XX AC AAF59099;  
XX DT 23-APR-2001 (first entry)  
XX DE Rat MLP nucleotide sequence SEQ ID NO:48.  
XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX KW cardiant; gene therapy; secretory cell function regulator; promoter;  
XX KW inhibitor; ds.  
XX OS Rattus sp.  
XX PN WO200102564-A1.  
XX PD 11-JAN-2001.  
XX PF 29-JUN-2000; 2000WO-JP04278.  
XX PR 30-JUN-1999; 99JP-0186718.  
XX PA (TAKE ) TAKEDA CHEM IND LTD.  
XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
XX PI Tanaka H;  
XX DR WPI; 2001-159271/16.  
XX DR P-PSDB; AAB69131.  
XX XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX PS Claim 12; Page 107; 111pp; Japanese.

XX

The present invention describes novel MLP proteins and their encoding DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac activities, and can be used in gene therapy and as secretory cell function regulators. The MLP proteins and DNAs can be used in drugs, in the diagnosis and development of promoters and inhibitors for preventing or treating bone and joint diseases as well as pathologic angiogenesis. AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used in the exemplification of the present invention.

XX Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;

## Alignment Scores:

Pred. No.:	2,37e-70	Length:	330
Score:	574.00	Matches:	106
Percent Similarity:	99.09%	Conservative:	3
Best Local Similarity:	96.36%	Mismatches:	1
Query Match:	84.91%	Indels:	0
DB:	22	Gaps:	0

US-10-019-455A-12 (1-128) x AAF59099 (1-330)

Qy	19	HisGlyValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluGluCysVal	38
Db	1	CATGGCATGTTTATGATPAACATTTCTTCTAGAAAGTTGTGTGCAGATGAGAGTGTGTC	60
Qy	39	TyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle	58
Db	61	TATACCATTTCTCTGGCAAGAGCACAGGAAGACTACATGCCCCGGACTGTAGGTTTCATC	120
Qy	59	AspValIysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAla	78
Db	121	AATGTCGAAGAAAGGGCAGCAGATCTATGTTTATTCCAAGCTGTTACAGAAATGGAGCT	180
Qy	79	GlyGluPheThrPalaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGly	98
Db	181	GGGGCATTCCTGGGCTGGCACTGTTTATGGTGACCCAGGATGAGATGGGAATTGTGGGT	240
Qy	99	TyrPheProSerAsnLeuValLysGluGlnArgValTyrGlnGluIleThrLysGluIle	118
Db	241	TATTTCCCCAGCAACTGGTTAGAGAGCAACGAGTGTACAGAGGGCCCAAGAGGATT	300
Qy	119	ProThrThrAspIleAspPhePheCysGlu	128
Db	301	CCAACCAACGGATATTGACTTCCTCTGTGAA	330

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Job time : 161.353 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 19:57:30 ; Search time 287.193 Seconds  
(without alignments)  
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Title: US-10-019-455a-12

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Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
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Database : Published Applications NA:

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq2.\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	ID	Description
No.	Score				

ALIGNMENTS

RESULT 1

US-10-216-038-1  
; Sequence 1, Application US/10216038  
; Publication No. US20030124573A1  
; GENERAL INFORMATION:  
; APPLICANT: Mize, Nancy K  
; APPLICANT: Boyle, Bryan J  
; APPLICANT: Ford, John E  
; APPLICANT: Arterburn, Matthew C  
; APPLICANT: Tang, Y Tom  
; APPLICANT: Liu, Chenghua  
; APPLICANT: Drmanac, Radoje T  
; APPLICANT: Song, Yong  
; APPLICANT: Sjaastad, Michael  
; TITLE OF INVENTION: Methods and Materials Relating to No. US20030124573A1e1 Growth R  
; TITLE OF INVENTION: Polypeptides and Polynucleotides  
; FILE REFERENCE: HVS-7CIP  
; CURRENT APPLICATION NUMBER: US/10/216,038  
; CURRENT FILING DATE: 2002-08-08  
; PRIOR APPLICATION NUMBER: US 09/563,786  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: US 09/491,404  
; PRIOR FILING DATE: 2000-01-25  
; NUMBER OF SEQ ID NOS: 8

1	602	89.1	426	15	US-10-216-038-1	Sequence 1, Appl
2	602	89.1	521	13	US-10-216-163-71	Sequence 71, Appl
3	602	89.1	521	13	US-10-218-765-71	Sequence 71, Appl
4	602	89.1	521	13	US-10-219-063-71	Sequence 71, Appl
5	602	89.1	521	13	US-10-219-066-71	Sequence 71, Appl
6	602	89.1	521	13	US-10-219-067-71	Sequence 71, Appl
7	602	89.1	521	13	US-10-219-068-71	Sequence 71, Appl
8	602	89.1	521	13	US-10-219-069-71	Sequence 71, Appl
9	602	89.1	521	13	US-10-219-073-71	Sequence 71, Appl
10	602	89.1	521	13	US-10-219-475-71	Sequence 71, Appl
11	602	89.1	521	13	US-10-219-483-71	Sequence 71, Appl
12	602	89.1	521	13	US-10-219-525-71	Sequence 71, Appl
13	602	89.1	521	13	US-10-219-526-71	Sequence 71, Appl
14	602	89.1	521	13	US-10-219-530-71	Sequence 71, Appl
15	602	89.1	521	13	US-10-219-531-71	Sequence 71, Appl
16	602	89.1	521	13	US-10-219-532-71	Sequence 71, Appl
17	602	89.1	521	13	US-10-219-533-71	Sequence 71, Appl
18	602	89.1	521	13	US-10-223-081-359	Sequence 359, App
19	602	89.1	521	13	US-10-223-082-359	Sequence 71, Appl
20	602	89.1	521	13	US-10-230-437-71	Sequence 71, Appl
21	602	89.1	521	13	US-10-232-228-71	Sequence 71, Appl
22	602	89.1	521	13	US-10-223-082-359	Sequence 71, Appl
23	602	89.1	521	15	US-10-227-884-71	Sequence 71, Appl
24	602	89.1	521	15	US-10-230-163-71	Sequence 71, Appl
25	602	89.1	521	15	US-10-230-331-71	Sequence 71, Appl
26	602	89.1	521	15	US-10-218-631-71	Sequence 71, Appl
27	602	89.1	521	15	US-10-216-159A-71	Sequence 71, Appl
28	602	89.1	521	15	US-10-218-849-71	Sequence 71, Appl
29	602	89.1	521	15	US-10-227-873-71	Sequence 71, Appl
30	602	89.1	521	15	US-10-227-883-71	Sequence 71, Appl
31	602	89.1	521	15	US-10-219-076-71	Sequence 71, Appl
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35	602	89.1	521	15	US-10-219-466-71	Sequence 71, Appl
36	602	89.1	521	15	US-10-219-479-71	Sequence 71, Appl
37	602	89.1	521	15	US-10-219-481-71	Sequence 71, Appl
38	602	89.1	521	15	US-10-230-260-71	Sequence 71, Appl
39	602	89.1	521	15	US-10-232-231-71	Sequence 71, Appl
40	602	89.1	521	15	US-10-232-233-71	Sequence 71, Appl
41	602	89.1	521	15	US-10-216-163-71	Sequence 71, Appl
42	602	89.1	521	15	US-10-216-163-71	Sequence 71, Appl
43	602	89.1	521	15	US-10-218-956-71	Sequence 71, Appl
44	602	89.1	521	15	US-10-219-468-71	Sequence 71, Appl
45	602	89.1	521	15	US-10-219-468-71	Sequence 71, Appl

SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 426  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (426)..(426)  
OTHER INFORMATION: n = A, T, G, or C  
US-10-216-038-1

Alignment Scores:  
Pred. No.: 2,31e-83 Length: 426  
Score: 602.00 Matches: 111  
Percent Similarity: 93.75% Conservatve: 9  
Best Local Similarity: 86.72% Mismatches: 8  
Query Match: 89.05% Indels: 0  
DB: 15 Gaps: 0

US-10-019-455A-12 (1-128) x US-10-216-038-1 (1-426)

QY 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20  
DB 19 ATGGCAAGAAATATTGTTACTTTCTCCCGGCTCTGTGGCTGTGTGCTGTGCATGGA 78  
QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40  
DB 79 ATATTATTGACCGCTAGCTTCCCAAGAAAGCTCTGTGCAGATGATGATGTTCTATCT 138  
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
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DB 199 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATATGGAGCTGGAGAA 258  
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
DB 259 TTTTGGCTGGCAGGTATTATGTTGATGGCCAGGACGAGATGGAGTCTGGGTATTATTC 318  
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
DB 319 CCCAGGAACCTTGGTCAAGAACAGCGTGTGTACCGAGGAGCTACCAAGAAAGTCCACC 378  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 379 ACGGATATTGACTTCTCTCGCAG 402

## RESULT 2

US-10-216-163-71  
Sequence 71, Application US/10216163  
Publication No. US20030149239A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC3  
CURRENT APPLICATION NUMBER: US/10/216,163  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 246  
SEQ ID NO 71  
LENGTH: 521  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-216-163-71

Alignment Scores:  
Pred. No.: 3.11e-83 Length: 521  
Score: 602.00 Matches: 111  
Percent Similarity: 93.75% Conservatve: 9  
Best Local Similarity: 86.72% Mismatches: 8  
Query Match: 89.05% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x US-10-216-163-71 (1-521)

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QY 21 ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValThr 40  
DB 98 ATATTATTGACCGCTAGCTTCCCAAGAAAGCTCTGTGCAGATGATGATGTTCTATCT 157  
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60  
DB 158 ATTTCTCTGGCTAGTGTCTCAAGAAATATTATGCCCCGAGCTGTAGATTCAATTAACGTT 217  
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyValAlaGlyGlu 80  
DB 218 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAATATGGAGCTGGAGAA 277  
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100  
DB 278 TTTTGGCTGGCAGGTATTATGTTGATGGCCAGGACGAGATGGAGTCTGGGTATTATTC 337  
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
DB 338 CCCAGGAACCTTGGTCAAGAACAGCGTGTGTACCGAGGAGCTACCAAGAAAGTCCACC 397  
QY 121 ThrAspIleAspPheCysGlu 128  
DB 398 ACGGATATTGACTTCTCTCGCAG 421

## RESULT 3

US-10-218-765-71  
Sequence 71, Application US/10218765  
Publication No. US20030187201A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Desnoyers, Luc  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530PIC3  
CURRENT APPLICATION NUMBER: US/10/218,765  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113

APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Smith, Victoria  
APPLICANT: Stephan, Jean-Philippe F.  
APPLICANT: Watanabe, Colin L.  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3530P1C19  
CURRENT APPLICATION NUMBER: US/10/218,765  
PRIOR FILING DATE: 2002-08-12  
PRIOR APPLICATION NUMBER: 10/119,480  
PRIOR FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063549  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/064103  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/069873  
PRIOR FILING DATE: 1997-12-17  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
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PRIOR FILING DATE: 1998-04-15  
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PRIOR FILING DATE: 1998-08-04  
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PRIOR FILING DATE: 1998-08-17  
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PRIOR FILING DATE: 1998-08-26  
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PRIOR FILING DATE: 1998-08-31  
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PRIOR APPLICATION NUMBER: 60/100390  
PRIOR FILING DATE: 1998-09-15  
PRIOR APPLICATION NUMBER: 60/100627  
PRIOR FILING DATE: 1998-09-16  
PRIOR APPLICATION NUMBER: 60/100848  
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PRIOR FILING DATE: 1998-11-03  
PRIOR APPLICATION NUMBER: 60/108787  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108801  
PRIOR FILING DATE: 1998-11-17  
PRIOR APPLICATION NUMBER: 60/108849  
PRIOR FILING DATE: 1998-11-18  
PRIOR APPLICATION NUMBER: 60/112422  
PRIOR FILING DATE: 1998-12-15  
PRIOR APPLICATION NUMBER: 60/113296  
PRIOR FILING DATE: 1998-12-22  
PRIOR APPLICATION NUMBER: 60/113605  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/113621  
PRIOR FILING DATE: 1998-12-23  
PRIOR APPLICATION NUMBER: 60/115558  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115565  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/115733  
PRIOR FILING DATE: 1999-01-12  
PRIOR APPLICATION NUMBER: 60/119549  
PRIOR FILING DATE: 1999-02-10  
PRIOR APPLICATION NUMBER: 60/123618  
PRIOR FILING DATE: 1999-03-10  
PRIOR APPLICATION NUMBER: 60/125259  
PRIOR FILING DATE: 1999-03-19  
PRIOR APPLICATION NUMBER: 60/125775

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Db 278 TTTTGGGCTGGCAGTGTTTATGGTGATGGCCAGGACGAGATGGGAGTCGTGGGTATTTC 337
QY 101 ProSerAsnLeuVallyysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACATTGGTCAAGGAACACGCGTGTGTACCAAGGAAGTTCACCAAGTTCACACC 397
QY 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTTCGCGAG 421

RESULT 4
US-10-219-063-71
; Sequence 71, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-063-71

Alignment Scores:
Pred. No.: 3,11e-83 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x US-10-219-063-71 (1-521)
QY 1 MetalAlaArgIleLeuIleLeuLeuLeuGlyClyIleuValValLeuCysAlaGlyHisGly 100

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[illegible]



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; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Alignment Scores:
Pred. No.:      3,11e-83      Length:      521
Score:          602.00      Matches:     111
Percent Similarity: 93.75%      Conservative: 9
Best Local Similarity: 86.72%      Mismatches:  8
Query Match:    89.05%      Indels:      0
DB:             13          Gaps:         0

US-10-019-455A-12 (1-128) x US-10-219-067-71 (1-521)
QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
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QY 21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValThr 40
Db 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
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QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
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QY 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100
Db 278 TTTTGGCTGGCAGTGTATTGTTGATGCCAGGACGAGATGGAGTGGTGGTATTTC 337
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGGTGTGTACCAAGGAAGCTACCAAGGAAGTCCCCACC 397
QY 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTGGCAG 421

RESULT 7
US-10-219-068-71
; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin E.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC31
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; CURRENT APPLICATION NUMBER: US/10/219,068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/091113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-068-71

Alignment Scores:
Pred. No.:      3,11e-83      Length:      521
Score:          602.00      Matches:     111
Percent Similarity: 93.75%      Conservative: 9
Best Local Similarity: 86.72%      Mismatches:  8
Query Match:    89.05%      Indels:      0
DB:             13          Gaps:         0

US-10-019-455A-12 (1-128) x US-10-219-068-71 (1-521)
QY 1 MetAlaArgIleLeuIleLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGATATTGTTCTCTCCGGGCTCTTGGCTGTATGCTGTCATGGA 97
QY 21 ValPheMetAspLysLeuSerSerLysLeuCysAlaAspGluGluCysValThr 40
Db 98 ATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTCTATACT 157
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAGNTATATATGCCCCGACTGTAGATTCAATACGTT 217
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 218 AAAAAAGGCGCAGCAGATCTATGTGTACTCAAGAGTGTAAAGAAATGGAGCTGGAGAA 277
QY 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyThrPhe 100
Db 278 TTTTGGCTGGCAGTGTATTGTTGATGCCAGGACGAGATGGAGTGGTGGTATTTC 337
QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 338 CCCAGGAACCTTGGTCAAGGAACAGCGGTGTGTACCAAGGAAGCTACCAAGGAAGTCCCCACC 397
QY 121 ThrAspIleAspPheCysGlu 128
Db 398 ACGGATATTGACTTCTTCTGGCAG 421

RESULT 8
US-10-219-069-71
; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
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Db 98 ATATTATGACCGTCTAGCTTCAAGAAGCTCTGTCAGATGATGAGTGTCATACT 157
      ::::::::::::::::::::
Qy 41 lIeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
      ::::::::::::::::::::
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
      ::::::::::::::::::::
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
      ::::::::::::::::::::
Db 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGTATAAAGAAATGGAGCTGGAGAA 277
      ::::::::::::::::::::
Qy 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
      ::::::::::::::::::::
Db 278 TTTTGGCTGCGAGTCTTATGTATGATGCGCAGAGATGGAGTCTGGGTATTTC 337
      ::::::::::::::::::::
Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
      ::::::::::::::::::::
Db 338 CCCAGGAACCTTGGTCAAGGAACACGCGTGTACACGGAAGCTACCAAGGAAGTTCCACC 397
      ::::::::::::::::::::
Qy 121 ThrAspIleAspPheCysGlu 128
      ::::::::::::::::::::
Db 398 ACGGATATTGACTTCTCTGGCAG 421
      ::::::::::::::::::::

```

## RESULT 10

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US-10-219-475-71
; Sequence 71, Application US/10219475
; Publication NO. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C49
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/10/219,475
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; TYPE: DNA
; LENGTH: 521
; ORGANISM: Homo Sapien
US-10-219-475-71
Alignment Scores:

```

```

Pred. No.: 3,11e-83 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservative: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 13 Gaps: 0

US-10-019-455A-12 (1-128) x US-10-219-475-71 (1-521)

Qy 1 MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
      ::::::::::::::::::::
Db 38 ATGGCAAGAAATATTGTATTCTTCTCCCGGCTCTTGGGCTGTATGCTGTGCTCATGGA 97
      ::::::::::::::::::::
Qy 21 ValPheMetAspLysLeuSerLysLysLeuCysAlaAspGluCysValTyrThr 40
      ::::::::::::::::::::
Db 98 ATATTATGAGCCGCTAGCTTCCAAAGAAGCTCTGTGCAGATGATGAGTGTCTATACT 157
      ::::::::::::::::::::
Qy 41 lIeSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
      ::::::::::::::::::::
Db 158 ATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGAGCTGTAGATTCAATTAACGTT 217
      ::::::::::::::::::::
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
      ::::::::::::::::::::
Db 218 AAAAAAGGGCAGCAGATCTATGTGTACTCAAAAGCTGTATAAAGAAATGGAGCTGGAGAA 277
      ::::::::::::::::::::
Qy 81 PheTyrAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
      ::::::::::::::::::::
Db 278 TTTTGGCTGCGAGTGTATTATGCTGATGCCAGGACGAGATGGAGTCTGGGTATTTC 337
      ::::::::::::::::::::
Qy 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
      ::::::::::::::::::::
Db 338 CCCAGGAACCTTGGTCAAGGAACACGCGTGTACACGGAAGCTACCAAGGAAGTTCCACC 397
      ::::::::::::::::::::
Qy 121 ThrAspIleAspPheCysGlu 128
      ::::::::::::::::::::
Db 398 ACGGATATTGACTTCTCTGGCAG 421
      ::::::::::::::::::::

RESULT 11
US-10-219-480-71
; Sequence 71, Application US/10219480
; Publication NO. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C38
; CURRENT APPLICATION NUMBER: US/10/219,480
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

```



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; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-03-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-483-71

Alignment Scores:
Pred. No.:      3,11e-83      Length:      521
Score:          602.00      Matches:    111
Percent Similarity: 93.75%      Conservative: 9
Best Local Similarity: 86.72%      Mismatches: 8
Query Match:      89.05%      Indels:     0
DB:              13          Gaps:       0

US-10-019-455A-12 (1-128) x US-10-219-483-71 (1-521)
QY      1  MetAlaArgIleLeuIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db      38  ATGCGAAGATATATGTTACTTTTCCTCCCGGGTCTTGTGGCTGTATGTGCTGTGATGGA 97
QY      21  ValPheMetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValIleThr 40
Db      98  ATAATTATGACCGCTGATGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTCTATACT 157
QY      41  IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db      158  ATTTCTCTGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTTCATTAAACGTT 217
QY      61  LysLysGlyGlnGlnIleTyrValTyrSerLysIleuValThrGluAsnGlyAlaGlyGlu 80
Db      218  AAAAAAGGGCAGCAGATCTATGTACTCTCAAGAGCTGGTAAAGAAATGGAGCTGGAGAA 277
QY      81  PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db      278  TTTTGGGCTGCGAGTGTTATGTGTATGGCCAGCAGATGGGAGTCTGGGTTATTTC 337
QY      101  ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db      338  CCCAGGAAC TTGGTCAAGGAACACGCGTGTGTACCAAGGAAGCTTACCAGGAAGTTCACCAAGGAAGTTC 397
QY      121  ThrAspIleAspPheCysGlu 128
Db      398  ACGGATATTGACTTCTTCTGCGAG 421

RESULT 13
US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PlC29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
;
US-10-219-525-71

Alignment Scores:
Pred. No.: 3,11e-83 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservatives: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-12 (1-128) x US-10-219-525-71 (1-521)
Qy 1 MetAlaArgIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGAATATTGTACTTCTCCCGGTCCTTGTGGCTGTGTGTCATGGA 97
Qy 21 ValPheMetAspLysLeuSerLysLeuCysAlaGlyHisGly 40
Db 98 ATATTATGACCGCTAGTCTTCCCAAGAGCTTGTGCAGATGATGATGATGAT 157
Qy 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 158 ATTTCTCTGGCTAGTCTCAAGAAGATTTATATCCCGGACTGTAGATTCATTAAGTT 217
Qy 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 218 AAAAAGGCGACAGACTATGTGTACTCAAGCTGGTTAAAGAAATGGAGCTGGAGAA 277
Qy 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 278 TTTTGGGCTGGCAGTGTATTATGGTATGGCCAGGACGAGATGGGAGTGGTGGTTATTC 337
Qy 101 ProSerAsnLeuValLysGluAlaArgValTyrGlnGluAlaThrLysGluIleProThr 120
Db 111

US-10-019-526-71
; Sequence 71, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PlC41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
;
US-10-219-526-71

Alignment Scores:
Pred. No.: 3,11e-83 Length: 521
Score: 602.00 Matches: 111
Percent Similarity: 93.75% Conservatives: 9
Best Local Similarity: 86.72% Mismatches: 8
Query Match: 89.05% Indels: 0
DB: 13 Gaps: 0

US-10-019-455a-12 (1-128) x US-10-219-526-71 (1-521)
Qy 1 MetAlaArgIleLeuLeuLeuGlyGlyLeuValValLeuCysAlaGlyHisGly 20
Db 38 ATGGCAAGAATATTGTACTTCTCCCGGTCCTTGTGGCTGTGTGTCATGGA 97
Qy 21 ValPheMetAspLysLeuSerLysLeuCysAlaGlyHisGly 40
Db 98 ATATTATGACCGCTAGTCTTCCCAAGAGCTTGTGCAGATGATGATGATGAT 157
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: December 29, 2003, 16:24:24 ; Search time 40.6947 Seconds  
(without alignments)  
1388.315 Million cell updates/sec

Title: US-10-019-455A-12

Perfect score: 676  
Sequence: 1 MARILLILLGLLVLCAGH.....RVYQATKEIPTTIDIFFCE 128

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPTXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTCUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	277.5	41.1	459	1	US-08-578-649-1 Sequence 1, Appl
2	261.5	38.7	330	1	US-08-578-649-18 Sequence 18, Appl
3	247	36.5	581	1	US-08-578-649-4 Sequence 4, Appl
4	219.5	32.5	305	1	US-08-578-649-8 Sequence 8, Appl
5	210	31.1	596	1	US-08-578-649-24 Sequence 24, Appl
6	177.5	26.3	3565	1	US-08-578-649-3 Sequence 3, Appl
7	91.5	13.5	2793	1	US-07-646-537B-1 Sequence 1, Appl
8	89.5	13.2	2757	5	PCT-US93-06251-79 Sequence 48, Appl
9	89.5	13.2	2757	5	PCT-US93-06251-79 Sequence 79, Appl
10	89.5	13.2	4762	4	US-09-300-958A-30 Sequence 30, Appl
11	82	12.1	467	4	US-09-300-958A-28 Sequence 28, Appl
12	78.5	11.6	5398	3	US-09-356-952-11 Sequence 11, Appl

13	77	11.4	2085	1	US-08-164-839-3 Sequence 3, Appl
14	77	11.4	2085	1	US-08-583-799-3 Sequence 3, Appl
15	77	11.4	2520	1	US-08-164-839-5 Sequence 5, Appl
16	77	11.4	2520	1	US-08-583-799-5 Sequence 5, Appl
17	76	11.2	1664976	4	US-08-916-421B-1 Sequence 1, Appl
18	75	11.1	2873	4	US-08-630-915A-193 Sequence 193, Appl
19	75	11.1	11864	4	US-08-961-527-61 Sequence 61, Appl
20	74.5	11.0	3981	4	US-09-328-352-760 Sequence 760, Appl
21	71.5	10.6	747	4	US-08-630-915A-39 Sequence 39, Appl
22	71.5	10.6	2064	1	US-08-164-839-30 Sequence 30, Appl
23	71.5	10.6	2064	1	US-08-164-839-32 Sequence 32, Appl
24	71.5	10.6	2064	1	US-08-583-799-30 Sequence 30, Appl
25	71.5	10.6	2064	1	US-08-583-799-32 Sequence 32, Appl
26	71.5	10.6	2148	1	US-08-164-839-69 Sequence 69, Appl
27	71.5	10.6	2148	1	US-08-164-839-71 Sequence 71, Appl
28	71.5	10.6	2148	1	US-08-583-799-69 Sequence 69, Appl
29	71.5	10.6	2148	1	US-08-583-799-71 Sequence 71, Appl
30	71	10.5	3398	5	PCT-US95-08493-12 Sequence 12, Appl
31	68	10.1	999	4	US-09-830-217-15 Sequence 15, Appl
32	67.5	10.0	1170	4	US-09-252-991A-2073 Sequence 2073, Appl
33	67.5	10.0	1593	4	US-09-252-991A-5394 Sequence 5394, Appl
34	67	9.9	3345	4	US-08-630-915A-29 Sequence 29, Appl
35	66.5	9.8	4119	4	US-09-076-259-1 Sequence 1, Appl
36	66	9.8	971	4	US-08-630-915A-197 Sequence 197, Appl
37	66	9.8	1457	3	US-09-444-053-3 Sequence 3, Appl
38	66	9.8	1878	3	US-08-996-139-14 Sequence 14, Appl
39	66	9.8	1878	3	US-08-995-659-14 Sequence 14, Appl
40	66	9.8	1878	3	US-09-215-649A-14 Sequence 14, Appl
41	66	9.8	1878	4	US-09-577-780-14 Sequence 14, Appl
42	66	9.8	1878	4	US-09-577-800-14 Sequence 14, Appl
43	66	9.8	1878	4	US-09-466-496-14 Sequence 14, Appl
44	66	9.8	1878	4	US-09-871-856-14 Sequence 14, Appl
45	66	9.8	1878	4	US-09-871-291-14 Sequence 14, Appl

## ALIGNMENTS

### RESULT 1

US-08-578-649-1  
; Sequence 1, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajoleff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-3200  
; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 459 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 40..432  
 ; FEATURE:  
 ; NAME/KEY: sig peptide  
 ; LOCATION: 40..111  
 ; FEATURE:  
 ; NAME/KEY: mat peptide  
 ; LOCATION: 112..432  
 ;  
 ; US-08-578-649-1

Alignment Scores:  
 Pred. No.: 5,94e-31 Length: 459  
 Score: 277.50 Matches: 59  
 Percent Similarity: 64.71% Conservative: 29  
 Best Local Similarity: 43.38% Mismatches: 35  
 Query Match: 41.05% Indels: 6  
 DB: 1 Gaps: 6

US-10-019-455a-12 (1-128) x US-08-578-649-1 (1-459)

QY 1 MetAlaArgTLeLeuLeuLeuGlyGlyValValLeuCys-----Ala 17  
 DB 40 ATGGCCCGGTCCTGGTGTGCTT-----GGTGTCAATCACTTGTGTGCTTCTTC 93  
 QY 18 GlyHisGlyValPhe-----MetAspLysLeuSerSerLysLysLeuCysAlaAsp 34  
 DB 94 GGACCTGTGTGTCAGGGTGTGTCCTATGCCCAAGTGTGCTACCGGAAGCTGTGTGGGAC 153  
 QY 35 GluGluCysValTyrThrIleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAsp 54  
 DB 154 CAGGAGTACAGCCCTATCTCCATGGCTGTGGCCCTTCAGGACTACATGGCCCGGAC 213  
 QY 55 CysArgPheIleAspValLysGlyGlnGlnIleTyrValTyrSerLysLeuValThr 74  
 DB 214 TGCCGATTCCTGACCAITCACCGGGCCCAAGTGTGTATGTTCTTCTCAAGCTG----- 267  
 QY 75 GluAsnGlyAlaGlyGlu---PheTrpAlaGlySerValTyrGlyAspHisGlnAspGlu 93  
 DB 268 ---AAGGGCCGTGGCGGCTCTTCTGGGGAGGCGCTTCAGGAGATTACTATGGAGAT 324  
 QY 94 MetGlyIle---ValGlyTyrPheProSerAsnLeuValLysGluGlnArgValTyrGln 112  
 DB 325 CTGGCTGTGCTCGCTGGGCTATTCTCCCAAGTAGCATTGTCGAGAGGACGACCCCTGAAA 384  
 QY 113 GluAlaThrLysGluIleProThrThrAspIleAspPheCysGlu 128  
 DB 385 CTGGCAAAAGTCGATGTGAAGACACAAATGGGATTCTTACTGCCAG 432

# RESULT 2

US-08-578-649-18  
 ; Sequence 18, Application US/08578649  
 ; Patent No. 5770366

; GENERAL INFORMATION:  
 ; APPLICANT: Ulrich Bogdan  
 ; APPLICANT: Reinhard Buttner  
 ; APPLICANT: Brigitte Kaluza  
 ; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Felfe & Lynch  
 ; STREET: 805 Third Avenue  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10022

; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: PC-DOS  
 ; SOFTWARE: Wordperfect  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/578,649  
 ; FILING DATE: 29-July-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE P 43 24 247.2  
 ; FILING DATE: 20-July-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Andrew L. Tajoloff  
 ; REGISTRATION NUMBER: 31,575  
 ; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 688-9200  
 ; TELEFAX: (212) 838-3884  
 ; INFORMATION FOR SEQ ID NO: 18:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 330 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; FEATURE:  
 ; NAME/KEY: mat peptide  
 ; LOCATION: 7..327  
 ; FEATURE:  
 ; NAME/KEY: misc RNA  
 ; LOCATION: 4..6  
 ; OTHER INFORMATION: /function= "Startcodon Met"  
 ;  
 ; US-08-578-649-18

Alignment Scores:  
 Pred. No.: 7,49e-29 Length: 330  
 Score: 261.50 Matches: 49  
 Percent Similarity: 67.59% Conservative: 24  
 Best Local Similarity: 45.37% Mismatches: 30  
 Query Match: 38.69% Indels: 5  
 DB: 1 Gaps: 3

US-10-019-455a-12 (1-128) x US-08-578-649-18 (1-330)

QY 23 MetAspLysLeuSerSerLysLysLeuCysAlaAspGluGluCysValTyrThrIleSer 42  
 DB 13 ATGCCAAATAGCAGATCGTAAATATGTGAGATCAGGAGTGAGCCATCTCTCC 72  
 QY 43 LeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspValLys 62  
 DB 73 ATGGCTGTGGCCCTTCAGGACTACATGCCCCCGACTGCCGATTCCTGACCATCACCG 132  
 QY 63 GlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu---Phe 81  
 DB 133 GCCCAAGTGGTGTATGTTCTTCTCCAAAGCTG-----AAGGGCCGTGGCGGCTCTTC 183  
 QY 82 TrpAlaGlySerValTyrGlyAspHisGlnAspMetGlyIle---ValcIlyTyrPhe 100  
 DB 184 TGGGAGGCGCGCTTCAGGAGATTACTATGGAGATCTGGCTGCTCGCTATCTTC 243  
 QY 101 ProSerAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThr 120  
 DB 244 CCCAGTAGCATGTCCGAGGACCCAGACCCCTGGAACCTGGCAAGTCGATGTGAAGACA 303  
 QY 121 ThrAspIleAspPheCysGlu 128  
 DB 304 GACAAATGGGATTCTTACTGCCAG 327

# RESULT 3

US-08-578-649-4  
 ; Sequence 4, Application US/08578649  
 ; Patent No. 5770366

Db	305	CGCCAAAGTGGTGTATGTTCTTCTTCAAGTTG-----AAGGGCCGCGGGCGGCTTTTC	355
Db	305	CGCCAAAGTGGTGTATGTTCTTCTTCAAGTTG-----AAGGGCCGCGGGCGGCTTTTC	355
Qy	82	TrpAlaGlySerValTyGlyAspHisGlnAspGluMetGlyIle---ValGlyTyrPhe	100
Db	356	TGGGGAGGCAGTGTTCAGGGAGGTACTATGAGGACCTGGGAGCCCGCTGGCTATTTTC	415
Qy	101	ProSerAsnLeuValLysGluGlnArgValTyGlnGluAlaThrLysGluIleProThr	120
Db	416	CCAGTAGCATTTGTCGGGAGGACCTGAACTCGAAACCTGGCAAAATTGATATGAAGACC	475
Qy	121	ThrAspIleAspPheCysGlu	128
Db	476	GATCAATGGGATTCTACTGCCAG	499
RESULT 4			
US-08-578-649-8			
Sequence 8, Application US/08578649			
Patent No. 5770366			
GENERAL INFORMATION:			
APPLICANT: Ulrich Bogdan			
APPLICANT: Reinhard Butner			
APPLICANT: Brigitte Kaluza			
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN			
NUMBER OF SEQUENCES: 24			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Felte & Lynch			
STREET: 805 Third Avenue			
CITY: New York			
STATE: New York			
COUNTRY: USA			
ZIP: 10022			
COMPUTER READABLE FORM:			
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette			
COMPUTER: IBM PS/2			
OPERATING SYSTEM: PC-DOS			
SOFTWARE: Wordperfect			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/578,649			
FILING DATE: 29-July-1994			
CLASSIFICATION: 435			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: DE P 43 24 247.2			
FILING DATE: 20-July-1993			
ATTORNEY/AGENT INFORMATION:			
NAME: Andrew L. Tiajolloff			
REGISTRATION NUMBER: 31,575			
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (212) 688-9200			
TELEFAX: (212) 838-3884			
INFORMATION FOR SEQ ID NO: 8:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 305 base pairs			
TYPE: nucleic acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: cDNA			
FEATURE:			
NAME/KEY: CDS			
LOCATION: 110..499			
FEATURE:			
NAME/KEY: sig_peptide			
LOCATION: 110..178			
FEATURE:			
NAME/KEY: mat_peptide			
LOCATION: 179..499			
US-08-578-649-4			
Alignment Scores:			
Pred. No.: 2,1e-26			
Score: 581			
Percent Similarity: 247.00			
Best Local Similarity: 60.94%			
Query Match: 42.97%			
DB: 36.54%			
Gaps: 1			



[illegible]



Alignment Scores:  
 Pred. No.: 0.00544 Length: 2793  
 Score: 91.50 Matches: 23  
 Percent Similarity: 52.86% Conservative: 14  
 Best Local Similarity: 32.86% Mismatches: 20  
 Query Match: 13.54% Indels: 13  
 DB: 1 Gaps: 3

US-10-019-455A-12 (1-128) x US-07-646-537B-1 (1-2793)

QY 44 AlaAraGAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVallyLysGly 63  
 DB 2369 GCCAAGCCCGCTACGACTTCTGCGCGGACAGGTGCGAAGTCTTAAAGAGGCT 2428  
 QY 64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83  
 DB 2429 GATATCATC-----AAGATCCTCAATAAGAGGACAGCAAGCGTGGTGGCT 2476  
 QY 84 GlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103  
 DB 2477 GGGGAGATCTACGCGCG-----ATCGGCTGGTTCCTTCTTAAC 2515  
 QY 104 LeuVallyysGluGlnArgValTyrGlnGlu 113  
 DB 2516 TATGTGGAGGAGAC-----TATTCGAA 2539

## RESULT 8

US-08-306-691B-48  
 ; Sequence 48, Application US/08306691B  
 ; Patent No. 5734039  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Calabretta, Bruno  
 ; APPLICANT: Skorski, Tomasz  
 ; TITLE OF INVENTION: ANTIGENSE  
 ; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
 ; NUMBER OF SEQUENCES: 55  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
 ; STREET: Two Penn Center, Suite 1800  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19102  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
 ; COMPUTER: IBM PS/2  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/306,691B  
 ; FILING DATE: September 15, 1994  
 ; CLASSIFICATION: 514  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Monaco, Daniel A.  
 ; REGISTRATION NUMBER: 30,480  
 ; REFERENCE/DOCKET NUMBER: 8321-8  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-8383  
 ; TELEFAX: (215) 568-5549  
 ; TELEX: No. 5734039e  
 ; INFORMATION FOR SEQ ID NO: 48:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2757 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; US-08-306-691B-48  
 Alignment Scores:  
 Pred. No.: 0.00544 Length: 2793  
 Score: 91.50 Matches: 23  
 Percent Similarity: 52.86% Conservative: 14  
 Best Local Similarity: 32.86% Mismatches: 20  
 Query Match: 13.54% Indels: 13  
 DB: 1 Gaps: 3

Pred. No.: 0.0104 Length: 2757  
 Score: 89.50 Matches: 23  
 Percent Similarity: 52.86% Conservative: 14  
 Best Local Similarity: 32.86% Mismatches: 20  
 Query Match: 13.24% Indels: 13  
 DB: 1 Gaps: 3  
 US-10-019-455A-12 (1-128) x US-08-306-691B-48 (1-2757)  
 QY 44 AlaAraGAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVallyLysGly 63  
 DB 2325 GCCAAGCCCGCTACGACTTCTGCGCGGACAGGTGCGAAGTCTTAAAGAGGCT 2384  
 QY 64 GlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83  
 DB 2385 GACATCATC-----AAGATCCTTAAAGAGGACAGCAAGCGTGGTGGCGA 2432  
 QY 84 GlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103  
 DB 2433 GGGGAGATCTATGCGCG-----GTTGGCTGGTTCCTTCTTCAAC 2471  
 QY 104 LeuVallyysGluGlnArgValTyrGlnGlu 113  
 DB 2472 TACGTGGAGGAGAT-----TATTCGAA 2495

## RESULT 9

PCT-US93-06251-79  
 ; Sequence 79, Application PC/TUS9306251  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wickstrom, Eric and Rife, Jason P.  
 ; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing  
 ; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates  
 ; NUMBER OF SEQUENCES: 93  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: NY  
 ; COUNTRY: USA  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US93/06251  
 ; FILING DATE: 19930630  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Digiglio, Frank S.  
 ; REGISTRATION NUMBER: 31,345  
 ; REFERENCE/DOCKET NUMBER: 8586  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 516-742-4343  
 ; TELEFAX: 516-742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 79:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2757 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; PCT-US93-06251-79  
 Alignment Scores:  
 Pred. No.: 0.0104 Length: 2757  
 Score: 89.50 Matches: 23  
 Percent Similarity: 52.86% Conservative: 14  
 Best Local Similarity: 32.86% Mismatches: 20  
 Query Match: 13.24% Indels: 13  
 DB: 1 Gaps: 3

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US-10-019-455A-12 (1-128) x PCT-US93-06251-79 (1-2757)
QY 44 AlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspValIlyslsGly 63
Db 2325 GCGAAGCCCGTATGACTTCTGCGCCGCTGACCGTTCAGAGTCTGCTCAAGAGGGT 2384
QY 64 GlnGlnIleTyrValTyrSerIlyLeuValThrGluAsnGlyAlaGlyGluPheTrpAla 83
Db 2385 GACATCATC-----AAGATCCTTAAACAAGAGGACGAAGGCTGGTGGCGA 2432
QY 84 GlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsn 103
Db 2433 GCGGAGATCTATGCGCG-----GTTGGTGGTTCCTCCGCCAAC 2471
QY 104 LeuValIlyslsGlnArgValTyrGlnGlu 113
Db 2472 TACGTGAGGAGAT-----TATTCTGAA 2495

RESULT 10
US-09-300-958A-30
; Sequence 30, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 4762
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (428)
; NAME/KEY: unsure
; LOCATION: (462)
; US-09-300-958A-30

Alignment Scores:
Pred. No.: 0.0229 Length: 4762
Score: 89.50 Matches: 22
Percent Similarity: 52.24% Conservative: 13
Best Local Similarity: 32.84% Mismatches: 21
Query Match: 13.24% Indels: 11
DB: 4 Gaps: 2

US-10-019-455A-12 (1-128) x US-09-300-958A-30 (1-4762)
QY 41 IleSerLeuAlaArgAlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspVal 60
Db 2405 CTGGGCATTGCCATCGCTCGGTATGACTTCTGTCGAAGAGATATGAGAGTGTGCTCTG 2464
QY 61 LysIlyslsGlnGlnIleTyrValTyrSerIlyLeuValThrGluAsnGlyAlaGlyGlu 80
Db 2465 TTGAAGAGGAGATGTGGTGAAGATTACACAAAGATG-----AGTGCAAATGGC 2512
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 2513 TGGTGGAGAGAGAGAGTAAATGGCAGG-----GTGGGCTGGTGT 2551
QY 101 ProSerAsnLeuValIlyslsGlu 107
Db 2552 CCATCCACATATGTGAAGAG 2572

RESULT 11
US-09-300-958A-28
; Sequence 28, Application US/09300958A
; Patent No. 6495319
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John
; APPLICANT: Trenkle, Thomas
; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
; FILE REFERENCE: P-PH 3457
; CURRENT APPLICATION NUMBER: US/09/300,958A
; CURRENT FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/083,331
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/098,070
; PRIOR FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: 60/118,624
; PRIOR FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (428)
; NAME/KEY: unsure
; LOCATION: (462)
; US-09-300-958A-28

Alignment Scores:
Pred. No.: 0.00961 Length: 467
Score: 82.00 Matches: 24
Percent Similarity: 50.00% Conservative: 15
Best Local Similarity: 30.77% Mismatches: 27
Query Match: 12.13% Indels: 12
DB: 4 Gaps: 3

US-10-019-455A-12 (1-128) x US-09-300-958A-28 (1-467)
QY 46 AlaGlnGluAspTyrAsnAlaProAspCysArgPheIleAspValIlyslsGlnGln 65
Db 152 GCTCGGTATGACTTCTGTCGAAGAGATATGAGAGTGTCTCTGTTGAAAGGAGATGTG 211
QY 66 IleTyrValTyrSerIlyLeuValThrGluAsnGlyAlaGlyGluPheTrpAlaGlySer 85
Db 212 GTGAAGATTACACAAAGATG-----AGTGCAAATGGCTGTGGAGGGAGAA 259
QY 86 ValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPheProSerAsnLeuVal 105
Db 260 GTAAATGGCAGG-----GTGGGCTGGTTCATCCACATATGTG 298
QY 106 LysGluGlnArgValTyrGlnGluAlaThrLysGluIleProThrThrAspIle 123
Db 299 ---GGAAGGAGGATGAATAATTCAAATCCCGTGTTCGACCCCTGCACCAAAATT 349

RESULT 12
US-09-356-952-11
; Sequence 11, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Borlack-Sjodin, Ann
; APPLICANT: Margarit, S. M.
; APPLICANT: Bor-Sogli, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228N
; CURRENT APPLICATION NUMBER: US/09/356,952
; CURRENT FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631

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; EARLIER FILING DATE: 1998-07-21
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 5398
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-11

Alignment Scores:
Pred. No.: 1.06 Length: 5398
Score: 78.50 Matches: 24
Percent Similarity: 47.19% Conservative: 18
Best Local Similarity: 26.97% Mismatches: 36
Query Match: 11.61% Indels: 11
DB: 3 Gaps: 4

US-10-019-455A-12 (1-128) x US-09-356-952-11 (1-5398)
QY 26 LeuSerSerLysLysLeuCyAlaAspGluGluCysValTyrThrIleSerLeuAlaArg 45
Db 445 CTTTCTTTCTCCCTCCAGAGTGAGTTGACCGAGATTGTCCTCAATTGGAATAGTAGTC 504
QY 46 AlaGlnGluAspTyrAsnAlaPro-----AspCysArgPheIleAspVal 60
Db 505 GCTGCTTATGACTTTAATTATCCCAATTAAAAAGACAGAGTTCTTCGCAACTTTTGTCTGTA 564
QY 61 LysLysGlyGlnGlnIleTyrValTyrSerLysLeuValThrGluAsnGlyAlaGlyGlu 80
Db 565 CAAACAGGGGGAACCACTTATATCTACTTAACAAA-----AACTCATCTGGG--- 609
QY 81 PheTrpAlaGlySerValTyrGlyAspHisGlnAspGluMetGlyIleValGlyTyrPhe 100
Db 610 TGGTGGGATGGATTAGTTATTGACGACAGATTAATGGAAAGTTAAC---AGAGGCTGGTTT 666
QY 101 ProSerAsnLeuValLysGluGlnArg 109
Db 667 CCTCAAAACTTCGGTAGACCTTTAAGA 693

RESULT 13
US-08-164-839-3
; Sequence 3, Application US/08164839
; Patent No. 5514573
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; TITLE OF INVENTION: GENE ENCODING TRANSGlutAMINASE DERIVED
; TITLE OF INVENTION: FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/164,839
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/004,729
; FILING DATE: 14-JAN-1993
; ATTORNEY/AGENT INFORMATION:

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; NAME: Oblon, No. 5514573man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-599-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)412-3000
; TELEFAX: (703)413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2085 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Pagrus major
; TISSUE TYPE: liver
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2082
US-08-164-839-3

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Score: 77.00 Matches: 22
Percent Similarity: 52.50% Conservative: 20
Best Local Similarity: 27.50% Mismatches: 28
Query Match: 11.39% Indels: 10
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RESULT 14
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; Sequence 3, Application US/08583799
; Patent No. 5607849
; GENERAL INFORMATION:
; APPLICANT: YASUEDA, HISASHI
; APPLICANT: NAKANISHI, KAZUO
; APPLICANT: MOTOKI, MASAO
; APPLICANT: NAGASE, KAZUO
; APPLICANT: MATSUI, HIROSHI
; TITLE OF INVENTION: GENE ENCODING TRANSGlutAMINASE DERIVED
; TITLE OF INVENTION: FROM FISH
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: IBM PC compatible
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/593,799

FILING DATE: 14-JAN-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/004,729

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5607849man P.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-599-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)412-3000

TELEFAX: (703)413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 2085 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORGANISM: Pagrus major

TISSUE TYPE: liver

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2082

US-08-583-799-3

Alignment Scores:  
 Pred. No.: 0.44 Length: 2085  
 Score: 77.00 Matches: 22  
 Percent Similarity: 52.50% Conservative: 20  
 Best Local Similarity: 27.50% Mismatches: 28  
 Query Match: 11.39% Indels: 10  
 DB: 1 Gaps: 3

US-10-019-455A-12 (1-128) x US-08-583-799-3 (1-2085)

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RESULT 15

US-08-164-839-5

Sequence 5, Application US/08164839

Patent No. 5514573

GENERAL INFORMATION:

APPLICANT: YASUEDA, HISASHI

APPLICANT: NAKANISHI, KAZUO

APPLICANT: MOTOKI, MASAO

APPLICANT: NAGASE, KAZUO

APPLICANT: MATSUI, HIROSHI

TITLE OF INVENTION: GENE ENCODING TRANSGLUAMINASE DERIVED

NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 Jefferson Davis Highway, Fourth Floor  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: U.S.A.  
 ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/164,839

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/004,729

FILING DATE: 14-JAN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5514573man P.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 10-599-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)412-3000

TELEFAX: (703)413-2220

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2520 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORGANISM: Pagrus major

TISSUE TYPE: liver

FEATURE:

NAME/KEY: CDS

LOCATION: 34..2121

US-08-164-839-5

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US-10-019-455A-12 (1-128) x US-08-164-839-5 (1-2520)

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Tue Dec 30 10:20:39 2003

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 5777422

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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4	330	100.0	384	6	BD093103	BD093103 Novel pol
5	330	100.0	521	6	AX358818	AX358818 Sequence
6	330	100.0	521	6	AX362311	AX362311 Sequence
7	330	100.0	521	6	AX454774	AX454774 Sequence
8	330	100.0	521	6	AX491252	AX491252 Sequence
9	330	100.0	846	9	AF233261	AF233261 Homo sapi
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ALIGNMENTS

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LOCUS

DEFINITION

Novel polypeptide and DNA thereof.

ACCESSION

BD010816

VERSION

BD010816.1 GI:19639189

KEYWORDS

JP 2001069994-A/17.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 330)

Yoshimura,K. and Tanaka,H.

Novel polypeptide and DNA thereof

BD010816 330 bp DNA linear PAT 31-JAN-2002

JOURNAL Patent: JP 2001069994-A 17 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/17  
PD 21-MAR-2001  
PF 29-JUN-2000 JP 2000195911  
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI  
SHINICHI MOGI,  
HIDEYUKI TANAKA  
PI YOKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P19/02, PC  
A61P19/08,  
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC  
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DEFINITION Novel polypeptide and its DNA.  
ACCESSION BD093117  
VERSION BD093117.1 GI:22638705  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 330)  
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
Yoshimura, K. and Tanaka, H.  
TITLE Novel polypeptide and its DNA  
JOURNAL Patent: JP 2001069994-A 17 21-JAN-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/3

JOURNAL Patent: JP 2001069994-A 17 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/17  
PD 21-MAR-2001  
PF 29-JUN-2000 WO 2000JP004278  
PR 30-JUN-1999 JP 99P 186718  
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI  
MOGI,  
HIDEYUKI TANAKA  
PI YOKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA  
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC  
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Best Local Similarity 100.0%; Pred. No. 6.7e-90;  
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LOCUS Novel polypeptide and DNA thereof.  
DEFINITION Novel polypeptide and DNA thereof.  
ACCESSION BD010802  
VERSION BD010802.1 GI:18639175  
KEYWORDS JP 2001069994-A/3.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 384)  
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,  
Yoshimura, K. and Tanaka, H.  
TITLE Novel polypeptide and DNA thereof  
JOURNAL Patent: JP 2001069994-A 3 21-MAR-2001;  
TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2001069994-A/3

PD	11-JAN-2001
PF	29-JUN-2000 WO 2000JP004278
PR	30-JUN-1999 JP 99P 186718
PI	YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO,SHINICHI
PI	MOGI,
PI	YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC	C12N15/12,C12N25/10,C12P21/02,C07K14/47,C07K16/18,A61K45/00,PC
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Matches 330; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5
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ACCESSION  AX358818
VERSION     AX358818.1  GI:18675310
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
JOURNAL     Patent: WO 0193983-A 71 13-DEC-2001;
            Genentech Inc. (US)
FEATURES    Location/Qualifiers
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Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 CCCACCAAGGATATGACTTCTTCTGCGAG 330
Db 392 CCCACCAAGGATATGACTTCTTCTGCGAG 421

RESULT 7
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LOCUS      AX454774
DEFINITION Sequence 359 from Patent WO0208284.
ACCESSION  AX454774
VERSION     AX454774.1 GI:21714011
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE       Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL     Patent: WO 0208284-A 359 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
Hillan, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
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BASE COUNT  167 a      86 c      131 g      137 t
ORIGIN
Query Match      100.0%; Score 330; DB 6; Length 521;
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Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGC 60
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QY 121 AACGTTAAAAAGGCGCAGAGATCTATGTACTCAAAGCTGTGTAAGAAATGGAGCT 180
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Db 332 TATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTT 391
QY 301 CCCACCAAGGATATGACTTCTTCTGCGAG 330
Db 392 CCCACCAAGGATATGACTTCTTCTGCGAG 421

RESULT 6
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LOCUS      AX362311
DEFINITION Sequence 71 from Patent WO0208288.
ACCESSION  AX362311
VERSION     AX362311.1 GI:18694613
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL     Patent: WO 0208288-A 71 31-JAN-2002;
Genentech, Inc. (US)
FEATURES
source      1..521
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Best Local Similarity 100.0%; Pred. No. 7.1e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGC 60
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QY 301 CCCACCGGATATTGACTTCTCTCGCGAG 330
Db 392 CCCACCGGATATTGACTTCTCTCGCGAG 421

RESULT 8
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LOCUS Sequence 359 from Patent WO0200690.
DEFINITION AX491252
ACCESSION AX491252
VERSION AX491252.1 GI:223223963
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerttsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0200690-A 359 03-JAN-2002;
Genentech, Inc. (US)
FEATURES
Location/Qualifiers
source
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/organism="Homo sapiens"
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BASE COUNT 167 a 86 c 131 g 137 t
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Best Local Similarity 100.0%; Pred. No. 7.1e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTAGCTTCCAGAGAGCTCTGCGAGATGAGTGTC 60
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QY 61 TATACTATTTCTGCTAGTCTCAAGAGAGATTATATGCCCGGACTGTAGATTCA 120
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QY 181 GGAGAAATTTGGCTGGCAGTGTATGTGTATGTCGAGAGATGGAGTCTGGGT 240
Db 272 GGAGAAATTTGGCTGGCAGTGTATGTGTATGTCGAGAGATGGAGTCTGGGT 331

QY 241 TATTTCCCGAGAACTTGTCTCAAGAAAGAGCTGTGTACCGAGAGCTACCAAGGAATT 300
Db 332 TATTTCCCGAGAACTTGTCTCAAGAAAGAGCTGTGTACCGAGAGCTACCAAGGAATT 391

QY 301 CCCACCGGATATTGACTTCTCTCGCGAG 330
Db 392 CCCACCGGATATTGACTTCTCTCGCGAG 421

RESULT 9
AF233261 846 bp mRNA linear PRI 06-JUL-2000
LOCUS Homo sapiens otoraplin (OTOR) mRNA, complete cds.
DEFINITION AF233261
ACCESSION AF233261
VERSION AF233261.1 GI:8927427
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 846)
Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,
Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
A novel conserved cochlear gene, OTOR: identification, expression
analysis, and chromosomal mapping
Genomics 66 (3), 242-248 (2000)
20334619
MEDLINE
PUBMED
2 (bases 1 to 846)
Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,
Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
Direct Submission
Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75
Francis Street, Boston, MA 02115, USA
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Location/Qualifiers
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BASE COUNT 235 a 147 c 205 g 259 t
ORIGIN
Query Match 100.0%; Score 330; DB 9; Length 846;
Best Local Similarity 100.0%; Pred. No. 7.6e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTAGCTTCCAGAGAGCTCTGCGAGATGAGTGTC 60
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QY 301 CCCACCGGATATTGACTTCTCTCGCGAG 330
Db 399 CCCACCGGATATTGACTTCTCTCGCGAG 428

RESULT 10
AF243505 865 bp mRNA linear PRI 26-DEC-2000
LOCUS Homo sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.
DEFINITION AF243505
ACCESSION AF243505

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VERSION AF243505.1 GI:11991843
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 865)
AUTHORS Cohen-Salmon, M., Frenzy, D., Liu, W., Verpy, E., Voegelings, S. and
Petit, C.
TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
in vitro effect on the early differentiation of the inner ear
mesenchyme
J. Biol. Chem. 275 (51), 40036-40041 (2000)
JOURNAL
MEDLINE 20568254
PUBMED 10998416
REFERENCE 2 (bases 1 to 865)
AUTHORS Cohen-Salmon, M., Frenzy, D., Verpy, E., Voegelings, S. and Petit, C.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
du Dr. Roux, Paris 75015, France
FEATURES
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QY 1 CATGGAATATTATGGACCGCTAGCTTCCAGAGATTATAATGCCCGGACTGTAGATTCATT 120
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QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 180
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QY 301 CCCACACGATATTGACTTCTTCGCGAG 330
DB 362 CCCACACGATATTGACTTCTTCGCGAG 391
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DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093121
LOCUS BD093121

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DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010820
VERSION BD010820.1 GI:18639193
KEYWORDS JP 200106994-A/21.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 923)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 200106994-A 21 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 200106994-A/21
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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Best Local Similarity 100.0%; Pred. No. 7.6e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 388 CCCACACGATATTGACTTCTTCGCGAG 417
RESULT 12
BD093121
LOCUS BD093121
DEFINITION Novel polypeptide and its DNA.
ACCESSION BD093121

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VERSION	BD093121.1	GI:22638709
KEYWORDS	WO 0102564-A/21	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 923)	
AUTHORS	Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y., Yoshimura, K. and Tanaka, H.	
TITLE	Novel polypeptide and its DNA	
JOURNAL	Patent: WO 0102564-A 21 11-JAN-2001; TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA	
COMMENT	OS Homo sapiens (human) PN WO 0102564-A/21 PD 11-JAN-2001 PF 29-JUN-2000 WO 2000JP004278 PR 30-JUN-1999 JP 99P 186718 PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC A61K38/17, A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/02, C12R1:19) PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/02, C12R1:19) CC FH	
FEATURES	source	
BASE COUNT	303 a 147 c 213 g 260 t	
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Best Local Similarity	100.0%; Pred. NO. 7.6e-90;	
Matches 330; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
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QY	61 TATACTATTCTCTGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 120	
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QY	121 AAGCTTAAAAAGGGCAGCAGATCTATGTCTACTCAAGCTGGTAAAGAAAATGGAGCT 180	
Db	208 AAGCTTAAAAAGGGCAGCAGATCTATGTCTACTCAAGCTGGTAAAGAAAATGGAGCT 267	
QY	181 GGAATATTTGGCGTGGCTGTTATGTTGATGGCCAGCAGATGGAGTCGTGGGT 240	
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QY	241 TATTTCCCAAGCACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAATT 300	
Db	328 TATTTCCCAAGCACTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAATT 387	
QY	301 CCCACACGATATTTGACTTCTCTCTGGAG 330	
Db	388 CCCACACGATATTTGACTTCTCTCTGGAG 417	
RESULT 13		
LOCUS	HS2424552	
DEFINITION	Homo sapiens mRNA for melanoma inhibitory activity like protein (MIAL gene).	
ACCESSION	AJ242452	
VERSION	AJ242452.1	GI:12619172

KEYWORDS	melanoma inhibitory activity like protein; Mial gene.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 1422)
AUTHORS	Rendtorff, N.D., Frodin, M., Attie-Bitach, T., Vekemans, M. and Tommerup, N.
TITLE	Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation
JOURNAL	Genomics 71 (1), 40-52 (2001)
MEDLINE	21100875
PUBMED	11161796
REFERENCE	2 (bases 1 to 1422)
AUTHORS	Rendtorff, N.D.
TITLE	Direct Submission
JOURNAL	Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK
REMARK	Revised by author 03-AUG-1999
COMMENT	Related sequences: AJ243939 (Mus musculus mRNA) Related sequences: AJ252324 to AJ252327 (genomic sequence).
FEATURES	Location/Qualifiers
source	1..1422 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="20" /map="20p11.22-12.2" /tissue type="brain and cochlea" /dev stage="fetal" 1..1422 /gene="MIAL" <1..1422 /gene="MIAL" /product="melanoma inhibitory activity like protein" 1..387 /gene="MIAL" /codon_start=1 /product="melanoma inhibitory activity like protein" /protein_id="CAC27443.1" /db_xref="GI:12619173" /translation="MARILLFLPGLVAVCAVHGFMRLASKKLCADCECVTTISLA SAQEDYNAPDCRFINVKQQIIVYVSKLVKENGACEFWAGSVYGDQDMGVGVFPR NLVKEQRTVEATKEVFTTIDDFCE" 1..75 /gene="MIAL" 76..384 /gene="MIAL" /product="melanoma inhibitory activity like protein" <1..115 /gene="MIAL" /number=1 116..257 /gene="MIAL" /number=2 115..116 /gene="MIAL" /number=1 258..363 /gene="MIAL" /number=3 257..258 /gene="MIAL" /number=2 364..387 /gene="MIAL" /number=4 363..364 /gene="MIAL" /number=3 388..1422
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3'UTR	

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BASE COUNT      417 a      220 c      306 g      479 t
ORIGIN
Query Match      100.0%; Score 330; DB 9; Length 1422;
Best Local Similarity 100.0%; Pred. No. 8.1e-90;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010817
VERSION BD010817.1 GI:18639190
KEYWORDS JP 2001069994-A/18.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
JOURNAL Novel polypeptide and DNA thereof
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Mus sp. (mouse)
PN JP 2001069994-A/18
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PI PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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Best Local Similarity 85.4%; Pred. No. 4.5e-66;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 CATGGAATATTATTTGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 60
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ACCESSION BD093118
VERSION BD093118.1 GI:22638706
KEYWORDS WO 0102564-A/18.
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and its DNA
JOURNAL Patent: WO 0102564-A 18 11-JAN-2001;
TAKEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO
OGI, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,
HIDEYUKI TANAKA
COMMENT OS Mus sp. (mouse)
PN WO 0102564-A/18
PD 11-JAN-2001
PF 29-JUN-2000 WO 2000JP004278
PF 30-JUN-1999 JP 99P 186718
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PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI
MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC
A61K38/17,
PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088// (C12P21/
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BASE COUNT 91 a 60 c 92 g 87 t
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Tue Dec 30 10:20:39 2003

us-10-019-455a-23.rge

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Best Local Similarity 85.4%; Pred. No. 4.5e-66;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

Qy      1 CATGGAATATTATGGACCGTCTAGCTTCAAGAAGCTCTGTGCAGATGATGATGTGTC 60
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Qy    241 TATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 300
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Job time : 1046 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: December 30, 2003, 01:02:37 ; Search time 1098.31 Seconds  
(without alignments)  
7302.593 Million cell updates/sec

Title: US-10-019-455A-23  
Perfect score: 330  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues  
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
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16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
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23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rpd:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	252.2	76.4	514	13	BQ568498
4	252.2	76.4	534	13	BQ564134

5	252.2	76.4	560	13	BQ569741	BQ569741	g1135f01.
6	252.2	76.4	608	13	BQ564944	BQ564944	g127g09.y
7	252.2	76.4	630	13	BQ568471	BQ568471	g1108g04.
8	252.2	76.4	684	13	BQ563768	BQ563768	g106c09.y
9	252.2	76.4	696	10	BQ611549	BQ611549	BQ611549
10	250.6	75.9	474	13	BQ565637	BQ565637	g142g03.y
11	238.6	72.3	409	13	BQ566932	BQ566932	g173g09.y
12	236.6	71.7	604	13	BQ567343	BQ567343	g188d08.y
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16	192.4	58.3	485	13	BQ565179	BQ565179	g132a07.y
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18	164.6	49.9	588	13	BQ566776	BQ566776	g169b07.y
19	158	47.9	280	13	BQ568785	BQ568785	g1114f04.
20	157.4	47.7	349	9	AW023324	AW023324	df53d01.y
21	131.6	39.9	338	9	AW021345	AW021345	df21c01.y
22	129	39.1	1201	13	EX418941	EX418941	EX418941
23	128.6	39.0	978	13	EX444840	EX444840	EX444840
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32	83.6	25.3	646	13	BQ563767	BQ563767	g106c09.x
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ALIGNMENTS

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DEFINITION clone g1143b10 5', mRNA sequence.  
ACCESSION BQ570035  
VERSION BQ570035.1 GI:21473352  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 398)  
AUTHORS Kachar,B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 143 row: b column: 10  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers

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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACGTACGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."
BASE COUNT      105 a      69 c      116 g      108 t
ORIGIN
Query Match      76.4%; Score 252.2; DB 13; Length 398;
Best Local Similarity 85.4%; Pred. No. 9.5e-64;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 CATGGAATATTATGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60

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Db 67 CATGGTATTATGGATAAACCTTCTTCTAAGAGTTGTGTCGGATGAGGAGTGTGTC 126

QY 61 TATACTATTTCTCGGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCAATT 120

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QY 121 AACGTTAAAAAGGCGCAGCATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 180

Db 187 GATGTCAAGAAGGCGCAGCATCTATGTGTACTTCCAGCTGTGTAAAGAAACGGAGCT 246

QY 181 GGAGAAATTTGGGCTGGCAGTGTATTATGGTATGGCCAGCAGCATGGAGTGTGGGT 240

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QY 301 CCCACACGAGTATTGACTTCTTCTGCGA 329

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RESULT 2

BQ564607

LOCUS

DEFINITION

gi19h02.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi19h02 5', mRNA sequence.

ACCESSION

BQ564607

VERSION

BQ564607.1 GI:21467924

KEYWORDS

EST.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 488)

Kachar,B.S.

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

TITLE

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL

Unpublished

COMMENT

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

5074249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 19 row: h column: 02

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

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/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACGTACGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."





recombinants. Stratagene's ExAssist Interference resistance helper phage (Catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t

## ORIGIN

Query Match 76.4%; Score 252.2; DB 13; Length 514;  
Best Local Similarity 85.4%; Pred. No. 1.1e-63;  
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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QY 301 CCCACACGGATATTGACTTCTTCTGCGA 329  
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Db 359 CCAACACGGATATTGACTTCTTCTGCGA 387  
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RESULT 4  
BQ564134 534 bp mRNA linear EST 19-JUN-2002  
LOCUS gill1d01.y1 Mouse Organ of Corti cDNA pluescript Mus musculus cDNA  
DEFINITION clone gill1d01 5', mRNA sequence.  
ACCESSION BQ564134  
VERSION BQ564134.1 GI:21467451  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 534)  
AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharbenid@nih.gov  
Plate: 11 row: d column: 01  
Seq primer: M13RPL reverse primer (ABI).  
Location/Qualifiers

FEATURES  
source

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/clone\_lib="Mouse Organ of Corti cDNA pluescript"  
organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the Micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 µg mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 µl of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 155 a 87 c 148 g 144 t

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Query Match	76.4%; Score 252.2; DB 13; Length 534;
Best Local Similarity	85.4%; Pred. No. 1.1e-63;
Matches 281; Conservative	0; Mismatches 48; Indels 0; Gaps 0;
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DB	
QY	57 CATGGTGATTATGATAAATCTTCTTAAGAAGTTGTGTGGGATGAGGAGTGTGC 116
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QY	61 TATACTATTCTCTGCTAGTCTCAGAGAGATTATAATGCCCGGACTGTAGATTCATT 120
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QY	117 TATACTATTCTCTGCAAGAGACAGAGAGATTACAATGCCCGGACTGTAGTTCATC 176
DB	
QY	121 AACGTTAAAAAGCGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAATGAGCT 180
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QY	177 GATGTCAGAAAGGCGACGAGATCTATGTTTACTCAAGCTGTGTAAGAAATGAGCT 236
DB	
QY	181 GGAGAAATTTGGCTGGCAGTGTATGTTGATGGCCAGCAGATGGGAGTCGGGT 240
DB	
QY	237 GGAGAGTTTGGCTGGCAGTGTATGTTGATGGCCAGCAGATGGGAGTTGAGGT 296
DB	
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DB	
QY	297 TATTTCCCGAGCACTTGTGTCAAGGACACGCTGTGTATACCAAGGAGATC 356
DB	
QY	301 CCCACACGAGATTTGACTTCTTCTGCGA 329
DB	
QY	357 CCAACACGAGTATTGACTTCTTCTGGA 385
DB	
RESULT 5	
BO569741	560 bp mRNA linear EST 19-JUN-2002
LOCUS	g1135f01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION	clone g1135f01 5', mRNA sequence.
ACCESSION	BO569741
VERSION	BO569741.1 GI:21473058
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 560)
JOURNAL	Kachar,B.
COMMENT	EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing
Unpublished	
Contact: Kachar,B.	
Structural Cell Biology	
National Institute of Deafness and other Communication Disorders	
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA	
Tel: 301-402-1599	
Fax: 301-402-1765	
Email: kachar@nidcd.nih.gov	
Seg primer: M13RP1 reverse primer (ABI).	
Location/Qualifiers	
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/clone_lib="Mouse Organ of Corti cDNA pBluescript"	
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla	
FEATURES	
source	

BASE COUNT	160 a	92 c	154 g	153 t	
ORIGIN					
Query Match	76.4%;	Score 252.2;	DB 13;	Length 560;	
Best Local Similarity	85.4%;	Pred. No. 1.1e-63;			
Matches 281; Conservative	0;	Mismatches 48;	Indels	0;	Gaps 0;
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DB	120	TATACTATTCTCTGGCAAGAGACAGAGAGATTACATGCCCGGACTGTAGTTCATC	179		
QY	121	AACGTTAAAAAGCGCAGCAGATCTATGTGTACTCAAGCTGTGTAAGAAATGAGCT	180		
DB	180	GATGTCAGAAAGGCGCAGCAGATCTATGTTTACTCAAGCTGTGTAAGAAATGAGCT	239		
QY	181	GGAGAAATTTGGCTGGCAGTGTATGTTGATGGCCAGCAGATGGGAGTCGGGT	240		
DB	240	GGAGAGTTTGGCTGGCAGTGTATGTTGATGGCCAGCAGATGGGAGTTGAGGT	299		

was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug RNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25x strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

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QY 241 TATTTCACAGGAACTGGTCAAGAACACGCTGTGTACACGAGGAGCTACCAAGGAGTT 300
DB |||||||
QY 300 TATTTCACAGGAACTGGTGTGAGGACGACGCTGTGTATACGAGGAGGCCACCAAGGAGATC 359
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QY 301 CCCACACGAGATATTGACTTCTTCTGCGA 329
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RESULT 6
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LOCUS g127g09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
DEFINITION clone g127g09 5', mRNA sequence.
ACCESSION BQ564944
VERSION BQ564944.1 GI:21468261
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 608)
Kachar,B.
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished
Contact: Kachar,B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 27 row: g Column: 09
Seq primer: M13RPA reverse primer (ABI).
Location/Qualifiers
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/dev_stage="Post natal day 5 to 13"
/clone_lib="Mouse Organ of Corti cDNA pBluescript"
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

```

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BASE COUNT 169 a 107 c 166 g 166 t  
ORIGIN

Query Match 76.4%; Score 252.2; DB 13; Length 608;  
Best Local Similarity 85.4%; Pred. No. 1.2e-63;  
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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QY 67 CATGGTATTATTATGATAAACTTCTTCTAAGAAGTTGTGTGCGATGAGAGTGTCTC 126
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QY 121 AACGTTAAAAGGCGACAGATCTATGTGTACTCAAAGCTGGTAAAAAGAAATGGAGCT 180
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QY 187 GATGTCAGAAAGGCGACAGATCTATGTTTACTCAAGCTGGTAAACAGAAACGAGCT 246
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DB |||||||
QY 367 CCAACACGAGATATTGACTTCTTCTGTGA 395
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RESULT 7  
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DEFINITION clone g1108g04 5', mRNA sequence.  
ACCESSION BQ568471  
VERSION BQ568471.1 GI:21471788  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 630)

Kachar, B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 108 row: g column: 04  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
1. 630  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/clone="g108g04"  
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/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti: Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with GigaPack III Gold and, upon titration on Xl1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

178 a 111 c 167 g 174 t

BASE COUNT  
ORIGIN

Query Match 76.4%; Score 252.2; DB 13; Length 630;  
Best Local Similarity 85.4%; Pred. No. 1.2e-63;  
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGGAATTTATGACCGCTCTAGCTTCCAGAAAGCTCTGTCCAGATGATGATGATGTC 60  
DB 67 CATGGGTATTTATGGATAAATCTTCTTAAAGATTTGTGCGGATGAGGATGTC 126  
QY 61 TATACTATTTCTGTGGCTAGTGTCTCAAGAGATTTATAATGCCCGGAGCTGTAGATTCATT 120  
DB 127 TATACTATTTCTGTGGCAAGAGCACAGGAAGATTACATGCCCGGAGCTGTAGGTTTCATC 186  
QY 121 AAGTTTAAAGGGGAGGAGATCTATGTCTACTCAAGCTGTGTAAGAAATGAGCT 180  
DB 187 GATGTCAAGAAAGGGGAGGAGATCTATGTTTACTTCAAGCTGTGTAAGAAATGAGCT 246  
QY 181 GGGAATTTGGGCTGGCAGTGTATGTGTGATGGCCAGGAGATGGGAGTCTGGGT 240  
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QY 241 TATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCAAGAAAGCTACCAAGGAAGTT 300  
DB 307 TATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTATACCAAGGAAGCTACCAAGGAAGTT 366  
QY 301 CCACACGAGATATGACTTCTTCTCGGA 329  
DB 367 CCAACACGAGATATGACTTCTTCTGTGA 395

RESULT 8  
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DEFINITION BQ563768.1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi06c09 5', mRNA sequence.  
ACCESSION BQ563768  
VERSION BQ563768.1 GI:21466749  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 684)  
AUTHORS Kachar, B.  
TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 06 row: c column: 09  
Seq primer: M13RPI reverse primer (ABI).  
Location/Qualifiers  
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FEATURES  
source

/clone.lib="Mouse Organ of Corti cDNA pluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (AMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25x Strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 194 a 120 c 178 g 192 t  
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 Best Local Similarity 85.4%; Pred. No. 1.2e-63;  
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 QY 61 TATACATTTTCTGGTAGTGTCTCAGAGAGATTATATCCCGCGACTCTAGATTCATT 120  
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 DEFINITION BB611549 RIKEN full-length enriched, 13 days embryo head Mus musculus cDNA clone 3110083012 5', mRNA sequence.  
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 VERSION BB611549.1 GI:15393547  
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 REFERENCE 1 (bases 1 to 696)  
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.  
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)  
 Unpublished  
 Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
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 Fax: 81-45-503-9216  
 Email: genome-res@gsr.riken.go.jp  
 URL:http://genome.gsc.riken.go.jp/  
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
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 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishii,Y. and Hayashizaki,Y.  
 Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Funct. Genomics 2 pre, L72-L86 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
 e mouse tissues.  
 Location/Qualifiers

FEATURES

JOURNAL  
COMMENT

Unpublished

Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 42 row: 9 column: 03  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

FEATURES  
source

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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 50.0. Second strand
cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTTAATTAATTAATTCCTCCCTCCCCCCC 3']. cDNA
was cleaved with XhoI and SstI."
204 a 122 c 176 g 194 t
BASE COUNT
ORIGIN

Query Match 76.4%; Score 252.2; DB 10; Length 696;
Best Local Similarity 85.4%; Pred. No. 1.2e-63;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 1 CATGGAATATTATGACCGCTAGCTTCCAGAGAGCTGTGCGAGATGAGTGTGTC 60
DB 78 CATGCTGATTATGATGAATCTTCTTCTTAAGAGTTGTGTGCGATGAGGAGTGTGTC 137
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RESULT 10
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clone gi42903 5', mRNA sequence.
ACCESSION B0565637
VERSION B0565637.1 GI:21468954
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 474)
AUTHORS Kachar, B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing

```

Unpublished

Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 42 row: 9 column: 03  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers

FEATURES  
source

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organ of Corti (OC) was fine dissected from a total of 386
OC as follows: 102 samples from post-natal (P) day 5; 72
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
14 from P12 and 24 from P13. After killing animals by
cervical dislocation followed by decapitation, the bulla
was removed and opened in Leibowitz medium. The bony
capsule of the cochlea was chipped away, stria vascularis
and spiral ligament were removed and the sensory
epithelium was carefully dissected out of the modiolus.
Total RNA was extracted using the micro Fasttrack kit
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according
to manufacturer's instructions. Reverse transcription and
library construction were carried out with the Uni-Zap XR
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
Gigapack III Gold Cloning kit (catalog # 237612), both
from Stratagene (La Jolla, CA, USA), according to
manufacturer's instructions. Briefly: 1.5 ug mRNA was
reverse transcribed using a hybrid oligo(dT) linker-primer
that contains an Xho I site. First strand synthesis was
primed with the linker- primer and transcribed using
Moloney murine leukemia virus reverse transcriptase
(MMLV-RT) and 5-methyl dCTP. The second strand was
synthesized with DNA polymerase and RNase H. Complementary
DNA was blunt ended with Pfu DNA polymerase, ligated with
EcoR I adaptors in the presence of ligase and digested
with Xho I. The cDNA was sequentially size fractionated
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)
and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA)
columns to enrich for cDNAs greater than 400bp and 1000 bp
, respectively. The cDNA was then directionally ligated to
the Uni-ZAP XR vector, which had been predigested with
EcoR I and Xho I. The phagemid was packaged with Gigapak
III Gold and, upon titration on XL1 Blue MRF+ cells, the
yield of the phage library was estimated to be 11,100,000
recombinants. Stratagene's ExAssist Interference
resistance helper phage (catalogue # 211203) was adopted
to rescue plasmid DNA from the phages. Upon plating of the
rescued library, individual cDNA clones were selected and
grown in 96-well, 2 ml growth plate. Plasmid DNA was
purified from 200 ul of saturated culture with the
Concert96(TM) plasmid purification kit (Invitrogen,
Carlsbad, CA) as instructed by the manufacturer. ESTs from
the 5' end of the cDNA clones were generated with the
universal M13 reverse primer (CAGGAACAGCTATGACC) and 25'
strength BigDye terminator sequencing chemistry (Applied
Biosystems, Foster City, CA). Sequencing reactions were
performed on MJ Tetrad thermal cyclers (MJ Research,
Waltham, MA), and analyzed on 3700 automated capillary
sequencers using POPs polymer (Applied Biosystems, Foster
City, CA). The frequency distribution of the library is
as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10;
1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of

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genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

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Query Match      75.9%; Score 250.6; DB 13; Length 474;
Best Local Similarity 85.1%; Pred. No. 3.1e-63;
Matches 280; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
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clone gi73g09 5', mRNA sequence.
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VERSION   BQ566932.1 GI:21470249
KEYWORDS  EST.
SOURCE    Mus musculus (house mouse)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 409)
Kachar.B
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished
Contact: Kachar.B.
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kacharbenidcd.nih.gov
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## FEATURES

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Matches 279; Conservative 0; Mismatches 49; Indels 1; Gaps 1;

OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have know function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."



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clone gi88d08 5', mRNA sequence.
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VERSION BQ567343
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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REFERENCE
AUTHORS Kachar,B.
TITLE EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
JOURNAL Unpublished
COMMENT Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
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Seq primer: M13RP1 reverse primer (ABI).

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```

DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on Xli Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

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BASE COUNT 178 a 108 c 152 g 166 t
ORIGIN

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Query Match 71.7%; Score 236.6; DB 13; Length 604;
Best Local Similarity 87.0%; Pred. No. 4.8e-59;
Matches 260; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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Qy 91 GATTATATGCCCCGAGCTGTAGATTCTATTAACGTTAAAGGCGCAGCATCTATGTG 150
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RESULT 13
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LOCUS
DEFINITION gi37b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi37b12 5', mRNA sequence.
ACCESSION
VERSION BQ565411
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

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BQ565411 490 bp mRNA linear EST 19-JUN-2002
gi37b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi37b12 5', mRNA sequence.
BQ565411
BQ565411.1 GI:21468728
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 490)
REFERENCE

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Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
22354683  
12466851  
Contact: Yoshitake Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.go.jp/  
URL: http://genome.gsc.riken.go.jp/  
Aizawa, K., Akimura, T., Akakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha, NE 68131 USA ) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

# FEATURES

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/mol\_type="mRNA"  
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Best Local Similarity 85.0%; Pred. No. 1.1e-53;  
Matches 244; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

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DB TATACATATTTCTCGGCAAGAGCACAGGAAGATTACAAATGCCCCAGACTGTAGTTTCATC 197  
QY 121 AACGTTAAAAAGGGCAGCAGATCTATGTCTCAAGCTGTGTAAAGAAATGGAGCT 180  
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QY 181 GGAGAAATTTGGGCTGGCAGTGTATGCTGATGGCCAGGACGAGATGGGAGTCGTGGGT 240  
DB 258 GGAGAGTTTGGGGCTGGCAGTGTATGCTGATGGCCAGGATGAGATGGGAATGTAGGT 317  
QY 241 TATTTCCCGAGGAAGTGTGTCAAGAACAGCGTGTGTACAGGAAGC 287  
DB 318 TATTTCCCGAGGAAGTGTGTGTGAAGGAGCAGCGTGTATACAGGAGGC 364

## RESULT 15

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CH3#018 G05T7 Canine heart normalized cDNA library in pBluescript  
Canis familiaris cDNA clone CH3#018\_G05 5', mRNA sequence.  
ACCESSION BU748241 GI:23700286  
VERSION BU748241.1  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 795)  
AUTHORS Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.  
TITLE Expressed sequence tags from Canine heart  
JOURNAL Unpublished  
COMMENT Other ESTs: CH3#018\_G05T3  
Contact: George A.L. G05T3  
Division of Genetic Medicine  
Vanderbilt University  
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA  
Tel: 615 936 2660  
Fax: 615 936 2661  
Email: al.george@vanderbilt.edu  
Insert Length: 1892 Std Error: 0.00  
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High quality sequence stop: 559.

## FEATURES

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/note="Organ: heart; Vector: pBluescript; Site 1: 5' of vector NotI; Site 2: 3' of vector EcoRI; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction: oligo-dT primed"  
BASE COUNT 199 a 176 c 195 g 225 t  
ORIGIN

Query Match 60.2%; Score 198.6; DB 13; Length 795;  
Best Local Similarity 86.2%; Pred. No. 9.9e-48;  
Matches 232; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

QY 62 ATACTATTTCTCGGTAGTGTCAAGAGATTAATATGCCCGGACTGTAGATTCATTA 121  
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QY 122 ACCTTAAAAAGGGCAGCAGATCTATGTCTCAAGCTGTGTAAAGAAATGGAGCTG 181  
DB 316 ATGTGAAAAAGGACAGCAGATTTACGTTTACTCGAGCTGTGTAAAGAAATGGAGCTG 375  
QY 182 GGAATATTTGGGCTGGCAGTGTATGCTGATGGCC---AGGACGAGATGGGAGTCGTGG 238  
DB 376 GAAATATTTGGGCTGGCAGTGTATGCTGATGGACACGAGGATGAGATGGGAACCGGG 435

Qy	239	GTTATTTC	CCCCAGGA	ACTTCG	TCAAGGA	CAGCGT	GTGTAC	CCAGGA	AGCTAC	CAAGGA	G 298
Db	436	GCTATTTC	CCCCAGCA	GCTTCG	TGGAGG	AGCAAC	ACACGT	GTACCA	AGAGCC	CAAGGA	G 495
Qy	299	TTCCAC	CCAGGA	TATTGA	CTTCTT	CTGC	327				
Db	496	TCCCCA	CTACGA	CATTGA	CTTCTT	CTGC	524				

Search completed: December 30, 2003, 06:07:15  
Job time : 1098.64 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 29, 2003, 22:01:01 ; Search time 109.538 Seconds  
(without alignments)  
8132.484 Million cell updates/sec

Title: US-10-019-455A-23

Perfect score: 330

Sequence: 1 catggaatattatgacgcg.....attatgacttttttgcgag 330

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 19Jun03:\*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA1981.DAT:\*
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- 25: /SIDS1/gcgdata/geneseq/geneseq-emb1/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Match	Length	DB ID	Description
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2	330	100.0	384	22	AAF59065	Human MLP nucleoti
3	330	100.0	387	24	AA517583	DNA encoding novel
4	330	100.0	426	22	AAH26341	Human growth regul
5	330	100.0	521	24	ABL95740	Human angiogenesis
6	330	100.0	521	24	ABL88251	Human PRO9873 cDNA
7	330	100.0	521	24	ABK33571	cDNA encoding huma
8	330	100.0	891	22	AAH98228	Human EST-derived

9	330	100.0	891	22	AAH26342	Human growth regul
10	330	100.0	923	22	AAF59083	Human MLP nucleoti
11	330	100.0	1201	22	AAH26343	Human growth regul
12	252.2	76.4	330	22	AAF59080	Mouse MLP nucleoti
13	252.2	76.4	384	22	AAF59068	Mouse MLP nucleoti
14	252.2	76.4	947	22	AAF59084	Mouse MLP nucleoti
15	249	75.5	330	22	AAF59099	Rat MLP nucleotide
16	249	75.5	384	22	AAF59098	Rat MLP nucleotide
17	214.6	65.0	307	22	AAF59093	Rat MLP nucleotide
18	193.8	58.7	261	22	AAF59092	Rat MLP nucleotide
19	63.4	19.2	433	22	AAH47783	Recombinant human
20	63.4	19.2	459	16	AAQ84050	Sequence encoding
21	63.4	19.2	459	22	AAI70083	Melanoma inhibitor
22	63.4	19.2	459	22	AAI18732	Human antisense ol
23	63.4	19.2	555	23	ABV59229	Human prostate exp
24	63.2	19.2	581	16	AAQ84052	Sequence encoding
25	61.8	18.7	442	24	ABL63602	Breast cancer rela
26	61.8	18.7	442	24	ABL64012	Breast cancer rela
27	57.4	17.4	330	16	AAQ84061	Sequence encoding
28	54.2	16.4	305	16	AAQ84055	Amplified fragment
29	53.6	16.2	300	20	AAZ14828	Human gene express
30	53.6	16.2	429	22	AA522695	Human cDNA encodin
31	53.6	16.2	884	22	AA522459	Human TANGO 130 pa
32	53.6	16.2	1230	24	ABQ79850	Human TANGO 130 CD
33	53.6	16.2	1263	21	AAZ51245	Human TANGO 130 po
34	53.6	16.2	1263	24	ABQ79849	Human prostate exp
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37	53.6	16.2	4409	23	ABV26878	Human prostate exp
38	53.6	16.2	4409	23	ABV29625	Human prostate exp
39	53.6	16.2	5724	24	ABQ79852	Human TANGO 130 po
40	53.6	16.2	8121	24	ABQ79851	Human TANGO 130 po
41	52	15.8	417	22	AAH93775	Human protein enco
42	46	13.9	1060	22	AAF92140	Human PRO19670 cDN
43	46	13.9	1060	24	AB574460	Human cDNA encodin
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#### ALIGNMENTS

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XX AAF59079;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human MLP nucleotide sequence SEQ ID NO:23.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX cardiant; gene therapy; secretory cell function regulator; promoter;  
XX inhibitor; ds.

XX OS Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

XX Tanaka H;

XX WPI; 2001-159271/16.

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; PRIOR FILING DATE: 1999-08-17
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; PRIOR APPLICATION NUMBER: 60/169835

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Best Local Similarity 100.0%; Pred. No. 7.2e-100;
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; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28

; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-063-71

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QY 1 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGC 60
Db CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGC 151
QY 61 TATACTATTTCTGGCTAGTGTCTCAAGAGATTATTAATGCCCGGACTGTAGATTCATT 120
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QY 121 AACGTTAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCT 180
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QY 181 GGAGAAATTTGGCTGGCAGTGTATGTGTATGCGCAGACAGATGGAGTGTGGGT 240
Db GGAGAAATTTGGCTGGCAGTGTATGTGTATGCGCAGACAGATGGAGTGTGGGT 331
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC27
; CURRENT APPLICATION NUMBER: US/10/219,066
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; PRIOR APPLICATION NUMBER: 10/119,480
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; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-066-71

Query Match      100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGATATTATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 60
DB 92 CATGGATATTATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACTATTTCTGTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGAGCTGTAGATTCAAT 120
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QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCT 271

QY 181 GGAGAAATTTTGGGCTGGCAGTGTATTTATGGTGTATGTCAGGAGCAGATGGGAGTCTGGGT 240
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DB 332 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAAAGCTACCAAGGAAGTT 391

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DB 392 CCCACACGGATATTGACTTCTTCTGCGAG 421

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; Publication No. US20030187204A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C51

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; CURRENT APPLICATION NUMBER: US/10/219,067
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-067-71

Query Match      100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGATATTATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 60
DB 92 CATGGATATTATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACTATTTCTGTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGAGCTGTAGATTCAAT 120
DB 152 TATACTATTTCTGTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGAGCTGTAGATTCAAT 211

QY 121 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCT 180
DB 212 AACGTTAAAAAGGCGACAGATCTATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCT 271

QY 181 GGAGAAATTTTGGGCTGGCAGTGTATTTATGGTGTATGTCAGGAGCAGATGGGAGTCTGGGT 240
DB 272 GGAGAAATTTTGGGCTGGCAGTGTATTTATGGTGTATGTCAGGAGCAGATGGGAGTCTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAAAGCTACCAAGGAAGTT 300
DB 332 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAAAGCTACCAAGGAAGTT 391

QY 301 CCCACACGGATATTGACTTCTTCTGCGAG 330
DB 392 CCCACACGGATATTGACTTCTTCTGCGAG 421

RESULT 7
US-10-219-068-71
; Sequence 71, Application US/10219068
; Publication No. US20030187205A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.

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Tue Dec 30 10:20:39 2003

```
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C31
; CURRENT APPLICATION NUMBER: US/10/219,068
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-068-71
```

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Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGC 60
Db 92 CATGGAATATTTATGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGC 151

QY 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAAAGATTTAATGCCCGGACTGTAGATTCATT 120
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAAAGATTTAATGCCCGGACTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGAGCAGATCTATGTCTCAAGCTGTTAAAGAAATGGAGCT 180
Db 212 AACGTTAAAAAGGCGAGCAGATCTATGTCTCAAGCTGTTAAAGAAATGGAGCT 271

QY 181 GGAGAAATTTGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGT 331

QY 241 TATTTCCCAAGAACTTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGAAATTT 300
Db 332 TATTTCCCAAGAACTTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGAAATTT 391

QY 301 CCCACACGAGATATTGACTTCTCTCGGAG 330
Db 392 CCCACACGAGATATTGACTTCTCTCGGAG 421
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RESULT 8
US-10-219-069-71
; Sequence 71, Application US/10219069
; Publication No. US20030187206A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
```

```
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C40
; CURRENT APPLICATION NUMBER: US/10/219,069
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-069-71
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Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTTATGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGC 60
Db 92 CATGGAATATTTATGACCGCTCTAGCTTCCAGAAAGCTCTGTGCAGATGATGAGTGTGC 151

QY 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAAAGATTTAATGCCCGGACTGTAGATTCATT 120
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAAAGATTTAATGCCCGGACTGTAGATTCATT 211

QY 121 AACGTTAAAAAGGCGAGCAGATCTATGTCTCAAGCTGTTAAAGAAATGGAGCT 180
Db 212 AACGTTAAAAAGGCGAGCAGATCTATGTCTCAAGCTGTTAAAGAAATGGAGCT 271

QY 181 GGAGAAATTTGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGCTGGCAGTGTATGTTGATGGCCAGACGAGATGGAGTCGTGGGT 331

QY 241 TATTTCCCAAGAACTTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGAAATTT 300
Db 332 TATTTCCCAAGAACTTTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGAAATTT 391

QY 301 CCCACACGAGATATTGACTTCTCTCGGAG 330
Db 392 CCCACACGAGATATTGACTTCTCTCGGAG 421
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RESULT 9
US-10-219-073-71
; Sequence 71, Application US/10219073
; Publication No. US20030187207A1
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C52
; CURRENT APPLICATION NUMBER: US/10/219,073
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-073-71

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 271

QY 181 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 391

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-475-71

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 271

QY 181 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 391

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-475-71

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 271

QY 181 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 391

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C49
; CURRENT APPLICATION NUMBER: US/10/219,475
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-219-475-71

Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60
Db 92 CATGGAATATTATGGACCGTCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151

QY 61 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 120
Db 152 TATACATATTTCTCGGTAGTGTCTCAAGAAGATTATATGCCCCGGACTGTAGATTCAAT 211

QY 121 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 180
Db 212 AACGTTAAAAAGGCGCAGACATCTATGTGTACTCAAGAGCTGTGTAAGAGAAATCGAGCT 271

QY 181 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATGTTGATGTCAGGACGAGATGGGAGTCGTGGGT 331

QY 241 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 300
Db 332 TATTTCCCGAGAACTTGGTCAAGAAACAGCGTGTGTACCCAGAGAGCTACCAAGGAAGTT 391
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Db 272 GGAGAAATTTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGGAGTGGTGGGT 331  
Qy 241 TATTTCCCGAGGACTTGGTCAAGGACAGCGTGTGTACCAAGGAGCTTACCAAGGAGCTT 300  
Db 332 TATTTCCCGAGGAACTTGGTCAAGGACAGCGTGTGTACCAAGGAGCTTACCAAGGAGCTT 391  
Qy 301 CCACACCGGATATTGACTTCTTCTCGCGAG 330  
Db 392 CCCACCGGATATTGACTTCTTCTCGCGAG 421  
RESULT 12  
US-10-219-483-71  
; Sequence 71, Application US/10219483  
; Publication No. US20030187210A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC43  
; CURRENT APPLICATION NUMBER: US/10/219,483  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-483-71  
Query Match 100.0%; Score 330; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.2e-100;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CATGGAATTTTATGACCGCTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 60  
Db 92 CATGGAATTTTATGACCGCTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 151  
Qy 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 120  
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 211  
Qy 121 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCT 180

Qy 301 CCACACCGGATATTGACTTCTTCTCGCGAG 330  
Db 392 CCCACCGGATATTGACTTCTTCTCGCGAG 421  
RESULT 11  
US-10-219-480-71  
; Sequence 71, Application US/10219480  
; Publication No. US20030187209A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC38  
; CURRENT APPLICATION NUMBER: US/10/219,480  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 71  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-219-480-71  
Query Match 100.0%; Score 330; DB 13; Length 521;  
Best Local Similarity 100.0%; Pred. No. 7.2e-100;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CATGGAATTTTATGACCGCTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 60  
Db 92 CATGGAATTTTATGACCGCTCTAGCTTCCAAGAGCTCTGTGCAGATGATGATGTC 151  
Qy 61 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 120  
Db 152 TATACTATTTCTCTGGCTAGTGTCTCAAGAGATTAATAATGCCCGGACTGTAGATTCATT 211  
Qy 121 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCT 180  
Db 212 AACGTTAAAAAGGGCAGCAGATCTATGTGTACTCAAGCTGTGTAAAGAAATGGAGCT 271  
Qy 181 GGAGAAATTTTGGGCTGGCAGTGTATTATGTTGATGGCCAGGACGAGATGGGAGTGGTGGGT 240

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Db 212 AACGTTAAAAAGGCGACGAGATCTATGTGTACTCAAAAGTGTGTAAGAAAGAAATGGAGCT 271
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Db 272 GGAGAAATTTTGGGCTGCGAGTGTATGTGTATGCGGACGACGAGATGGGAGTCTGTGGGT 331
Qy 241 TATTTCCCGGAGAACTTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTTTCAAGAAAGTT 300
Db 332 TATTTCCCGGAGAACTTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTTTCAAGAAAGTT 391
Qy 301 CCCACCGAGATATTGACTTCTCTGCGAG 330
Db 392 CCCACCGAGATATTGACTTCTCTGCGAG 421

RESULT 13
US-10-219-525-71
; Sequence 71, Application US/10219525
; Publication No. US20030187211A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC29
; CURRENT APPLICATION NUMBER: US/10/219,525
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-525-71
Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Mismatches 0; Indels 0; Gaps 0;
Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Mismatches 0; Indels 0; Gaps 0;

Qy 61 TATACTATTTCTCTGGCTAGTGTCAAGAAAGATTATTAATGCCCGGAGTCTGTAGATTCAATT 120
Db 152 TATACTATTTCTCTGGCTAGTGTCAAGAAAGATTATTAATGCCCGGAGTCTGTAGATTCAATT 211
Qy 121 AACGTTAAAAAGGCGACGAGATCTATGTGTACTCAAAAGTGTGTAAGAAAGAAATGGAGCT 180
Db 212 AACGTTAAAAAGGCGACGAGATCTATGTGTACTCAAAAGTGTGTAAGAAAGAAATGGAGCT 271
Qy 181 GGAGAAATTTTGGGCTGCGAGTGTATGTGTATGCGGACGACGAGATGGGAGTCTGTGGGT 240
Db 272 GGAGAAATTTTGGGCTGCGAGTGTATGTGTATGCGGACGACGAGATGGGAGTCTGTGGGT 331
Qy 241 TATTTCCCGGAGAACTTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTTTCAAGAAAGTT 300
Db 332 TATTTCCCGGAGAACTTTGGTCAAGAAACAGCGTGTGTACCAAGAAAGTTTCAAGAAAGTT 391
Qy 301 CCCACCGAGATATTGACTTCTCTGCGAG 330
Db 392 CCCACCGAGATATTGACTTCTCTGCGAG 421

RESULT 14
US-10-219-526-71
; Sequence 71, Application US/10219526
; Publication No. US20030187212A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-526-71
Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Mismatches 0; Indels 0; Gaps 0;
Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100;
Mismatches 0; Indels 0; Gaps 0;
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Qy 1 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTCTC 60
Db 92 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTCTC 151
Qy 61 TATACTATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 120
Db 152 TATACTATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 211
Qy 121 AAGCTTAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 180
Db 212 AAGCTTAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 271
Qy 181 GGAGAAATTTGGGCTGGCAGTGTATGTGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATGTGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 331
Qy 241 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 300
Db 332 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 391
Qy 301 CCCACACGAGATATTGACTTCTTCTGCGAG 330
Db 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421
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## RESULT 15

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US-10-219-530-71
; Sequence 71, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PLC54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 71
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo Sapien
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## US-10-219-530-71

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Query Match 100.0%; Score 330; DB 13; Length 521;
Best Local Similarity 100.0%; Pred. No. 7.2e-100; Indels 0; Gaps 0;
Matches 330; Conservative 0; Mismatches 0;

Qy 1 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTCTC 60
Db 92 CATGGAATATTATGACCGCTCTAGCTTCCAGAGCTCTGTGCAGATGATGAGTGTCTC 151
Qy 61 TATACTATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 120
Db 152 TATACTATTCTCTGGCTAGTGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCAAT 211
Qy 121 AAGCTTAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 180
Db 212 AAGCTTAAAGGCGAGCAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 271
Qy 181 GGAGAAATTTGGGCTGGCAGTGTATGTGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 240
Db 272 GGAGAAATTTGGGCTGGCAGTGTATGTGTGTGATGGCCAGGACGAGATGGGAGTCTGGGT 331
Qy 241 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 300
Db 332 TATTTCGCCAGGAACCTTGGTCAAGAACAGCGTGTGTACAGGAAGCTACCAAGGAAGTT 391
Qy 301 CCCACACGAGATATTGACTTCTTCTGCGAG 330
Db 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421
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Job time : 271.994 secs

Tue Dec 30 10:20:39 2003

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 30, 2003, 01:34:27 ; Search time 26.6527 Seconds  
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5464.987 Million cell updates/sec

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Perfect score: 330  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	63.2	19.2	581	1	US-08-578-649-4
3	57.4	17.4	330	1	US-08-578-649-18
4	54.2	16.4	305	1	US-08-578-649-8
5	40.4	12.2	596	1	US-08-578-649-24
6	40.4	12.2	3565	1	US-08-578-649-3
7	34	10.3	7218	1	US-08-232-463-14
8	33.6	10.2	1136	3	US-08-860-820-1
9	33.6	10.2	1929	4	US-09-359-161-4
10	32.6	10.2	2159	3	US-08-286-870A-7
11	32.8	9.9	6501	4	US-09-767-515-1
12	32.8	9.9	6501	4	US-09-767-515-2
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18	30.4	9.2	289	3	US-09-007-008-17
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27	29.4	8.9	2718	4	US-09-650-855-14

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Sequence 131, App  
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Sequence 2654, Ap  
Sequence 1103, Ap  
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Sequence 1, Appli  
Sequence 3, Appli

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31 29.2 8.8 3489 4 US-09-134-001C-1171  
32 29 8.8 810 4 US-09-252-991A-10933  
33 29 8.8 10357 4 US-08-961-527-191  
34 29 8.8 45175 4 US-09-453-702B-116  
35 28.8 8.7 1497 4 US-09-220-132-94  
36 28.8 8.7 1941 4 US-09-107-532A-2654  
37 28.6 8.7 849 4 US-09-252-991A-1103  
38 28.6 8.7 1518 2 US-08-929-501-4  
39 28.6 8.7 1518 2 US-08-929-501-5  
40 28.6 8.7 1518 3 US-09-140-177-4  
41 28.6 8.7 1518 3 US-09-140-177-5  
42 28.6 8.7 1518 3 US-09-397-979-4  
43 28.6 8.7 1518 3 US-09-397-979-5  
44 28.6 8.7 1753 2 US-08-929-501-1  
45 28.6 8.7 1753 2 US-08-929-501-3

ALIGNMENTS

RESULT 1  
US-08-578-649-1  
; Sequence 1, Application US/08578649  
; Patent No. 5770366  
; GENERAL INFORMATION:  
; APPLICANT: Ulrich Bogdan  
; APPLICANT: Reinhard Buttner  
; APPLICANT: Brigitte Kaluza  
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/578,649  
; FILING DATE: 29-July-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 43 24 247.2  
; FILING DATE: 20-July-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Andrew L. Tiajoloiff  
; REGISTRATION NUMBER: 31,575  
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; TELEFAX: (212) 838-3884  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 40..432  
; FEATURE:  
; NAME/KEY: sig\_peptide  
; LOCATION: 40..111  
; FEATURE:

Tue Dec 30 10:20:39 2003

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; LOCATION: 112...432
US-08-578-649-1

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Best Local Similarity 58.2%; Pred. No. 5e-11;
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QY 12 TATGACCGTCTAGCTTCCAAAGAGATTATATGCCCCGAGCTGATGCTGTCTATATCTTTC 71
DB 117 TATGCCCAAGCTGGCTGACCGAGCTGTGTGGACCGAGGAGTGACGCCACCTATCTC 176
QY 72 TCTGCTAGTCTCAAGAGATTATATGCCCCGAGCTGTAGATTCATTAACTTTAAA 131
DB 177 CATGCTGTGGCCCTTCAGGACTACATGCCCCGAGCTGCCGATTCCTGACCATTCACCG 236
QY 132 AGGCAGCAGATCTATGTGTACTCAAGCTGTAAAGAAATGAGCTGGAGATTTTG 191
DB 237 GGGCCCAAGTGGTGTATGCTCTTCCAAAGCTG-----AAGGCCGTGGCGGCTCTTCTG 290
QY 192 GGCTGGCAGTGTATTATGTGTATGGCCAGGACGAGATGGGAG---TCGTGGGTATTTC 248
DB 291 GGGAGGCAGCGTTTCAGGAGATTACTATGAGATCTGGGTCTGCGCTGGGCTATTTC 350
QY 249 CAGGAACCTGGTCAAGGACACG 271
DB 351 CAGTAGCATTTGCCGAGAGGACC 373

RESULT 2
US-08-578-649-4
; Sequence 4, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:

; NAME/KEY: CDS
; LOCATION: 110...499
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 110...178
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 179...499
US-08-578-649-4

Query Match      19.2%; Score 63.2; DB 1; Length 581;
Best Local Similarity 54.3%; Pred. No. 6.5e-11;
Matches 175; Conservative 0; Mismatches 138; Indels 9; Gaps 2;

QY 12 TATGACCGTCTAGCTTCCAAAGAGCTCTGTGAGATGATGAGTGTCTATATCTTTC 71
DB 184 TATGCCCAAGCTGGCTGACTGGAAGCTGTGTGCGGAGGAGAAATGACGCCATCCTATCTC 243
QY 72 TCTGCTAGTCTCAAGAGATTATATGCCCCGAGCTGTAGATTCATTAACTTTAAA 131
DB 244 CATGCTGTGGCCCTTCAGGACTAGCTGGCCCTGATTGGCGCTTCTTGACTATATATAG 303
QY 132 AGGCAGCAGATCTATGTGTACTCAAGCTGTAAAGAAATGAGAGCTGGAGATTTTG 191
DB 304 GGGCCCAAGTGGTGTATGCTCTTCCAAAGTTG-----AAGGCCCTGGCGGCTTTTCTG 357
QY 192 GGCTGGCAGTGTATTATGTGTATGGCCAGGACGAGATGGGAG---TCGTGGGTATTTC 248
DB 358 GGGAGGCAGTGTTCAGGAGGTTACTATGAGACTGGAGCCGCCCTGGGCTATTTC 417
QY 249 CAGGAACCTGGTCAAGGAAACAGCGTGTGTACCCAGGAAGCTACCAAGGAAGTTCCACCCAC 308
DB 418 CAGTAGCATTTGCCGAGGAGCTGAACTCGAAACCTGCAAAATTTGATATGAAGACCGA 477
QY 309 GGATATTGACTTCTTCTGCGAG 330
DB 478 TCATGGGATTTCTACTGCCAG 499

RESULT 3
US-08-578-649-18
; Sequence 18, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 581 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
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Tue Dec 30 10:20:39 2003

```
;
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 330 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 7..327
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: 4..6
; OTHER INFORMATION: /function= "Startcodon Met"
;
US-08-578-649-18

Query Match 17.4%; Score 57.4; DB 1; Length 330;
Best Local Similarity 58.5%; Pred. No. 3.8e-09;
Matches 141; Conservative 0; Mismatches 91; Indels 9; Gaps 2;

QY 34 AAGCTCTGTGCAGATGATGTGTCTATATCTCTCTGTGGCTAGTGTCTCAAGAAGAT 93
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 34 AAATATGTGCAGATCAGAGTGCAGCCACCCCTATCTCCATGGCTGTGGCCCTTCAGGAC 93
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 94 TATAATGCCCGGACTGTAGATTCAATTAACGTTAAAGGAGGAGCAGATCTATGTGTAC 153
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 94 TACATGGCCCCGACTGCGGATTCCTGACCATTCACCGGGGCCAAGTGGTGTATGTCTTC 153
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 154 TCAAGCTGTGTAAAGAAAATGGAGCTGGAGATTTTGGGCTGGCAGTGTATGTGTAT 213
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 208 TACTATGGAGATCGCTGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 270
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 C 271
Db 268 C 268

RESULT 4
US-08-578-649-8
; Sequence 8, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnar
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
;

;
; NAME: Andrew L. Tiajoloiff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc RNA
; LOCATION: join(1..29, 277..305)
; OTHER INFORMATION: /function= "Primer"
;
US-08-578-649-8

Query Match 16.4%; Score 54.2; DB 1; Length 305;
Best Local Similarity 57.7%; Pred. No. 4e-08;
Matches 139; Conservative 0; Mismatches 93; Indels 9; Gaps 2;

QY 34 AAGCTCTGTGCAGATGATGTGTCTATATCTCTCTGTGGCTAGTGTCTCAAGAAGAT 93
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 94 TATAATGCCCGGACTGTAGATTCAATTAACGTTAAAGGAGGAGCAGATCTATGTGTAC 153
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 67 TACATGGCCCCGACTGCGGATTCCTGACCATTCACCGGGGCCAAGTGGTGTATGTCTTC 126
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 154 TCAAGCTGTGTAAAGAAAATGGAGCTGGAGATTTTGGGCTGGCAGTGTATGTGTAT 213
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 214 GCGCAGGACGAGATGGGAG---TCGTGGTGTATTTCCCGAGAACTTGGTCAAGGAACAG 270
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 TACTATGGAGATCGTGTCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 271 C 271
Db 241 C 241

RESULT 5
US-08-578-649-24
; Sequence 24, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttnar
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
```

ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Tiajolloff  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 596 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(40..111, 40..166, 214..347, 393..503, 549  
LOCATION: ..569)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 40..111  
FEATURE:  
NAME/KEY: exon  
LOCATION: 40..166  
FEATURE:  
NAME/KEY: exon  
LOCATION: 214..347  
FEATURE:  
NAME/KEY: exon  
LOCATION: 393..503  
FEATURE:  
NAME/KEY: exon  
LOCATION: 549..569  
FEATURE:  
NAME/KEY: -  
LOCATION: one-of(194, 369, 527)  
OTHER INFORMATION: /note= "N in positions 194, 369  
OTHER INFORMATION: and 527 denotes an indefinite number and sequence  
OTHER INFORMATION: of nucleotides "  
US-08-578-649-24  
Query Match 12.2%; Score 40.4; DB 1; Length 596;  
Best Local Similarity 63.3%; Pred. No. 0.0016;  
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 65 CTATTCTCTGGCTAGTGTCTCAAGAGATTATATGCCCCGAGCTGTAGATTCAATTAACG 124  
Db 217 CTATCTCCATGGCTGTGGCCCTTCAGGACTACATGCCCCCGACTGCCGATTCCTGACCA 276  
QY 125 TTAATAAAGGCGAGCATCTATGTGTACTCAAGCTG 162  
Db 277 TTCACCGGGCCCAAGTGTGTATGTCTTCTCCAAGCTG 314  
RESULT 6  
US-08-578-649-3  
Sequence 3, Application US/08578649  
Patent No. 5770366  
GENERAL INFORMATION:  
APPLICANT: Ulrich Bogdan  
APPLICANT: Reinhard Buttner  
APPLICANT: Brigitte Kaluza  
TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/578,649  
FILING DATE: 29-July-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 43 24 247.2  
FILING DATE: 20-July-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Andrew L. Tiajolloff  
REGISTRATION NUMBER: 31,575  
REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3565 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1378..1449  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1378..1504  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1586..1719  
FEATURE:  
NAME/KEY: exon  
LOCATION: 2804..2914  
FEATURE:  
NAME/KEY: exon  
LOCATION: 3232..3252  
FEATURE:  
NAME/KEY: -  
LOCATION: one-of(2216)  
OTHER INFORMATION: /note= "N in position 2216  
OTHER INFORMATION: denotes an indefinite number and sequence of  
OTHER INFORMATION: nucleotides"  
US-08-578-649-3  
Query Match 12.2%; Score 40.4; DB 1; Length 3565;  
Best Local Similarity 63.3%; Pred. No. 0.0037;  
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 65 CTATTCTCTGGCTAGTGTCTCAAGAGATTATATGCCCCGAGCTGTAGATTCAATTAACG 124  
Db 1589 CTATCTCCATGGCTGTGGCCCTTCAGGACTACATGCCCCCGACTGCCGATTCCTGACCA 1648  
QY 125 TTAATAAAGGCGAGCATCTATGTGTACTCAAGCTG 162  
Db 1649 TTCACCGGGCCCAAGTGTGTATGTCTTCTCCAAGCTG 1686  
RESULT 7  
US-08-232-463-14/c  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: ptzgt-F1s  
US-08-232-463-14

Query Match 10.3%; Score 34; DB 1; Length 7218;  
Best Local Similarity 8.1%; Pred. No. 0.6;  
Matches 19; Conservative 120; Mismatches 95; Indels 0; Gaps 0;

Qy 65 CTATTTCTGTGGTGTCTCAAGAGATTATAATGCCCGGACTGTAGATTCTTAACG 124  
Db 1471 CTTATGCAAGTAGTTAAAGAGATAGAAGAAATTTGGTACRRRRRRRRRRRRRRRRRR 1412

Qy 125 TTAAGAAAGGCACACACATCTATGTGTACTCAAGCTGTTAAAGAAATCGAGCTGAG 184  
Db 1411 RRR 1352

Qy 185 AATTTTGGGCTGGCAGTGTATTATGCTGATGCCAGGACGAGTGGAGTCTGTGGTTATT 244  
Db 1351 RRR 1292

Qy 245 TCCCAGGAACCTGGTCAAGGAACAGCGGTGTGTACCAAGGAGCTACCAAGGAAG 298  
Db 1291 RRR 1238

RESULT 8  
US-08-860-820-1  
Sequence 1, Application US/08960820  
Patent No. 6245967  
GENERAL INFORMATION:  
APPLICANT: Sonnewald, Uwe  
APPLICANT: Kossmann, Jens  
APPLICANT: Bowien, Botho  
TITLE OF INVENTION: PROCESS AND DNA MOLECULES FOR INCREASING  
TITLE OF INVENTION: THE PHOTOSYNTHESIS RATE IN PLANTS  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York

COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/860,820  
FILING DATE: 04-SEP-1997  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19502053.7  
FILING DATE: 13-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: AGREVO-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1136 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 30..1121  
US-08-860-820-1

Query Match 10.2%; Score 33.6; DB 3; Length 1136;  
Best Local Similarity 56.2%; Pred. No. 0.34;  
Matches 63; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 172 AATGAGCTGAGAAATTTGGCTGGCAGTGTATATGCTGATGCCAGGACGAGTGGGA 231  
Db 204 AATCAAGCCGGAGAAGCAGGGCGGTCAACGTGCGGGCGAAATCCAGCAAGCTGAC 263

Qy 232 GTCTGTGGTATTTCCTCCAGCAACTTGTCTCAAGGAACAGCGGTGTGTACCAGG 283  
Db 264 GTCTGTGACATACCACTTCTCTCGCGTCAACAGTGGGGGGGTACCTGG 315

RESULT 9  
US-09-359-161-4/c  
Sequence 4, Application US/09359161A  
Patent No. 6342656  
GENERAL INFORMATION:  
APPLICANT: Bradford, Kent J.  
APPLICANT: Dahal, Peetambar  
APPLICANT: Yang, Hong  
APPLICANT: Cooley, Michael  
APPLICANT: Downie, Bruce  
APPLICANT: Gee, Oliver  
APPLICANT: The Regents of the University of California  
TITLE OF INVENTION: Regulation of Source-Sink Relationships and Responses  
TITLE OF INVENTION: to Stress Conditions in Plants  
FILE REFERENCE: 023070-095900US  
CURRENT APPLICATION NUMBER: US/09/359,161A  
CURRENT FILING DATE: 1999-07-21  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 1929  
TYPE: DNA  
ORGANISM: Lycopersicon esculentum  
FEATURE:  
OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast



```

; OTHER INFORMATION: SNF1 kinase subunit of protein kinase (LeSNF1)
US-09-359-161-4
Query Match 10.2%; Score 33.6; DB 4; Length 1929;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 72; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 84 TCAGAAGATTATTAATCCCGGACTGTAGATTCAATTAAGTTAAAAAGGCGCAGAT 143
Db 1793 TCTGTAAGTAGACTCTAGTAACTGAAATTCATTAAGCTTAAAAAAGAGAGTGAGCT 1734
QY 144 CTATGTTACTCAAGCTGTTAAAGAAATGGAGCTGGAGAAATTTGGGCTGSCAGTGT 203
Db 1733 AGATCTCTAGCGAATCAAAAGAAAAAAGAGTTGCTAGGCACCTCTGACCAACAGCGGT 1674
QY 204 TTATGGTGATGGCCAG 219
Db 1673 GGAATTGTTAACAAG 1658

RESULT 10
US-08-286-870A-7/c
; Sequence 7, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2159
US-08-286-870A-7

Query Match 10.2%; Score 33.6; DB 3; Length 2159;
Best Local Similarity 52.1%; Pred. No. 0.46;
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 174 TGGAGCTGGAGAAATTTGGGCTGGCAGTGTATTATGGTATGGCCAGACGAGATGGGAGT 233
Db 2002 TGGTCTGGTGAACAGCGCGGTGACCTTCTCCTGGGCTTCTCGAAGTCGTACTCGGCCT 1943
QY 234 CGTGGGTTATTTCCCGAGGAACCTTGGTCAAGGAACACGCGTGTGTACCAAGCACTACCA 293
Db 1942 CGTAGGTCACTCCACGCGGCACGAACCTCGATGCGGTGTACACCTCGTTGCCGCTGC 1883
QY 294 GGAAGTTCACCAACCGGATATTGA 317
Db 1882 TGAAGTTCAGGCGCGCATGTTGA 1859

RESULT 11
US-09-767-515-1
; Sequence 1, Application US/09767515
; Patent No. 6586207
; GENERAL INFORMATION:
; APPLICANT: Tirrell, David A
; APPLICANT: Klicik, Kristi L
; TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for
; TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
; TITLE OF INVENTION: Amino Acid Analogues
; FILE REFERENCE: 30431.6US01
; CURRENT APPLICATION NUMBER: US/09/767,515
; CURRENT FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/207,627
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 6501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pOE15-MRS
US-09-767-515-1

Query Match 9.9%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.4;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
QY 180 TGGAGAAATTTGGGCTGGCAGTGTATTATGGTATGGCCAGACGAGATGGGAGTGGTGG 239
Db 2259 TGGTGAAGCGTGGGAAAGCCGTGAATTTGGTAAAGCCGTGGCGGAAATCATGGCGCTGC 2318
QY 240 TTATTTCCCGAGGAACCTTGGTCAAGGAACGCGTGTGTACCAAGGAAGCTTACCAAGGAGT 299
Db 2319 TGATCTGGCTAACCGCTATGTCGTAACAGGCTCCGTGGGTGGTGGCGAACAAGG 2378
QY 300 TCCC 303
Db 2379 CCGC 2382

RESULT 12
US-09-767-515-2
; Sequence 2, Application US/09767515
; Patent No. 6586207
; GENERAL INFORMATION:
; APPLICANT: Tirrell, David A
; APPLICANT: Klicik, Kristi L
; TITLE OF INVENTION: Overexpression of Aminoacyl-tRNA Synthetases for
; TITLE OF INVENTION: Efficient Production of Engineered Proteins Containing
; TITLE OF INVENTION: Amino Acid Analogues
; FILE REFERENCE: 30431.6US01
; CURRENT APPLICATION NUMBER: US/09/767,515
; CURRENT FILING DATE: 2001-01-23
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Tue Dec 30 10:20:39 2003

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; PRIOR APPLICATION NUMBER: 60/207,627
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 6501
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pOE15-W305F
US-09-767-515-2

Query Match          9.8%; Score 32.8; DB 4; Length 6501;
Best Local Similarity 54.0%; Pred. No. 1.4;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 180 TGGAGAAATTTTGGCTGCGCAGTGTATGGTGTGGCCAGGACGAGATGGGAGTCGTGGG 239
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 240 TTATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCGAAGCTACCAAGGAAGT 299
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 2319 TGAATCGCTAACCGCTATGTCGATGAACAGGCTCCGTGGTGTGGCGAAACAGGAAGG 2378
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 300 TCCC 303
Db |||||
Qy 2379 CCGC 2382
Db |||||

RESULT 13
US-09-734-674-3
; Sequence 3, Application US/09734674
; Patent No. 6498022
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001018
; CURRENT APPLICATION NUMBER: US/09/734,674
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 202001
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(202001)
; OTHER INFORMATION: n = A,T,C or G
US-09-734-674-3

Query Match          9.8%; Score 32.2; DB 4; Length 202001;
Best Local Similarity 49.7%; Pred. No. 11;
Matches 82; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

Qy 65 CTATTTCTGTGCTAGTCTCAGAGATTATATGCCCCGACGTAGATTCATTAAAG 124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183409 CTAGAACTCAGGAGAGCTAAGGACAGACGTAGGTCGGTGAATCATTAGCAAGTCTGT 183468
Qy 125 TTAATAAGGGGACGACAGATCTATGTACTCAAAGCTGTAAAGAAATGGAGCTGGAG 184
Db 183469 GAAAGTCAAGCCATGGGTATGGATGAATCTATCCAGGAGAAAGAAACAGAGATGAG 183528
Qy 185 AATTTTGGGCTGGCAGTGTATGGTGTATGGCCAGACGAGATGG 229
Db 183529 AGTCAGGAATCCCAATGTTGAGGGGCAATTAAGAGAGATTG 183573

RESULT 14
US-09-252-991A-889/c
; Sequence 889, Application US/09252991A
```

```
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 889
; LENGTH: 1944
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-889

Query Match          9.5%; Score 31.4; DB 4; Length 1944;
Best Local Similarity 51.8%; Pred. No. 2.3;
Matches 71; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 181 GGAGAAATTTTGGCTGCGCAGTGTATGGTGTATGGCCAGGACGAGATGGGAGTCGTGGGT 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 241 TATTTCCCGAGGAACCTTGGTCAAGGAACAGCGTGTGTACCGAAGAGCTACCAAGGAAGTT 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 301 CCCACCAAGGATATTGA 317
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 300 CCGACCCCTGGCGGTGA 284
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          9.5%; Score 31.2; DB 3; Length 4403765;
Best Local Similarity 47.9%; Pred. No. 62;
Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 99 TGCCCGGACGTGTAGATTCATTAAAGGCGGAGATCTATGTGTACTCAAA 158
Db 426225 TGTCCAGCGGGGCCGCGCGCCATGCAGGGTGTATCGACCGGCGGCAAGA 426284
Qy 159 GCTGTAAAGAAATGGAGCTGGAGAAATTTGGGCTGGCAGTGTATGTATGGTGGCCA 218
Db 426285 CGGTGCCACTGAGGATGCTATGTCGAGCTTCCGCTGGCGTGTCTGGGGAACGTA 426344
```

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QY	219	GGACGAGATGGGAGTCGTGGGTTATTCCCGAGGAACCTTGGTCAAGGAACACCGTGTGTA	278
Db	426345	TGGCGGGGATGGAGACATTGGTGATGTCGCCCGTGATGGGGATGTTGACCGGGATGTCCA	426404
QY	279	CCAGGAAG	286
Db	426405	CATTGAGG	426412

Search completed: December 30, 2003, 06:10:50  
Job time : 36.6527 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 11.4006 Seconds  
(without alignments)  
927.898 Million cell updates/sec

Title: US-10-019-455A-24  
Perfect score: 590  
Sequence: 1 HGIFMDRLASKKLCADDECV.....RVYQEAKEVPTTIDIFFCE 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	253.5	43.0	131	2 I38019	melanoma-derived g
2	86.5	14.7	839	1 TVHUVV	transforming prote
3	85.5	14.5	844	1 TVMSVV	transforming prote
4	81.5	13.8	878	2 I51940	gene VAV2 protein
5	78.5	13.3	1589	1 RBYC5	cell division cont
6	74.5	12.6	1215	2 T32734	myosin-IA - Acanth
7	74	12.5	308	2 T48525	hypothetical prote
8	71.5	12.1	541	2 C64439	asparagine synthas
9	71.5	12.1	671	1 C69621	fructose-bisphosph
10	71	12.0	383	2 A23516	Balbani ring 1 ch
11	71	12.0	585	2 G96995	ATP-dependent RNA
12	71	12.0	769	2 C90186	AAA family ATPase
13	70.5	11.9	669	2 D72278	endo-1,4-beta-mann
14	70	11.9	209	2 D86758	orotate phosphorib
15	69.5	11.8	295	2 F90113	cell division cycl
16	69.5	11.8	1199	2 T47442	disease resistance
17	69	11.7	328	2 E86714	quinone oxidoreduc
18	69	11.7	392	2 I39521	rubredoxin-NAD+ re
19	69	11.7	444	1 A64417	phosphoribosylamin
20	69	11.7	670	2 S67383	probable signal tr
21	69	11.7	2541	2 T29340	hypothetical prote
22	68.5	11.6	461	2 AF2340	sugar ABC transpor
23	68.5	11.6	505	1 S24550	protein-tyrosine k
24	68.5	11.6	506	1 S24553	protein-tyrosine k
25	68	11.5	162	2 B29662	Balbani ring 2 ch
26	68	11.5	259	2 C64427	hypothetical prote
27	68	11.5	359	2 B29960	Balbani ring 2 ch
28	68	11.5	782	2 B83966	formate dehydrogen
29	67.5	11.4	374	2 B97258	glycosyltransferas

30 67.5 11.4 839 2 G96719 probable chromomet  
31 67 11.4 142 2 C75325 methylmalonyl-CoA  
32 67 11.4 373 2 T39655 VHS domain contain  
33 67 11.4 383 2 S24156 polygalacturonase  
34 67 11.4 509 2 G82104 glutamyl-tRNA synt  
35 67 11.4 518 1 P2WL8 L2 protein - human  
36 67 11.4 524 2 S36483 L2 protein - human  
37 67 11.4 542 2 D70873 probable ABC trans  
38 67 11.4 1187 2 T19413 probable ABC trans  
39 66.5 11.3 209 2 AG1303 orotate phosphorib  
40 66.5 11.3 258 2 E81308 hypothetical prote  
41 66.5 11.3 493 2 S11148 amIA protein - Str  
42 66.5 11.3 847 1 A53800 mixed-lineage prot  
43 66 11.2 162 2 A29662 Balbani ring 1 ch  
44 66 11.2 229 2 AG2737 acetyltransferase  
45 66 11.2 229 2 E97518 probable acetyltra

#### ALIGNMENTS

##### RESULT 1

I38019  
melanoma-derived growth regulatory protein MIA - human  
C:Species: Homo sapiens (man)  
C:Date: 17-May-1996 #sequence\_revision 17-May-1996 #text\_change 04-Mar-2000  
C:Accession: I38019; S40238  
R:Blesch, A.; Bosserhoff, A.K.; Apfel, R.; Behl, C.; Hoesdoerfer, B.; Schmitt, A.; Ja  
Cancer Res. 54, 5695-5701, 1994  
A:Title: Cloning of a novel malignant melanoma-derived growth-regulatory protein, MIA  
A:Reference number: I38019; MUID:95007612; PMID:7923218  
A:Accession: I38019  
A>Status: Preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-131 <RES>  
A:Cross-references: EMBL:X75450; NID:g438057; PIDN:CAAS3203.1; PID:g438058  
C:Genetics:  
A:Gene: mia  
C:Superfamily: human melanoma-derived growth regulatory protein MIA

Query Match 43.0%; Score 253.5; DB 2; Length 131;  
Best Local Similarity 45.4%; Pred. No. 4.2e-19;  
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADDECVYTISLASAQEDYNAPCRFTNVKGGQIVYVSKLVKENGGE-F 63  
Db 27 MPKLADRLKLCADQECSHPIISMAVALQDYNAPCRFTLHRRGQVVYVFSKL---KGRGRUF 83

QY 64 WAGSVYVGDGDMGV-VGYFPRNLVKEQRVYQEAKEVPTTIDIFFCE 110  
Db 84 WGSVQGGDYVGDLAARLGYFSPSSIVREDQTLKPGKVDVTKDKWDFYCO 131

##### RESULT 2

TVHUVV  
transforming protein vav - human (fragments)  
N:Alternate names: finger protein vav  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1991 #sequence\_revision 03-May-1996 #text\_change 18-Jun-1999  
C:Accession: B39576; S05382  
R:Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
Mol. Cell. Biol. 11, 1912-1920, 1991  
A:Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene  
A:Reference number: A39576; MUID:91172176; PMID:2005887  
A:Accession: B39576  
A:Molecule type: mRNA  
A:Residues: 1-61 <KAT>  
A:Cross-references: GB:M59834; NID:g340189; PIDN:AAA63267.1; PID:g340190  
A:Note: the authors translated the codon CAG for residue 6 as Glu, CAG for residue 13  
R:Katzav, S.; Martin-Lanca, D.; Barbacid, M.  
EMBO J. 8, 2283-2290, 1989  
A:Title: vav, a novel human oncogene derived from a locus ubiquitously expressed in h  
A:Reference number: S05382; MUID:90005432; PMID:2477241

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A;Accession: S05382  
 A:Molecule type: mRNA  
 A;Residues: 62-839 <KAT2>  
 A;Cross-references: EMBL:X16316  
 R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.  
 Oncogene 7, 611-618, 1992  
 A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl  
 A;Reference number: S23669; MUID:92228488; PMID:1565462  
 A;Contents: annotation  
 A;Note: in the sequence from mouse the authors find three additional nucleotides that pr  
 occurred in the published human sequences  
 C;Comment: In comparing these sequences with the mouse (see PIR:TVMSV), there appear to  
 C;Genetics:  
 A;Gene: GDB:VAV1; VAV  
 A;Cross-references: GDB:127112; OMIM:164875  
 A;Map position: 19p13.3-19p13.3  
 A;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding  
 C;Keywords: phosphoprotein; transforming protein; zinc finger  
 F;126-170/Region: acidic  
 F;188-452/Domain: CDC24 homology <CD24>  
 F;509-557/Domain: protein kinase C zinc-binding repeat homology <K22>  
 F;522-542/Region: zinc finger CCCC motif  
 F;547-560/Region: zinc finger HCCH motif  
 F;536-648/Domain: SH3 homology <SH3A>  
 F;664-756/Domain: SH2 homology <SH2>  
 F;783-831/Domain: SH3 homology <SH3B>  
 F;433/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 14.7%; Score 86.5; DB 1; Length 839;  
 Best Local Similarity 32.9%; Pred. No. 0.68;  
 Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;  
 Qy 26 ASAQEDYNAPDCRFINVKKQIIVYVSKLVKENGAGFWAGSVYGDQDGVVGYPPRN 85  
 Db 781 AKARYDFCARDRSLSLKGDI---KILNKKQQQGWRRGEIYGR-----VGWFFAN 829  
 Qy 86 LVKEQRYVQE 95  
 Db 830 YVEED--YSE 837

RESULT 3  
 TVMSV  
 transforming protein vav - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 03-May-1994 #sequence revision 16-Feb-1996 #text\_change 18-Jun-1999  
 C;Accession: A61187; A39576; S36941; S23669  
 R;Coppola, J.; Bryant, S.; Koda, T.; Conway, D.; Barbacid, M.  
 Cell Growth Differ. 2, 95-105, 1991  
 A;Title: Mechanism of activation of the vav protooncogene.  
 A;Reference number: A61187; MUID:91299578; PMID:2069873  
 A;Accession: A61187  
 A;Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A;Residues: 1-844 <COP>  
 R;Katzav, S.; Cleveland, J.L.; Heslop, H.E.; Pulido, D.  
 Mol. Cell. Biol. 11, 1912-1920, 1991  
 A;Title: Loss of the amino-terminal helix-loop-helix domain of the vav proto-oncogene ac  
 A;Reference number: A39576; MUID:91172176; PMID:2005887  
 A;Accession: A39576  
 A:Molecule type: mRNA  
 A;Residues: 1-28, 'E' 30-93 <KAT>  
 A;Cross-references: GB:M59833; NID:g202343; PIDN:AAA63402.1; PID:g202344  
 R;Adams, J.M.  
 submitted to the EMBL Data Library, January 1992  
 A;Reference number: S36941  
 A;Accession: S36941  
 A:Molecule type: mRNA  
 A;Residues: 1-323, 'D'LMVPMQVRVLYKLLQLQELVK', 346-347, 'QDAT', 352, 'K', 354, 'N', 355-453, 'R', 45  
 A;Cross-references: EMBL:X64361; NID:g95220; PIDN:CAA45713.1; PID:g95221  
 R;Adams, J.M.; Houston, H.; Allen, J.; Lints, T.; Harvey, R.  
 Oncogene 7, 611-618, 1992  
 A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the dbl

A;Reference number: S23669; MUID:92228488; PMID:1565462  
 A;Contents: annotation; the authors note the frameshift difference with sequence in A  
 A;Note: the complete sequence was submitted to Genbank; see S36941  
 C;Genetics:  
 A;Gene: vav  
 C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-bindin  
 C;Keywords: phosphoprotein; transforming protein; zinc finger  
 F;32-102/Region: leucine-rich  
 F;132-176/Region: acidic  
 F;194-458/Domain: CDC24 homology <CD24>  
 F;336-340/Region: proline-rich  
 F;486-493/Region: nuclear location signal  
 F;515-563/Domain: protein kinase C zinc-binding repeat homology <K21>  
 F;528-548/Region: zinc finger CCCC motif  
 F;553-566/Region: zinc finger HCCH motif  
 F;575-582/Region: nuclear location signal  
 F;604-654/Domain: SH3 homology <SH3A>  
 F;606-609/Region: proline-rich  
 F;670-761/Domain: SH2 homology <SH2>  
 F;788-836/Domain: SH3 homology <SH3B>  
 F;439/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicte

Query Match 14.5%; Score 85.5; DB 1; Length 844;  
 Best Local Similarity 31.4%; Pred. No. 0.87;  
 Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;  
 Qy 26 ASAQEDYNAPDCRFINVKKQIIVYVSKLVKENGAGFWAGSVYGDQDGVVGYPPRN 85  
 Db 786 AKARYDFCARDRSLSLKGDI---KILNKKQQQGWRRGEIYGR-----IGWFFSN 834  
 Qy 86 LVKEQRYVQE 95  
 Db 835 YVEED--YSE 842

RESULT 4  
 I51940  
 gene VAV2 protein - human  
 C;Species: Homo sapiens (man)  
 C;Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 16-Jul-1999  
 C;Accession: I51940  
 R;Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlaxhan, S.; Haines, J.L.; K  
 Ann. Hum. Genet. 59, 25-37, 1995  
 A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis g  
 A;Reference number: I51940; MUID:95282235; PMID:7762982  
 A;Accession: I51940  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A;Residues: 1-878 <RES>  
 A;Cross-references: GB:S76992; NID:g913345; PIDN:AA834377.1; PID:g913346  
 C;Genetics:  
 A;Gene: GDB:VAV2  
 A;Cross-references: GDB:370880; OMIM:600428  
 A;Map position: 9q34-9q34  
 C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-bindin  
 F;198-462/Domain: CDC24 homology <CD24>  
 F;524-572/Domain: protein kinase C zinc-binding repeat homology <K22>  
 F;673-764/Domain: SH2 homology <SH2>  
 F;823-872/Domain: SH3 homology <SH3>

Query Match 13.8%; Score 81.5; DB 2; Length 878;  
 Best Local Similarity 26.3%; Pred. No. 2.4;  
 Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;  
 Qy 20 VYT---ISLASAQEDYNAPDCRFINVKKQIIVYVSKLVKENGAGFWAGSVYGDQDEM 76  
 Db 812 VFTPRVIGTAVARYNFAARDMRELSREGDVRIYSRIGDQG---WMKG-----ETN 861  
 Qy 77 GWVGYFERNLVKEQRYV 92  
 Db 862 GRIGWFFPSTVVEERGI 877

A:Accession: T32734  
A>Status: Preliminary; translated from GB/EMBL/DBBJ  
A:Molecule type: DNA  
A:Residues: 1-1215 <LEE>  
A:CROSS-references: EMBL:AF085185; NID:g3599477; PID:g3599478; PIDN:AAC35357.1  
A:Experimental source: strain Neff  
C:Genetics:  
A:Gene: MIA  
A:Introns: 1/3; 41/3; 72/2; 103/2; 162/3; 184/1; 217/1; 296/1; 340/3; 390/3; 447/3; 501/3  
C:Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homo  
F:14-674/Domain: myosin motor domain homology <MMO>

Query Match 12.6%; Score 74.5; DB 2; Length 1215;  
Best Local Similarity 28.6%; Pred. No. 18;  
Matches 20; Conservative 12; Mismatches 25; Indels 13; Gaps 2;

Qy 20 VYTSLASAGDYNAPDCRFNVKKGGQQIYVYSKLVKENGAEFWAGSVYGDQDEMGVV 79  
Db 1158 VFTVGRCRALYYGAGEADLTREGVDIVIQ-----SGEWEGTNGR-----T 1204

Qy 80 GFPEPLVKES 89  
Db 1205 GVFFANYVED 1214

RESULT 7  
T48525  
hypothetical protein T22P22\_50 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T48525  
A:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24490  
A:Accession: T48525  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-308 <BEV>  
A:CROSS-references: EMBL:AL163814  
A:Experimental source: cultivar Columbia; BAC clone T22P22  
C:Genetics:  
A:Map position: 5  
A:Introns: 63/3; 117/3; 135/3; 180/3  
A>Note: T22P22\_50

Query Match 12.5%; Score 74; DB 2; Length 308;  
Best Local Similarity 37.2%; Pred. No. 4.5;  
Matches 16; Conservative 8; Mismatches 17; Indels 2; Gaps 1;

Qy 44 KGQQLYVYSKLVKENGAEFWAGSVYGDQDEMGVVGYPPRNLL 86  
Db 168 KQGERAVYASIVQEIKDNWVTVDYDRPDVH--IGYWPKEL 208

RESULT 8  
C64439  
asparagine synthase (glutamine-hydrolysing) (EC 6.3.5.4) [similarity] - Methanococcus  
C:Species: Methanococcus jannaschii  
C>Date: 13-Sep-1996 #sequence\_revision 09-Jun-2000 #text\_change 19-Jul-2002  
C:Accession: C64439  
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake  
Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.  
son, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.N.; Hurst, W.A.  
Science 273, 1058-1073, 1996  
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,  
A>Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii  
A:Reference number: A64300; MUID:96337999; PMID:8688087  
A:Accession: C64439  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 'WRD', 1-541 <BUL>  
A:CROSS-references: GB:U67554; GB:L77117; NID:g2826365; PIDN:AAB99117.1; PID:g1591755;  
A>Note: an incorrect initiation codon was used

C;Genetics:  
A;Map position: REV1058315-1056681  
C;Superfamily: asparagine synthetase (glutamine-hydrolyzing)  
C;Keywords: asparagine biosynthesis; ligase  
F;2-541/Product: asparagine synthase (glutamine-hydrolyzing) #status predicted <MAT>  
F;2/Active site: Cys #status predicted

Query Match 12.1%; Score 71.5; DB 2; Length 541;  
Best Local Similarity 25.7%; Pred. No. 15;  
Matches 27; Conservative 22; Mismatches 33; Indels 23; Gaps 6;

QY 3 IFMDRLAS-----KKLCADDEC-VYTISLASAQEDYNAPDCRFINVKKGQOIYVYVKL 54  
DB 298 IYAEKLDLNLKLRKTIISBEYEVFKAKAIDEVD-----LMKIGVGIPYVASEM 352

QY 55 VKENGAGFFWAGSVVGDQDMGVVGFPRNLVKEQRYQVQATKE 99  
DB 353 ANEDGLKV-----LSGQGADEL-FGY-----ARHERIYRGE 387

RESULT 9  
C9621  
fructose-bisphosphatase (EC 3.1.3.11) [validated] - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 03-Jun-2002  
C;Accession: C69621  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A.; Mathers: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron  
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
T.; Winters, P.; Wipat, A.; Yamano, K.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M  
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: C69621  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-671 <KUN>  
A;Cross-references: GB:Z99124; GB:AL009126; NID:G2636442; PIDN:CAB16056.1; PID:G2636566  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: fbp; Yyde  
C;Function:  
A;Description: catalyzes the hydrolysis of fructose-1,6-bisphosphate to fructose-6-phosph  
A;Pathway: gluconeogenesis  
A;Note: requires manganese ion for stability and phosphoenolpyruvate for activation  
C;Superfamily: Bacillus subtilis fructose-bisphosphatase; phosphoesterase core homology  
C;Keywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoest

Query Match 12.4%; Score 71.5; DB 1; Length 671;  
Best Local Similarity 22.8%; Pred. No. 19;  
Matches 26; Conservative 21; Mismatches 38; Indels 29; Gaps 4;

QY 4 FMRLASKKLCADDEC-VYTISLASAQEDYNAPDCRFINVKKGQOIYVYV 55  
DB 35 YLDLAAQYDCEEKVWVTEINLKA-----IINLPRGTGHEFVSDLHGEYQAFQHV 83

QY 56 KENGAG-----EFWAGSVVGDQDMGVVGFPRNLVKEQRYQVQATKE 99  
DB 84 LRNGSGRVKKEIRDFISGVYDREIDELALVYYPEDKLIKHKHDFPAKEALNE 137

RESULT 10  
A23516  
Balbiani ring 1 chain - midge (Chironomus tentans) (fragment)

C;Species: Chironomus tentans  
C;Date: 23-Aug-1987 #sequence\_revision 23-Aug-1987 #text\_change 21-Jul-2000  
C;Accession: A23516  
R;Hoog, C.; Engberg, C.; Wieslander, L.  
Nucleic Acids Res. 14, 703-719, 1986  
A;Title: A BR 1 gene in Chironomus tentans has a composite structure: a large repetiti  
A;Reference number: A23516; MUID:86120366; PMID:3003693  
A;Accession: A23516  
A;Molecule type: DNA  
A;Residues: 1-383 <HOO>  
A;Cross-references: GB:X03490; NID:G7043; PIDN:CAA27206.1; PID:G769785  
A;Note: the authors translated the codon GAA for residue 118 as Gly and TTC for residu  
C;Genetics:  
A;Introns: 273/1  
C;Superfamily: unassigned Balbiani ring proteins

Query Match 12.0%; Score 71; DB 2; Length 383;  
Best Local Similarity 28.0%; Pred. No. 12;  
Matches 26; Conservative 10; Mismatches 37; Indels 20; Gaps 3;

QY 6 DRLASKKLCADDEC-VYTISLASAQEDYNAPDCRFINVKKGQOIYVYVKENGAGETWA 65  
DB 303 DKDCCKNKNCDGAKF-----PECESNSKQSGMFDILAKLFRPQG-GDPEA 348

QY 66 GSVYGDQDMGVVGFPRNLVKEQRYQVQATK 98  
DB 349 GSVEVDGKK-----LSPEKKEKFGKALQDAVK 375

RESULT 11  
G96995  
ATP-dependent RNA helicase, superfamily II [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 14-Sep-2001  
C;Accession: G96995  
R;Nolling, J.; Bretton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Le  
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: G96995  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-585 <KUR>  
A;Cross-references: GB:AE001437; PIDN:BAK78754.1; PID:G15023664; GSPDB:GN00168  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0778

Query Match 12.0%; Score 71; DB 2; Length 585;  
Best Local Similarity 29.4%; Pred. No. 19;  
Matches 30; Conservative 13; Mismatches 37; Indels 22; Gaps 5;

QY 12 KLCADD-----ECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYVK-----LVKENGAGE 62  
DB 272 KCDEBVEIKVKRAIPLEVEDBSFYKD-----IXEGDAVVVFSKRVLEIAQSYSARG 326

QY 63 FWAGSVVGDQDMGVVGFPRNLVKEQRYQVQATKEVPTTD 104  
DB 327 IKASIIYGLPPEV-----RKLQYEQFIKKE-TKVLVTTD 360

RESULT 12  
C90186  
AAA family ATPase [imported] - Sulfolobus solfataricus  
C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 15-Jun-2001  
C;Accession: C90186  
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Cha  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder,  
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.

A;Reference number: A99139  
A;Accession: C90186  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-769 <KUR>  
A;Cross-references: GB:AE006641; NID:gl3813572; PIDN:AAK40746.1; GSPDB:GN00155  
C;Genetics:  
C;Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bind

Query Match 12.0%; Score 71; DB 2; Length 769;  
Best Local Similarity 35.0%; Pred. No. 25;  
Matches 28; Conservative 10; Mismatches 20; Indels 22; Gaps 5;  
  
QY 49 YVYSKLVKENG-----AGFEWAGSVVYDG--QDEMGVGVYFPRNL-----VKE 89  
DB 51 YTISRGIENGVDYVEIIGSGSALQAALIGDGIADNEIRVDGIYRRISGVIGIGDEVTVKR 110  
  
QY 90 QRVYQATKEV--PTDIDF 107  
DB 111 AQV-QDATKVLAPTQPISF 129

RESULT 13  
D72278  
endo-1,4-beta-mannosidase - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C;Accession: D72278  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
C.M.  
Nature 399, 323-329, 1999  
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A;Reference number: A72200; MUID:99287316; PMID:10360571  
A;Accession: D72278  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-669 <ARN>  
A;Cross-references: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36302.1; PID:g498178  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TM1227

Query Match 11.9%; Score 70.5; DB 2; Length 669;  
Best Local Similarity 27.6%; Pred. No. 24;  
Matches 32; Conservative 12; Mismatches 37; Indels 35; Gaps 6;  
  
QY 25 LASAQEDYNAPDCRFINVKKGQOI-----YVYSK-----LVKENGAGEF 63  
DB 393 LFWTGEDIREDTCSFILPKDGMIEIKTVEVRAGVFDYSNTFEKLSVKVEDLVFENEIHL 452  
  
QY 64 WAGSVYVG-----DGQDEMGVGVYFPRNLVKEQ---RVYQATKEVPTTDDIF 107  
DB 453 GYG-IYGFDLDTTRIPDGEHEMEFEGHFGQKTKVDSIKAKVNEA-RYVLAEEVDV 506

RESULT 14  
D86758  
orotate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Lactococcus lactis subsp. l  
C;Species: Lactococcus lactis subsp. lactis  
C;Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 17-May-2002  
C;Accession: D86758  
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaitlon, O.; Malarne, K.; Weissenbach, J.; Ehrli  
Genome Res. 11, 731-753, 2001  
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s  
A;Reference number: A86625; MUID:21235186; PMID:11337471  
A;Accession: D86758  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-209 <STO>  
A;Cross-references: GB:AE005176; PID:gl2724022; PIDN:AAK05166.1; GSPDB:GN00146  
A;Experimental source: strain IL1403

C;Genetics:  
A;Gene: pyrE  
C;Superfamily: orotate phosphoribosyltransferase; orotate phosphoribosyltransferase hom  
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 11.9%; Score 70; DB 2; Length 209;  
Best Local Similarity 26.9%; Pred. No. 7.7;  
Matches 21; Conservative 15; Mismatches 42; Indels 0; Gaps 0;  
  
QY 25 LASAQEDYNAPDCRFINVKKGQOIYVYSKLVKENGAGFEWAGSVVYDGQDEMGVGVYFPR 84  
DB 95 IRSKPKDHGAGNQVGRVTKGQRMVVVEDLSTGGSVLEAVAAAREGADVILGVVAIFTY 154  
  
QY 85 NLVKEQRVYQATKEVPT 102  
DB 155 ELEKANRRFADAGVKLAT 172

RESULT 15  
F90113  
cell division cycle 2 homolog [imported] - Guillardia theta nucleomorph  
C;Species: nucleomorph Guillardia theta  
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 15-Jun-2001  
C;Accession: F90113  
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re  
Nature 410, 1091-1096, 2001  
A;Title: The highly reduced genome of an enslaved algal nucleus.  
A;Reference number: A99082; MUID:11323671; PMID:11323671  
A;Accession: F90113  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-295 <DOU>  
A;Cross-references: GB:AJ010592; NID:gl2580757; PIDN:CAC27075.1; GSPDB:GN00151  
C;Genetics:  
A;Map position: 2  
A;Genome: nucleomorph  
C;Superfamily: kinase-related transforming protein; protein kinase homology  
C;Keywords: nucleomorph

Query Match 11.8%; Score 69.5; DB 2; Length 295;  
Best Local Similarity 28.0%; Pred. No. 13;  
Matches 28; Conservative 14; Mismatches 31; Indels 27; Gaps 6;  
  
QY 8 LASKKLCADECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKENGAG--GEFWA 65  
DB 157 LCSKKIKLSKIV-TLW-----YRAPE-----ILLGHFYDYSVDMWSFGCVIGELIT 203  
  
QY 66 GSVYGDQDEMGVGVYFPRNLVKEQRVYQATKEVPTTDDI 105  
DB 204 GEILFGKSELQDL-----NKIFQ--TIGTPTTEI 231

Search completed: December 29, 2003, 16:10:40  
Job time : 12.4006 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 4.31373 Seconds  
(without alignments)  
1199.181 Million cell updates/sec

Title: US-10-019-455A-24

Perfect score: 590

Sequence: 1 HGFMRLASKKLCADCEV.....RVQEQATKEVPTDIDFFCE 110

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query %	Length	DB ID	Description
1	590	100.0	128	1	OTOR_HUMAN
2	547	92.7	128	1	OTOR_MOUSE
3	477.5	80.9	132	1	OTOR_CHICK
4	390	66.1	133	1	OTOR_PANCA
5	253.5	43.0	131	1	MIA_HUMAN
6	252.5	42.8	130	1	MIA_BOVIN
7	250.5	42.5	130	1	MIA_RAT
8	235.5	39.9	130	1	MIA_MOUSE
9	88.5	15.0	847	1	VAV3_MOUSE
10	86.5	14.7	845	1	VAV3_HUMAN
11	86.5	14.7	847	1	VAV3_HUMAN
12	85.5	14.5	843	1	VAV3_RAT
13	85.5	14.5	845	1	VAV_MOUSE
14	82.5	14.0	868	1	VAV2_MOUSE
15	81.5	13.8	878	1	VAV2_HUMAN
16	78.5	13.3	1589	1	CC25_YEAST
17	74	12.5	2161	1	SHK1_HUMAN
18	71.5	12.1	541	1	ASN1_METJA
19	71	12.0	2167	1	SHK1_RAT
20	70.5	11.9	905	1	ZO3_MOUSE
21	70	11.9	209	1	PYRE_LACIA
22	70	11.9	209	1	PYRE_STRP3
23	70	11.9	209	1	PYRE_STRPY
24	70	11.9	1217	1	ITN1_RAT
25	70	11.9	1815	1	SHK3_RAT
26	69	11.7	392	1	PURE_ACICA
27	69	11.7	444	1	PURE_METJA
28	69	11.7	670	1	YBY2_SCHPO
29	68.5	11.6	505	1	SRK1_SPOLA
30	68.5	11.6	506	1	SRK4_SPOLA
31	68	11.5	162	1	BAR2_CHIPA
32	68	11.5	259	1	YA20_METJA
33	68	11.5	534	1	VL2_Hpv37

34	68	11.5	1714	1	ITN1_MOUSE
35	68	11.5	1721	1	ITN1_HUMAN
36	67	11.4	383	1	PGL3_ASPNG
37	67	11.4	474	1	SYE_VIBCH
38	67	11.4	518	1	VL2_HPV08
39	67	11.4	524	1	VL2_HPV17
40	66.5	11.3	209	1	PYRE_LISMO
41	66.5	11.3	793	1	VAV_DROME
42	66	11.2	209	1	PYRE_STRMU
43	66	11.2	326	1	BAR1_CHIPA
44	66	11.2	518	1	VL2_HPV36
45	66	11.2	898	1	ZO3_CANFA

#### ALIGNMENTS

##### RESULT 1

ID	OTOR_HUMAN	STANDARD;	PRT;	128 AA.
AC	Q9NRC9;	2001 (Rel. 40, Created)		
DT	16-OCT-2001	(Rel. 40, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Otoraplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory activity like protein).			
GN	OTOR OR FDP OR MIAL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cochlea;			
RX	MEDLINE=20334619; PubMed=10873378;			
RA	Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S., Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;			
RT	"A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping."			
RL	Genomics 66:242-248 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20568254; PubMed=10998416;			
RA	Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelings S., Petit C.;			
RT	"Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme."			
RL	J. Biol. Chem. 275:40036-40041 (2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Cochlea;			
RX	MEDLINE=21100875; PubMed=1161796;			
RA	Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;			
RT	"Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation."			
RL	Genomics 71:40-52 (2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21638749; PubMed=11780052;			
RA	Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L., Jones M., Stavridis G., Almeida J.P., Beare D.M., Beare D.M., Bailey J., Barlow K.F., Bates K.N., Bridgeman A.M., Brown A.J., Beasley O.P., Bird C.P., Blakey S.E., Carder C., Carter N.P., Buck D., Burrill W.D., Butler A.P., Clark G., Clark L.N., Clark S.Y., Clee C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Graffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			

RA Levaeslaih M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,  
 RA Milne K., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Scathaling S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
 CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL: AF233261; AAF82078.1; -;  
 CC EMBL: AF243505; AAG42356.1; -;  
 CC EMBL: AJ242582; CAC27443.1; -;  
 CC EMBL: AJ252324; CAC28085.1; -;  
 CC EMBL: AJ252325; CAC28085.1; JOINED.  
 CC EMBL: AJ252326; CAC28085.1; JOINED.  
 CC EMBL: AJ252327; CAC28085.1; JOINED.  
 CC EMBL: AL034428; CAC16848.1; -;  
 CC HSP: Q16674; 111J.  
 CC Genew; HGNC:8517; OTOR.  
 CC MIM; 606067; -;  
 CC GO; GO:0007605; P:hearing; TAS.  
 CC InterPro; IPR001452; SH3.  
 CC Pfam; PF00018; SH3; 1.  
 CC SMART; SM00326; SH3; 1.  
 CC PROSITE; PS50002; SH3; FALSE\_NEG.  
 CC Signal; SH3 domain.  
 CC SIGNAL 1 18 POTENTIAL.  
 CC CHAIN 19 128 OTORAPLIN.  
 CC DOMAIN 39 110 SH3.  
 CC DISULFID 32 37 BY SIMILARITY.  
 CC DISULFID 55 127 BY SIMILARITY.  
 CC SEQUENCE 128 AA; 14332 MW; 9B52C7F5D4FB700 CRC64;  
 SQ  
 Query Match 100.0%; Score 590; DB 1; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-54;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HGIFNDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 60  
 DB 19 HGIFNDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 78  
 QY 61 GEFWAGSVYGDQDGMGVGYPFRNLVKEQRYQVQATKEVPTTIDIDFCE 110  
 DB 79 GEFWAGSVYGDQDGMGVGYPFRNLVKEQRYQVQATKEVPTTIDIDFCE 128  
 RESULT 2  
 OTOR\_MOUSE  
 ID\_OTOR\_MOUSE STANDARD; PRT; 128 AA.  
 AC Q9JUE3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Otoraplin precursor (Melanoma inhibitory activity-like protein).  
 GN OTOR OR MIAL.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20334619; PubMed=10873378;  
 RA Robertson N.G.; Heller S.; Lin J.S.; Resendes B.L.; Weremowicz S.,  
 RA Denis C.S.; Bell A.M.; Hudspeth A.J.; Morton C.C.;  
 RA "A novel conserved cochlear gene, OTOR: identification, expression  
 RT analysis, and chromosomal mapping.";  
 RL Genomics 66:242-248(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Petal;  
 RX MEDLINE=21100875; PubMed=1161796;  
 RA Rentorff N.D.; Frodin M.; Attie-Bitach T.; Vekemans M.; Tommerup N.;  
 RA "Identification and characterization of an inner ear-expressed human  
 RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent  
 RT polymorphism that abolishes translation.";  
 RL Genomics 71:40-52(2001).  
 CC -!- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.  
 CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
 CC -!- SIMILARITY: Contains 1 SH3 domain.  
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 CC -----  
 CC EMBL: AF233333; AAF82079.1; -;  
 CC EMBL: AJ243939; CAC27444.1; -;  
 CC HSP: Q16674; 111J.  
 CC MGD; MGI:188678; Otor.  
 CC GO; GO:0001502; P:cartilage condensation; IMP.  
 CC InterPro; IPR001452; SH3.  
 CC Pfam; PF00018; SH3; 1.  
 CC SMART; SM00326; SH3; 1.  
 CC PROSITE; PS50002; SH3; 1.  
 CC Signal; SH3 domain.  
 CC SIGNAL 1 18 POTENTIAL.  
 CC CHAIN 19 128 OTORAPLIN.  
 CC DOMAIN 39 110 SH3.  
 CC DISULFID 32 37 BY SIMILARITY.  
 CC DISULFID 55 127 BY SIMILARITY.  
 CC SEQUENCE 128 AA; 14328 MW; 3DD47D4C77C4A7FD CRC64;  
 SQ  
 Query Match 92.7%; Score 547; DB 1; Length 128;  
 Best Local Similarity 90.0%; Pred. No. 1.7e-49;  
 Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 HGIFNDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 60  
 DB 19 HGIFNDRLASKKLCADDECVVTISLASAQEDYNAPDCRFINVKGGQIYVYVKLVKNGA 78  
 QY 61 GEFWAGSVYGDQDGMGVGYPFRNLVKEQRYQVQATKEVPTTIDIDFCE 110  
 DB 79 GEFWAGSVYGDQDGMGVGYPFRNLVKEQRYQVQATKEVPTTIDIDFCE 128  
 RESULT 3  
 OTOR\_CHICK  
 ID\_OTOR\_CHICK STANDARD; PRT; 132 AA.  
 AC Q918P6;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Otoraplin precursor.  
 GN OTOR.

```

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF233518; AAF82727.1; -.
DR HSSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain. 23
FT CHAIN 1 23
FT DOMAIN 42 114 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 131 BY SIMILARITY.
FT SEQUENCE 132 AA; 15177 MW; 9D1CB07FD353CE1C CRC64;
SQ
Query Match 80.9%; Score 477.5; DB 1; Length 132;
Best Local Similarity 80.0%; Pred. No. 2.6e-42;
Matches 88; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
QY 2 GTFMDRLASKKLCADDECVYITSLASQEDYNAPDCRFNVKKGQIYVYSLVKENGAG 61
Db 23 GTFMDRLASKKLCADDECVYITSLVRAEDYNAPDCRFNVKKGQIYVYSLVKERESG 82
QY 62 EFWAGSVYGDG-QDEMGVGVYFPRNLVKEQRYQVQATKEVPTTIDIDFFCE 110
Db 83 EFWAGSVYGEYEDHMGTVGVYFPRSLVSEQHVYQVQANKTPTTIDIDFFCE 132
RESULT 4
OTOR_RANCA
ID OTOR_RANCA STANDARD; PRT; 133 AA.
AC Q918P5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).

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CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; AF233519; AAF82728.1; -.
DR HSSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
DR SIGNAL; SH3 domain. 23
FT CHAIN 1 23
FT DOMAIN 48 115 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 132 BY SIMILARITY.
FT SEQUENCE 133 AA; 15243 MW; 25440C1A3CF911AE CRC64;
SQ
Query Match 66.1%; Score 390; DB 1; Length 133;
Best Local Similarity 58.9%; Pred. No. 2.6e-33;
Matches 66; Conservative 26; Mismatches 18; Indels 2; Gaps 2;
QY 1 HGTFMDRLASKKLCADDECVYITSLASQEDYNAPDCRFNVKKGQIYVYSLVKENG-G 59
Db 22 YGVYMQKLSKLCADDECVYITSLVRAEDYNAPDCRFNVKKGQIYVYSLVKENDD 81
QY 60 AGEFWAGSVYGDG-QDEMGVGVYFPRNLVKEQRYQVQATKEVPTTIDIDFFCE 110
Db 82 AGEFWAGSVYSDQYRQDQGLVGFPSLSVLTLYKDELQELPTTAVDFFCD 133
RESULT 5
MIA_HUMAN
ID MIA_HUMAN STANDARD; PRT; 131 AA.
AC Q16674;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity).
GN MIA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bosserhoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachimczak P., Lottspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
RL Cancer Res. 54:5695-5701(1994).
RN [2]_
RP SEQUENCE FROM N.A.
RX TISSUE=Placenta;
RX MEDLINE=96132947; PubMed=8550608;
RA Bosserhoff A.-K., Hein R., Bogdahn U., Buettner R.;
RT "Structure and promoter analysis of the gene encoding the human
RT melanoma-inhibiting protein MIA.";
RL J. Biol. Chem. 271:490-495(1996).
RN [3]_
RP SEQUENCE FROM N.A.
RX TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;

```

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Frange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimmel J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krywinski M.I., Skalska U., Smalls D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (1.39 ANGSTROMS) OF 25-131.  
RX MEDLINE=21244635; PubMed=11331761;  
RA Loughheed J.C., Holton J.M., Alber T., Bazan J.F., Handel T.M.;  
RT "Structure of melanoma inhibitory activity protein, a member of a  
RT recently identified family of secreted proteins.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520(2001).  
CC -!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO  
CC AS WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND  
CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND  
CC INFREQUENTLY IN GLIOMA CELL LINES.  
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
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CC -----  
DR EMBL; X75450; CAA53203.1; -.  
DR EMBL; X84707; CAA59195.1; -.  
DR EMBL; BC005910; AAH05910.1; -.  
DR PIR; I38019; I38019.  
DR PDB; 1IIJ; 16-MAY-01.  
DR PDB; 1HJD; 29-JUN-02.  
DR PDB; 1K0X; 24-JUL-02.  
DR Genew; HGNC:7076; MIA.  
DR MIM; 601340; -.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0008283; P:cell proliferation; TAS.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50002; SH3; 1.  
KW Growth factor; Signal; SH3 domain; 3D-structure.  
FT SIGNAL 1 24  
FT CHAIN 25 131 MELANOMA DERIVED GROWTH REGULATORY  
FT PROTEIN.  
FT SH3.  
FT DOMAIN 43 113  
FT DISULFID 36 41  
FT DISULFID 59 130  
FT STRAND 33 36  
FT TURN 39 40  
FT STRAND 46 50  
FT STRAND 54 54  
FT TURN 59 60  
FT STRAND 61 61  
FT STRAND 64 64

FT TURN 66 67  
FT STRAND 69 76  
FT HELIX 78 80  
FT TURN 81 82  
FT STRAND 83 89  
FT TURN 93 94  
FT STRAND 96 96  
FT STRAND 101 104  
FT HELIX 105 107  
FT STRAND 108 113  
FT STRAND 119 122  
FT HELIX 126 128  
SQ SEQUENCE 131 AA; 14509 MW; 4D3BB30BD6008BDC CRC64;  
  
Query Match 43.0%; Score 253.5; DB 1; Length 131;  
Best Local Similarity 45.4%; Pred. No. 2.9e-19;  
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;  
  
Qy 5 MDRLSKKLCADDECVTTSLSAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAGE-F 63  
Db 27 MPKLADRLKADQCESHPI SMAVALQDYMAPDCRFLLTHRGQVVYVFSKL---KGRGLP 83  
  
Qy 64 WAGSVYGDQDEMGV-VGYFPRNLVKEQRVYQATKEVPTTDDIFFCE 110  
Db 84 WGSVQGDYVYGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYCQ 131  
  
RESULT 6  
MIA\_BOVIN STANDARD; PRT; 130 AA.  
ID MIA\_BOVIN STANDARD; PRT; 130 AA.  
AC Q28038;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, last sequence update)  
DT 28-FEB-2003 (Rel. 41, last annotation update)  
DE Melanoma derived growth regulatory protein precursor (Melanoma  
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive  
DE protein) (CD-RAP).  
GN MIA OR CDRA.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96216414; PubMed=8621736;  
RA Dietz U.H., Sandell L.J.;  
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and  
RT during chondrogenesis.";  
RL J. Biol. Chem. 271:3311-3316(1996).  
CC -!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND  
CC MAINTENANCE.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.  
CC -!- INDUCTION: Repressed by retinoic acid.  
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.  
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.  
CC -!- SIMILARITY: Contains 1 SH3 domain.  
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CC -----  
DR EMBL; U51437; AAC48523.1; -.  
DR HSPF; Q16674; 1IIJ.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00018; SH3; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS50002; SH3; 1.

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KW Growth factor; Signal; SH3 domain.
FT SIGNAL 1 22 BY SIMILARITY
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
FT CHAIN 23 130 PROTEIN.
FT DOMAIN 42 112 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 129 BY SIMILARITY.
SQ SEQUENCE 130 AA; 14353 MW; 95D153161C78E02A CRC64;

Query Match 42.8%; Score 252.5; DB 1; Length 130;
Best Local Similarity 45.0%; Pred. No. 3.7e-19;
Matches 50; Conservative 22; Mismatches 28; Indels 11; Gaps 4;

QY 5 MRLASKKLCADCECVYTISLSAQEDYNAPDCRFNVKKGQOIYVYVKLVKENGAGE-F 63
Db 26 MPKLADRKLCADCECHSPISMAVALQDYVAPDCRFLLIHOGVYVIFSKL---KGRGLRF 82

QY 64 WAGSV---YGDQDEMGVGVYPPRNVLKQRYVQATKEVPTTIDFFCE 110
Db 83 WGGSVQDGYGDAARL---GYFPSSIVREDQTLKPAKTDVKTIDWDFYQC 130

RESULT 7
MIA RAT
ID MIA RAT STANDARD; PRT; 130 AA.
AC Q62946; P97591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
GN MIA OR CDAP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Mammary gland;
RA Lu J.X.;
RT "Gene expression changes associated with chemically-induced rat
RT mammary carcinogenesis.";
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 34-124 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=96216414; PubMed=8621736;
RA Dietz U.H.; Sandell L.J.;
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
RT during chondrogenesis.";
RL J. Biol. Chem. 271:3311-3316 (1996).
CC -!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
CC -!- MAINTENANCE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -!- INDUCTION: Repressed by retinoic acid.
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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CC -----
DR EMBL; U51438; AAC52481.1; -
DR EMBL; U67884; BAB40659.1; -
DR HSSP; Q16674; 111J.
DR InterPro; IPR001452; SH3.
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DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; FALSE NEG.
KW Growth factor; Signal; SH3 domain.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
FT CHAIN 23 130 PROTEIN.
FT DOMAIN 42 112 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 129 BY SIMILARITY.
FT CONFLICT 46 47 MA -> VT (IN REF. 2).
SQ SEQUENCE 130 AA; 14536 MW; 5F99149AECF74501 CRC64;

Query Match 42.5%; Score 250.5; DB 1; Length 130;
Best Local Similarity 44.4%; Pred. No. 5.9e-19;
Matches 48; Conservative 23; Mismatches 32; Indels 5; Gaps 3;

QY 5 MRLASKKLCADCECVYTISLSAQEDYNAPDCRFNVKKGQOIYVYVKLVKENGAGE-F 63
Db 26 MPKLADRKLCADCECHSPISMAVALQDYVAPDCRFLLIHOGVYVIFSKL---KGRGLRF 82

QY 64 WAGSVGDGQDEMGV-VGYPPRNVLKQRYVQATKEVPTTIDFFCE 110
Db 83 WGGSVQDGYGDLAAHLGYFPSSIVREDTLKPKQVDMKTDEWDFYQC 130

RESULT 8
MIA MOUSE
ID MIA MOUSE STANDARD; PRT; 130 AA.
AC Q61865; O09086; P97495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
GN MIA OR CDAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A.; Bosserhoff A.-K.; Apfel R.; Behl C.; Hessdoerfer B.;
RA Schmitt A.; Jachimczak P.; Lottspeich F.; Buettner R.; Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA.";
RL Cancer Res. 54:5695-5701 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97251341; PubMed=9097023;
RA Bosserhoff A.K.; Kondo S.; Moser M.; Dietz U.; Copeland N.G.;
RA Gilbert D.J.; Jenkins N.A.; Buettner R.; Sandell L.J.;
RT "Mouse CD-RAP/MIA gene: structure, chromosomal localization, and
RT expression in cartilage and chondrosarcoma.";
RL Dev. Dyn. 208:516-525 (1997).
CC -!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AS
CC WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
CC INFREQUENTLY IN GLIOMA CELL LINES.
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: Contains 1 SH3 domain.
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 CC -----

DR EMBL; X94322; CAA63983.1; --  
 DR EMBL; U85612; AAB42082.1; --  
 DR EMBL; X97965; CAA66608.1; --  
 DR HSSP; Q16674; I11J.  
 DR MGD; MGI:109615; Mia.  
 DR GO; GO:0007160; P:cell-matrix adhesion; IMP.  
 DR GO; GO:0030198; P:extracellular matrix organization and bioge. . .; IMP.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00018; SH3; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR PROSITE; PS50002; SH3; FALSE NEG.  
 KW Growth factor; Signal; SH3 domain.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY  
 FT PROTEIN.  
 FT DOMAIN 42 112 SH3.  
 FT DISULFID 35 40 BY SIMILARITY.  
 FT DISULFID 58 129 BY SIMILARITY.  
 FT CONFLICT 112 113 TL -> NS (IN REF. 1).  
 SQ SEQUENCE 130 AA; 14593 MW; 16C957459C5BB5F9 CRC64;

Query Match 39.9%; Score 235.5; DB 1; Length 130;  
 Best Local Similarity 43.5%; Pred. No. 2.1e-17;  
 Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;

Qy 5 MDRLASKKLCDDCVYITISLASQEDYNAPCRFINVKKGQIIVYVSKLVKENGAGB-F 63  
 Db 26 MKPLADWKLCADECSHPISVAVALQDYVADPCFLTYRGQVIVFVSKL---KGRGLP 82  
 Qy 64 WAGSVYGGDQEMGV-VGYFPRNLVKEQVRVQEATKEVPTTIDPFCE 110  
 Db 83 WGGSVQGGYVGLAARLGYFSSIVREDLTLPKGIKDMKTQWDFYQ 130

## RESULT 9

ID VAV3 MOUSE STANDARD; PRT; 847 AA.  
 AC Q9R0C8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Vav-3 protein.  
 GN VAV3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20179693; PubMed=10713454;  
 RA Trenkle T., McClelland M., Adlkofer K., Welsh J.;  
 RT "Major transcript variants of VAV3, a new member of the VAV family of  
 RT guanine nucleotide exchange factors.";  
 RL Gene 245:139-149(2000).  
 CC -!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,  
 CC -!- TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE  
 CC STATES OF THOSE GTPASES (BY SIMILARITY).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=Alpha;  
 CC IsoId=Q9R0C8-1; Sequence=Displayed;  
 CC Name=Beta;  
 CC IsoId=Q9R0C8-2; Sequence=Not described;  
 CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
 CC -!- SIMILARITY: Contains 1 DBU-nomology (DH) domain.  
 CC -!- SIMILARITY: Contains 1 PH domain.  
 CC -!- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
 CC binding domain.  
 CC -!- SIMILARITY: Contains 1 SH2 domain.

## -!- SIMILARITY: Contains 2 SH3 domains.

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 CC or send an email to license@isb-sib.ch).  
 CC -----

DR EMBL; AF067816; AAF09171.1; --  
 DR HSSP; P29355; ISEM.  
 DR MGD; MGI:1888518; Vav3.  
 DR InterPro; IPR001715; Calponin-like.  
 DR InterPro; IPR003247; CH type.  
 DR InterPro; IPR002219; DAG\_PE-bind.  
 DR InterPro; IPR001331; GDS\_CDC24.  
 DR InterPro; IPR001849; PH\_1.  
 DR InterPro; IPR000219; RhoGEF.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR003096; SM22\_calponin.  
 DR Pfam; PF003307; CH; 1.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00621; RhoGEF; 1.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR PRINTS; PR00401; SH2DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00888; SM22CALPONIN.  
 DR ProDom; PD001527; CH\_type; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00109; C1; 1.  
 DR SMART; SM00033; CH; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00325; RhoGEF; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50021; CH; 1.  
 DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
 DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
 DR PROSITE; PS50010; DH\_2; 1.  
 DR PROSITE; PS00741; DH\_1; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;  
 KW Guanine-nucleotide releasing factor; Alternative splicing.  
 FT DOMAIN 1 119 CH.  
 FT DOMAIN 192 371 DH.  
 FT DOMAIN 400 502 PH.  
 FT DOMAIN 514 562 PHORBOL-ESTER AND DAG BINDING.  
 FT DOMAIN 592 660 SH3 1.  
 FT DOMAIN 672 766 SH2.  
 FT DOMAIN 788 847 SH3 2.  
 SQ SEQUENCE 847 AA; 97946 MW; 9A6B63F0D9E60F8F CRC64;

## Query Match

Best Local Similarity 15.0%; Score 88.5; DB 1; Length 847;

Matches 21; Conservative 14; Mismatches 21; Indels 11; Gaps 2;

Qy 23 ISLASAQEDYNAPCRFINVKKGQIIVYVSKLVKENGAGBFWAGSVYGGDQEMGVYGYF 82  
 Db 790 LGIAIARYDFCARDRELKLGDMVKYTKM-----SANGWWRGEVNGR-----VGWF 838

Qy 83 PRNLVKE 89

Db 839 PSTYVEE 845

RESULT 10

VAV\_HUMAN  
ID VAV\_HUMAN STANDARD; PRT; 845 AA.  
AC P15498; Q15860;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Vav proto-oncogene.  
GN VAV1 OR VAV.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Denninger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;  
RT "Transcriptional regulation of the vav proto-oncogene.";  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 62-845 FROM N.A.  
RX MEDLINE=90005432; PubMed=2477241;  
RA Katrav S., Martin-Zanca D., Barbacid M.;  
RT "vav, a novel human oncogene derived from a locus ubiquitously  
RT expressed in hematopoietic cells.";  
RL EMBO J. 8:2283-2290(1989).  
RN [3]  
RP SEQUENCE OF 1-61 FROM N.A.  
RX MEDLINE=91172176; PubMed=2005887;  
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;  
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-  
RT oncogene activates its transforming potential.";  
RL Mol. Cell. Biol. 11:1912-1920(1991).  
RN [4]  
RP SEQUENCE OF 299-837 FROM N.A.  
RA Romero F.;  
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 299-334 FROM N.A.  
RX MEDLINE=96038895; PubMed=7478592;  
RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,  
RA Tortolero M., Fischer S.;  
RT "The proline-rich region of Vav binds to Grb2 and Grb3-3.";  
RL Oncogene 11:1665-1669(1995).  
RN [6]  
RP SIMILARITY TO CDC24 FAMILY.  
RX MEDLINE=9228488; PubMed=1565462;  
RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;  
RT "The hematopoietically expressed vav proto-oncogene shares homology  
RT with the db1 Gbp-GTP exchange factor, the bcr gene and a yeast gene  
RL (CDC24) involved in cytoskeletal organization.";  
CC Oncogene 7:611-618(1992).  
CC -1- FUNCTION: Couples tyrosine kinase signals with the activation of  
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or  
CC proliferation.  
CC -1- SUBUNIT: Interacts with SLA (By similarity). Interacts with Grb2  
CC and Grb3.  
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT  
CC NOT IN OTHER CELL TYPES.  
CC -1- PTM: Phosphorylated on tyrosine residues.  
CC -1- MISCELLANEOUS: 'Vav' stands for the sixth letter of the Hebrew  
CC alphabet.  
CC -1- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -1- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC -1- SIMILARITY: Contains 1 PH domain.  
CC -1- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
CC binding domain.  
CC -1- SIMILARITY: Contains 1 SH2 domain.  
CC -1- SIMILARITY: Contains 2 SH3 domains.  
CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts  
CC in position 322 and 355.  
CC  
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-----  
CC EMBL; AF030227; AAC25011.1; JOINED.  
CC EMBL; AF030201; AAC25011.1; JOINED.  
CC EMBL; AF030202; AAC25011.1; JOINED.  
CC EMBL; AF030203; AAC25011.1; JOINED.  
CC EMBL; AF030204; AAC25011.1; JOINED.  
CC EMBL; AF030205; AAC25011.1; JOINED.  
CC EMBL; AF030206; AAC25011.1; JOINED.  
CC EMBL; AF030207; AAC25011.1; JOINED.  
CC EMBL; AF030208; AAC25011.1; JOINED.  
CC EMBL; AF030209; AAC25011.1; JOINED.  
CC EMBL; AF030210; AAC25011.1; JOINED.  
CC EMBL; AF030211; AAC25011.1; JOINED.  
CC EMBL; AF030212; AAC25011.1; JOINED.  
CC EMBL; AF030213; AAC25011.1; JOINED.  
CC EMBL; AF030214; AAC25011.1; JOINED.  
CC EMBL; AF030215; AAC25011.1; JOINED.  
CC EMBL; AF030216; AAC25011.1; JOINED.  
CC EMBL; AF030217; AAC25011.1; JOINED.  
CC EMBL; AF030218; AAC25011.1; JOINED.  
CC EMBL; AF030219; AAC25011.1; JOINED.  
CC EMBL; AF030220; AAC25011.1; JOINED.  
CC EMBL; AF030221; AAC25011.1; JOINED.  
CC EMBL; AF030222; AAC25011.1; JOINED.  
CC EMBL; AF030223; AAC25011.1; JOINED.  
CC EMBL; AF030224; AAC25011.1; JOINED.  
CC EMBL; AF030225; AAC25011.1; JOINED.  
CC EMBL; AF030226; AAC25011.1; JOINED.  
CC EMBL; X16316; AAA34383.1; ALT\_FRAME.  
CC EMBL; M59834; AAA63267.1; -.  
CC EMBL; X83931; CAA58783.1; -.  
CC PIR; B39576; TVHUVV.  
CC HGSP; P29354; IGRI.  
CC TRANSFAC; T00880; -.  
CC Genew; HGNC:12657; VAV1.  
CC MIM; 164875; -.  
CC DR GO; 0003700; F:transcription factor activity; TAS.  
CC DR GO; 0007048; P:oncogenesis; TAS.  
CC DR InterPro; IPR001715; Calponin-like.  
CC InterPro; IPR003247; CH-type.  
CC InterPro; IPR002219; DAG\_PE-bind.  
CC InterPro; IPR001331; GDS\_CDC24.  
CC DR InterPro; IPR001849; PH.  
CC DR InterPro; IPR000219; RhoGEF.  
CC DR InterPro; IPR000980; SH2.  
CC DR InterPro; IPR001452; SH3.  
CC DR InterPro; IPR003096; SM22\_calponin.  
CC DR Pfam; PF00307; CH; 1.  
CC DR Pfam; PF00130; DAG\_PE-bind; 1.  
CC DR Pfam; PF00169; PH; 1.  
CC DR Pfam; PF00621; RhoGEF; 1.  
CC DR Pfam; PF00017; SH2; 1.  
CC DR Pfam; PF00018; SH3; 2.  
CC DR PRINTS; PR00401; SH2DOMAIN.  
CC DR PRINTS; PR00452; SH3DOMAIN.  
CC DR PRINTS; PR00888; SM22CALPONIN.  
CC DR ProDom; PD001527; CH type; 1.  
CC DR ProDom; PD000093; SH2; 1.  
CC DR ProDom; PD000066; SH3; 1.  
CC DR SMART; SM00109; CH; 1.  
CC DR SMART; SM00033; CH; 1.  
CC DR SMART; SM00233; PH; 1.  
CC DR SMART; SM00325; RhoGEF; 1.  
CC DR SMART; SM00252; SH2; 1.  
CC DR SMART; SM00326; SH3; 2.  
CC DR PROSITE; PS50021; CH; 1.  
CC DR PROSITE; PS00479; DAG PE BIND DOM 1; 1.  
CC DR PROSITE; PS50081; DAG PE BIND\_DOM\_2; 1.  
CC DR PROSITE; PS50010; DH\_2; 1.





```

Query Match          14.7%; Score 86.5; DB 1; Length 847;
Best Local Similarity 31.3%; Pred. No. 0.33;
Matches 2; Conservative 14; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLASAQEDYNAPDRFINVKKGQIIYVYVKLVKENGAGFEWAGSVYGDQDWMGVVGYF 82
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 790 LGIAIARYDFCARDMRELSLLKGDVVKIYTKM-----SANGWWRGVEVNGR-----VGWF 838

QY 83 PRNLVKE 89
    | : : : :
Db 839 PSTYVEE 845

RESULT 12
VAV_RAT          STANDARD;          PRT;          843 AA.
ID VAV_RAT
AC PS4100;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vav proto-oncogene (p95).
GN VAV1 OR VAV.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99323974; PubMed=10395673;
RA Song J.S., Haleem-Smith H., Arudchandran R., Gomez J., Scott P.M.,
RA Mill J.F., Tan T.-H., Rivera J.;
RT "Tyrosine phosphorylation of Vav stimulates IL-6 production in mast
RL J. Immunol. 163:802-810(1999).
CC -!- FUNCTION: Couples tyrosine kinase signals with the activation of
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or
CC proliferation.
CC -!- SUBUNIT: Interacts with SLA (By similarity).
CC -!- PTM: Phosphorylated on tyrosine residues.
CC -!- SIMILARITY: Contains 1 calponin-homology (CH) domain.
CC -!- SIMILARITY: Contains 1 DBL-homology (DH) domain.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 zinc-dependent phosphol-ester and DAG
CC binding domain.
CC -!- SIMILARITY: Contains 1 SH2 domain.
CC -!- SIMILARITY: Contains 2 SH3 domains.
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CC -----
DR EMBL; U39476; AAA98606.1; -.
DR HSSP; P29354; 1GRI.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG_PE_bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE_bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.

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DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00886; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50003; PH DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.
FT DOMAIN 1 119
FT DOMAIN 194 373 DH.
FT DOMAIN 402 504 PH.
FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 615 658 SH3 1.
FT DOMAIN 669 763 SH2.
FT DOMAIN 780 840 SH3 2.
SQ SEQUENCE 843 AA; 97953 MW; C4A5CACD45FCB80E CRC64;

Query Match          14.5%; Score 85.5; DB 1; Length 843;
Best Local Similarity 31.4%; Pred. No. 0.42;
Matches 2; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDRFINVKKGQIIYVYVKLVKENGAGFEWAGSVYGDQDWMGVVGYFPRN 85
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 785 AKARYDFCARDRSELSLKEDII-----KILNKKGQGGWWRGEIYGR-----IGWPPSN 833

QY 86 LVKEQRYQE 95
    | : | | |
Db 834 YVEED--YSE 841

RESULT 13
VAV_MOUSE
ID VAV_MOUSE          STANDARD;          PRT;          845 AA.
AC P27870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vav proto-oncogene.
GN VAV1 OR VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228488; PubMed=1565462;
RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the dbl GDP-GTP exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization.";
RL Oncogene 7:611-618(1992).
RN [2]
RP SEQUENCE OF 1-93 FROM N.A.
RX MEDLINE=91172176; PubMed=2005887;
RA Katrav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RL onogene activates its transforming potential.";
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [3]
RP INTERACTION WITH SLA.

```

RX MEDLINE=20130290; PubMed=10662792;  
RA Sosinowski T., Pandey A., Dixit V.M., Weiss A.;  
RT "Src-like adaptor protein (SLAP) is a negative regulator of T cell  
RL receptor signaling.";  
J. Exp. Med. 191:463-474(2000).  
CC -|- FUNCTION: Couples tyrosine kinase signals with the activation of  
CC the Rho/Rac GTPases, thus leading to cell differentiation and/or  
CC proliferation.  
CC -|- SUBUNIT: Interacts with SLA.  
CC -|- TISSUE SPECIFICITY: Widely expressed in hematopoietic cells but  
CC not in other cell types.  
CC -|- PTM: Phosphorylated on tyrosine residues (By similarity).  
CC -|- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -|- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC -|- SIMILARITY: Contains 1 PH domain.  
CC -|- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
CC binding domain.  
CC -|- SIMILARITY: Contains 1 SH2 domain.  
CC -|- SIMILARITY: Contains 2 SH3 domains.  
CC  
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DR EMBL; X64361; CAA45713.1; -;  
DR EMBL; M59833; AAA63402.1; -;  
DR PIR; A61187; TVMSV.  
DR PDB; 1F5X; 15-SEP-00.  
DR PDB; 1GCP; 28-JAN-03.  
DR PDB; 1GCP; 28-JAN-03.  
DR PDB; 1K1Z; 18-DEC-02.  
DR TRANSFAC; T01230; -;  
DR MGD; MGI:98923; Vav1.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR003247; CH type.  
DR InterPro; IPR002219; DAG\_PE-bind.  
DR InterPro; IPR001331; GDS\_CDC24.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR000219; RhoGEF.  
DR InterPro; IPR000980; SH2.  
DR InterPro; IPR001452; SH3.  
DR InterPro; IPR003096; SM22\_calponin.  
DR Pfam; PF00307; CH; 1.  
DR Pfam; PF00130; DAG\_PE-bind; 1.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhoGEF; 1.  
DR Pfam; PF00017; SH2; 1.  
DR Pfam; PF00018; SH3; 2.  
DR PRINTS; PR00401; SH2DOMAIN.  
DR PRINTS; PR00452; SH3DOMAIN.  
DR PRINTS; PR00888; SM22CALPONIN.  
DR ProDom; PD001527; CH type; 1.  
DR ProDom; PD000093; SH2; 1.  
DR ProDom; PD000066; SH3; 1.  
DR SMART; SM00109; C1; 1.  
DR SMART; SM00033; CH; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhoGEF; 1.  
DR SMART; SM00252; SH2; 1.  
DR SMART; SM00326; SH3; 2.  
DR PROSITE; PS50021; CH; 1.  
DR PROSITE; PS00479; DAG\_PE\_BIND\_DOM\_1; 1.  
DR PROSITE; PS50081; DAG\_PE\_BIND\_DOM\_2; 1.  
DR PROSITE; PS50010; DH\_2; 1.  
DR PROSITE; PS00741; DH\_1; 1.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
DR PROSITE; PS50001; SH2; 1.  
DR PROSITE; PS50002; SH3; 2.  
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;

KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation;  
KW 3D-structure. 1 119 CH.  
FT DOMAIN 194 373 DH.  
FT DOMAIN 402 504 PH.  
FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.  
FT DOMAIN 617 660 SH3 1.  
FT DOMAIN 671 765 SH2.  
FT DOMAIN 782 842 SH3 2.  
FT CONFLICT 29 29 Q -> E (IN REF. 2).  
SQ SEQUENCE 845 AA; 98136 MW; 3666DCCD1C5229DA CRC64;  
  
Query Match 14.5%; Score 85.5; DB 1; Length 845;  
Best Local Similarity 31.4%; Pred. No. 0.42;  
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;  
  
QY 26 ASAGEDYNAPDREFINVKKGQOIIVYKLVKENGAGFAGSVGDCQDEMGVVGYPN 85  
DB 787 AKARYDFCARDSELSLKEGDII---KILNKGQGGWRGEIYGR-----IGWFFSN 835  
QY 86 LVKEQRVYQE 95  
DB 836 YVEED--YSE 843  
  
RESULT 14  
VAV2 MOUSE STANDARD; PRT; 868 AA.  
ID VAV2 MOUSE STANDARD; PRT; 868 AA.  
AC Q60992;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Vav-2 protein.  
GN VAV2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6;  
RX MEDLINE=96313271; PubMed=8710375;  
RA Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,  
RT Goldman D., Lee I.J.;  
RT "Isolation and characterization of murine vav2, a member of the vav  
RL Oncogene 13:363-371(1996).  
CC -|- FUNCTION: Guanine nucleotide exchange factor for the Rho family  
CC of Ras-related GTPases (By similarity).  
CC -|- SIMILARITY: Contains 1 calponin-homology (CH) domain.  
CC -|- SIMILARITY: Contains 1 DBL-homology (DH) domain.  
CC -|- SIMILARITY: Contains 1 PH domain.  
CC -|- SIMILARITY: Contains 1 zinc-dependent phorbol-ester and DAG  
CC binding domain.  
CC -|- SIMILARITY: Contains 1 SH2 domain.  
CC -|- SIMILARITY: Contains 2 SH3 domains.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U37017; AAC52761.1; -;  
DR HSSP; Q60631; IGBQ.  
DR MGD; MGI:102718; Vav2.  
DR InterPro; IPR001715; Calponin-like.  
DR InterPro; IPR003247; CH type.  
DR InterPro; IPR002219; DAG\_PE-bind.  
DR InterPro; IPR001331; GDS\_CDC24.  
DR InterPro; IPR001849; PH.  
DR Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;



KW Guanine-nucleotide releasing factor; Repeat; Phosphorylation.

```
FT DOMAIN 1 119 CH.
FT DOMAIN 198 376 DH.
FT DOMAIN 405 512 PH.
FT DOMAIN 524 572 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 586 652 SH3 1.
FT DOMAIN 673 767 SH2.
FT DOMAIN 816 877 SH3 2.
FT MOD_RES 142 142 PHOSPHORYLATION (BY EGFR).
FT MOD_RES 159 159 PHOSPHORYLATION (BY EGFR).
FT MOD_RES 172 172 PHOSPHORYLATION (BY EGFR).
SQ SEQUENCE 878 AA; 101256 MW; C8FF7681032146B4 CRC64;

Query Match 13.8%; Score 81.5; DB 1; Length 878;
Best Local Similarity 26.3%; Pred. No. 1.1;
Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;

QY 20 VVT---ISLASQEDYNAPDCRFNVKGGQIYVYKLVKENGAGEFVAGSVYGDQDEM 76
Db 812 VETPRVIGTAVARYNFAARDMRELSLRGSDVVRVYSRIGGDOG---WWKG-----ETN 861

QY 77 GVVGYPFRNLVKEQV 92
Db 862 GRIGWFPSTYVEEGI 877
```

Search completed: December 29, 2003, 16:04:13  
Job time : 4.31373 secs

Result No.	Score	%		Length	DB	ID	Description
		Match	Query				
1	226.5	38.4	96	11	Q9J109	Q9J109 mesocricetu	
2	215	36.4	268	11	Q8BJE9	Q8BJE9 mus musculus	
3	215	36.4	1239	11	Q8BI84	Q8BI84 mus musculus	
4	185.5	31.4	119	4	Q96PC5	Q96PC5 homo sapien	
5	181	30.7	137	11	Q921X3	Q921X3 mus musculus	
6	171.5	29.1	119	11	Q91ZV0	Q91ZV0 mus musculus	
7	168.5	28.6	88	13	Q90XF1	Q90XF1 tetraodon n	
8	100	16.9	68	11	Q8C999	Q8C999 mus musculus	
9	88.5	15.0	287	11	Q8R076	Q8R076 mus musculus	
10	88.5	15.0	846	13	Q8UUX6	Q8UUX6 gallus gall	
11	88.5	15.0	1196	4	Q9OHZ2	Q9OHZ2 homo sapien	
12	88.5	15.0	1196	4	Q8H157	Q8H157 homo sapien	
13	86.5	14.7	719	4	Q96D37	Q96D37 homo sapien	
14	85.5	14.5	166	11	O08526	O08526 mus musculus	
15	85.5	14.5	806	11	Q8VDU4	Q8VDU4 mus musculus	
16	85.5	14.5	845	11	O8BTV7	O8BTV7 mus musculus	



Db 26 MPKLDKWKLCADBCSHPIISNAVALQDVAFDCRFLTYRGQVYVFSKL---KGRGLF 82

Qy 64 WAGSV 68

Db 83 WGSV 87

# RESULT 6

Q91ZV0 PRELIMINARY; PRT; 119 AA.  
 AC Q91ZV0;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Melanoma inhibitory activity protein 2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Bosserhoff A.K., Buettner R.;  
 RT "Characterization of the MIA gene family.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF390177; AAL26992.1; -;  
 DR InterPro: IPR001452; SH3.  
 DR SMART; SM00326; SH3; 1.  
 SQ SEQUENCE 119 AA; 13397 MW; 589F390C0B49D1C7 CRC64;

Query Match 29.1%; Score 171.5; DB 11; Length 119;  
 Best Local Similarity 39.2%; Pred. No. 5.7e-11;  
 Matches 40; Conservative 14; Mismatches 39; Indels 9; Gaps 3;

Qy 8 LASKKLCADBCVVTISLQAQEDYNAPDRFINVKGQIYYVSKLVKNGAGGEFWAGS 67

Db 26 LAHLKKGGLCEFTLISRLVALRDYTGDCRYLNFITGCEITSVYVVLGGDR--EDLWAGS 83

Qy 68 VYGDQDGMGVGVFPENLVKEQRYQATKEVPTTIDIDFFC 109

Db 84 ---KGKD----FGYFPRDAVQIEEVFISEIQMSTKESDFLC 118

# RESULT 7

Q90XF1 PRELIMINARY; PRT; 88 AA.  
 AC Q90XF1;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Melanoma inhibitory activity protein (Fragment).  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Bosserhoff A.K., Buettner R.;  
 RT "Characterization of the MIA gene family.";  
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF390176; AAL26991.1; -;  
 DR InterPro: IPR001452; SH3.  
 DR Pfam; PF00018; SH3; 1.  
 DR SMART; SM00326; SH3; 1.  
 FT NON\_TER 1  
 SQ SEQUENCE 88 AA; 10080 MW; C355C1FE04DA22EA CRC64;

Query Match 28.6%; Score 168.5; DB 13; Length 88;  
 Best Local Similarity 43.3%; Pred. No. 8.4e-11;  
 Matches 39; Conservative 15; Mismatches 29; Indels 7; Gaps 4;

Qy 23 ISLSAQEDYNAPDRFINVKGQIYYVSKLVKNGAG--EFWAGSVVD--QDEMGVV 79

Db 3 IMIARALQDYYPADCFIPRQGLIYYVYAML---KGRGSQFWAGSVQDSYVGOE-ARI 58

Qy 80 GYFPENLVKEQRYQATKEVPTTIDIDFFC 109

Db 59 GHFPSSIVEETHPLMAAQTEVKTNSWDFYC 88

# RESULT 8

Q8C899 PRELIMINARY; PRT; 68 AA.  
 AC Q8C899;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Otoraplin.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Head;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 DR EMBL; AK047965; BAC33202.1; -;  
 SQ SEQUENCE 68 AA; 7431 MW; 3CBE75527D3CBF7F CRC64;

Query Match 16.9%; Score 100; DB 11; Length 68;  
 Best Local Similarity 42.6%; Pred. No. 0.0019;  
 Matches 20; Conservative 9; Mismatches 8; Indels 10; Gaps 2;

Qy 1 HGIFMDRLASKKLCADBCV-----YTISLQAQEDYNA--PDC 37

Db 19 HGVFMDKLSKLCADBCVCKALLTWFSLSFYHIMGNLGKQPC 65

# RESULT 9

Q8R076 PRELIMINARY; PRT; 287 AA.  
 AC Q8R076;  
 DT 01-JUN-2002 (TREMBlrel. 21, Created)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Hypothetical 32.7 kDa protein.  
 GN VAV3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC027242; AAH27242.1; -;  
 DR MGD; MGI:1888518; Vav3  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PSS0001; SH2; 1.  
 DR PROSITE; PSS0002; SH3; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 287 AA; 32662 MW; BF2850B8F921F048 CRC64;



```
Query Match      15.0%; Score 88.5; DB 11; Length 287;
Best Local Similarity 31.3%; Pred. No. 0.19;
Matches 21; Conservative 14; Mismatches 21; Indels 11; Gaps 2;

QY 23 ISLASAQEDYNAPDCRFNVKKGQOIYVYSLVKENGAGERWAGSVYGDQDMGVGVYF 82
Db 230 LGIAIARYDFCARDWRELKGLKGDVVKIYTKM-----SANGWWRGEVNGR-----VGMF 278

QY 83 PRLVKE 89
Db 279 PSTYVEE 285

RESULT 10
ID Q8UUX6 PRELIMINARY; PRT; 846 AA.
AC Q8UUX6;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DE GDP/GTP exchange factor VAV3.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11805146;
RA Inabe K., Ishiai M., Scharenberg A.M., Freshney N., Downward J.,
RA Kurosaki T.;
RT "vav3 Modulates B Cell Receptor Responses by Regulating
RT Phosphoinositide 3-Kinase Activation.";
RL J. Exp. Med. 195;189-200(2002).
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; AY046915; XAL06249.1; -.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_RhoGEF.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom; PD001527; CH type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG PE BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG PE BIND_DOM_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.

Query Match      15.0%; Score 88.5; DB 4; Length 1196;
Best Local Similarity 33.3%; Pred. No. 1.1;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

QY 20 VYTISLASAQEDYNAPDCRFNVKKGQOIYVYSLVKENGAGERWAGSVYGDQDMGV 79
Db 1050 VDTAPTVALVDYTNRSDELTHRGDIIRVF---FKDN--EDWWYGSIGKQGE-----1098

QY 80 GYFPRNLVKEORVYQEAATKEV 100
Db 1099 GYFPANHVASETLVQELPPEI 1119

RESULT 11
ID Q9HOH2 PRELIMINARY; PRT; 1196 AA.
AC Q9HOH2;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DE Hypothetical protein.
GN DKFZF434N031.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166;
RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA Ansgorge W., Boecker M., Bloecker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.W., Ottenwaelder B., Obermaier B., Poustka A.;
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
RL Genome Res. 11:422-435(2001).
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AL136797; CAB66731.1; -.
DR HSSP; P06241; LSHF.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00400; WD40; 6.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; SH3 domain; WD repeat.
SQ SEQUENCE 1196 AA; 137114 MW; E27E3FB1D7932024 CRC64;

Query Match      15.0%; Score 88.5; DB 4; Length 1196;
Best Local Similarity 33.3%; Pred. No. 1.1;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

QY 20 VYTISLASAQEDYNAPDCRFNVKKGQOIYVYSLVKENGAGERWAGSVYGDQDMGV 79
Db 1050 VDTAPTVALVDYTNRSDELTHRGDIIRVF---FKDN--EDWWYGSIGKQGE-----1098

QY 80 GYFPRNLVKEORVYQEAATKEV 100
Db 1099 GYFPANHVASETLVQELPPEI 1119

RESULT 12
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Q8N157
ID Q8N157 PRELIMINARY; PRT; 1196 AA.
AC Q8N157;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ34943.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Nanomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie K.,
RA Osuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RA "NEDO human cDNA sequencing project.";
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RN
RP SEQUENCE FROM N.A.
RA Close J.P., Game I.G., Clark B., Thein S.L.;
RT "An integrated physical and transcript map of human 6q23 encompassing
RT a quantitative trait loci for foetal haemoglobin expression.";
RL Thesis (2002), Department of Clinical medicine, University of Oxford,
RL Oxford, United Kingdom.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; AK092262; BAC03840.1; -.
DR EMBL; AJ459824; CAD30871.1; -.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 5.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00002; SH3; 1.
DR PROSITE; PS00082; WD_REPEATS_2; 4.
DR PROSITE; PS00294; WD_REPEATS_REGION; 1.
KW Hypothetical protein; Repeat; SH3 domain; WD repeat.
SQ SEQUENCE 1196 AA; 137114 MW; 16A237C915DABF0F CRC64;

Query Match 15.0%; Score 88.5; DB 4; Length 1196;
Best Local Similarity 33.3%; Pred.No.1.1;
Matches 27; Conservative 12; Mismatches 31; Indels 11; Gaps 4;

QY 20 VYTIASAEQEDYNAPDCRFNVKKGQIYVYSLKLVKENGAGFEWAGSVYGDQDMGVV 79
Db 1050 VDTAPTVALYDYTNARSDLTTHRGDIIRVF---FKDN--EDWYVGS1-GKQE-----1098

QY 80 GYFPRNLVKEQRVQATKEV 100
Db 1099 GYFPANHVASATLYQLPEI 1119

RESULT 13
Q96D37
ID Q96D37 PRELIMINARY; PRT; 719 AA.
AC Q96D37;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tissue=Placenta;
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RA Strausberg R.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; BC013361; AAH13361.1; -.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_CDC24.
DR InterPro; IPR000219; RHOGEF.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RHOGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RHOGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00741; DH; 1; 1.
DR PROSITE; PS00010; DH; 2; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00001; SH2; 1.
DR PROSITE; PS00002; SH3; 2.
KW Hypothetical protein; SH3 domain.
SQ SEQUENCE 719 AA; 83727 MW; A51B757DAS43BA6C CRC64;

Query Match 14.7%; Score 86.5; DB 4; Length 719;
Best Local Similarity 32.9%; Pred.No.0.98;
Matches 23; Conservative 13; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFNVKKGQIYVYSLKLVKENGAGFEWAGSVYGDQDMGVVYFPRN 85
Db 661 AKARYDFCARDSELSLKEGDI---KILNKGQQQWVRGEIYGR-----VGWFPAN 709

QY 86 LYKEQRVYQE 95
Db 710 YVEED--YSE 717

RESULT 14
O08526
ID O08526 PRELIMINARY; PRT; 166 AA.
AC O08526;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vav-T.
GN VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=ddy; TISSUE=Testis;
RX MEDLINE=97190224; PubMed=9038379;
RA Okumura K., Kaneko Y., Nonoguchi K., Nishiyama H., Yokoi H.,
RA Higuchi T., Itoh K., Yoshida O., Miki T., Fujita J.;
RT "Expression of a novel isoform of Vav, Vav-T, containing a single
RT Src homology 3 domain in murine testicular germ cells.";
RL Oncogene 14:713-720(1997).
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DR EMBL; D83266; BAA18950.1; -.
DR HSSP; Q60631; 1GBQ.
```

```
DR MGD; MGI:98923; Vav.
DR InterPro; IPR000980; SH2.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR00452; SH3DDOMAIN.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 166 AA; 19434 MW; 2CJAF1FF07A5018F CRC64;

Query Match 14.5%; Score 85.5; DB 11; Length 166;
Best Local Similarity 31.4%; Pred. No. 0.21;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAGFEWAGSVYGDGDENGWVGYFPRN 85
Db 108 AKARYDFCARDRELSLSKEGDI-----KILNKGQGGWWRGGEIYGR-----IGWFFSN 156
QY 86 LVKEQRYVQE 95
Db 157 YVEED--YSE 164

RESULT 15
Q8VDU4
ID Q8VDU4 PRELIMINARY; PRT; 806 AA.
AC Q8VDU4;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Similar to vav oncogene.
GN VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBT_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
DR EMBL; BC020487; AAH20487.1; -.
DR MGD; MGI:98923; Vav.
DR InterPro; IPR005613; AIP3.
DR InterPro; IPR001715; Calponin-like.
DR InterPro; IPR003247; CH type.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH_CDC24.
DR InterPro; IPR000219; RhogEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR003096; SM22_calponin.
DR Pfam; PF03915; AIP3; 1.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhogEF; 1.
DR Pfam; PF00017; SH2; 1.
DR PRINTS; PR00452; SH3DDOMAIN.
DR ProDom; PD001527; CH_type; 1.
DR ProDom; PD000093; SH2; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhogEF; 1.

DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
SQ SEQUENCE 806 AA; 93868 MW; F4368CD13A62D695 CRC64;

Query Match 14.5%; Score 85.5; DB 11; Length 806;
Best Local Similarity 31.4%; Pred. No. 1.4;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFINVKKGQIYVYVKLVKENGAGFEWAGSVYGDGDENGWVGYFPRN 85
Db 748 AKARYDFCARDRELSLSKEGDI-----KILNKGQGGWWRGGEIYGR-----IGWFFSN 796
QY 86 LVKEQRYVQE 95
Db 797 YVEED--YSE 804

Search completed: December 29, 2003, 16:06:25
Job time : 16.9468 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2003, 16:03:18 ; Search time 21.5686 Seconds  
(without alignments)  
809.506 Million cell updates/sec

Title: US-10-019-455A-24

Perfect score: 590

Sequence: 1 HGIFMDRLASKKLCADDEC.....RVYQATKEVPTTIDDFCE 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A Geneseq 19Jun03.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
4: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	110	22	Human MLP protein
2	590	100.0	128	22	Human growth regul
3	590	100.0	128	22	Human MLP protein
4	590	100.0	128	23	Human angiogenesis
5	590	100.0	128	23	Human PRO873 prot
6	590	100.0	128	23	Human PRO protein,
7	590	100.0	128	23	Novel human secret
8	561	95.1	105	22	Human growth regul
9	547	92.7	110	22	Mouse MLP protein

10	547	92.7	128	22	AA669125	Mouse MLP protein
11	541	91.7	110	22	AA669131	Rat MLP protein se
12	541	91.7	128	22	AA669130	Rat MLP protein se
13	417	70.7	87	22	AA669129	Rat MLP protein se
14	253.5	43.0	131	16	AA669811	Melanoma inhibitor
15	253.5	43.0	131	22	AA669811	Human MIA protein
16	251.5	42.6	137	22	AA669812	Recombinant human
17	231.5	39.2	130	16	AA669812	Melanoma inhibitor
18	226.5	38.4	138	22	AA669812	Human protein sequ
19	225.5	38.2	125	23	AA669812	Human TANGO 130 MI
20	225.5	38.2	410	21	AA669812	Human TANGO 130 pr
21	225.5	38.2	410	21	AA669812	Human TANGO 130 pr
22	225.5	38.2	1907	23	AA669812	Human TANGO 130 po
23	217	36.8	499	22	AA669812	Human PRO polypept
24	217	36.8	499	22	AA669812	Human PRO20088 pro
25	217	36.8	499	24	AA669812	Human secreted/tra
26	217	36.8	499	24	AA669812	Human secreted/tra
27	217	36.8	499	24	AA669812	Human secreted/tra
28	217	36.8	499	24	AA669812	Human PRO polypept
29	217	36.8	499	24	AA669812	Human PRO polypept
30	217	36.8	499	24	AA669812	Human secreted/tra
31	217	36.8	499	24	AA669812	Human PRO polypept
32	217	36.8	499	24	AA669812	Human secreted/tra
33	215	36.4	125	23	AA669812	Mouse TANGO 130 MI
34	215	36.4	303	22	AA669812	Human PRO polypept
35	215	36.4	303	22	AA669812	Human PRO polypept
36	215	36.4	303	23	AA669812	Human secreted/tra
37	215	36.4	303	23	AA669812	Human secreted/tra
38	215	36.4	303	23	AA669812	Human secreted/tra
39	215	36.4	303	24	AA669812	Human PRO19670 pro
40	215	36.4	303	24	AA669812	Human secreted pol
41	215	36.4	303	24	AA669812	Novel human secret
42	215	36.4	303	24	AA669812	Human PRO polypept
43	215	36.4	303	24	AA669812	Human secreted/tra
44	215	36.4	303	24	AA669812	Novel human secret
45	215	36.4	303	24	AA669812	Human secreted/tra

#### ALIGNMENTS

RESULT 1

AA669126

ID AA669126 standard; Protein; 110 AA.

XX AA669126;

AC AA669126;

XX 23-APR-2001 (first entry)

DT Human MLP protein sequence SEQ ID NO:24.

XX Human MLP protein sequence SEQ ID NO:24.

XX MIP; MIA; melanoma inhibitory activity; cancer; bone disease;

XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

XX cardiant; gene therapy; secretory cell function regulator; promoter;

XX inhibitor.

XX Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

XX Tanaka H;

XX WPI; 2001-159271/16.

XX N-PSDB; AAF59079.

XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -

XX Claim 1; Page 97-98; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.

XX Sequence 110 AA;

Query Match 100.0%; Score 590; DB 22; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-68;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 60

Db 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 60

QY 61 GEFWAGSVYGDQDEMVGVPFPRNLVKEQRYQATKEVPTDIDFFCE 110

Db 61 GEFWAGSVYGDQDEMVGVPFPRNLVKEQRYQATKEVPTDIDFFCE 110

RESULT 2

AAB82671  
 ID AAB82671 standard; Protein; 128 AA.

XX AAB82671;

DT 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide.

KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..23

FT Protein /label= Signal\_peptide

FT /label= Mature protein

FT /note= "separately claimed in Claim 10"

XX WO200155332-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;

XX WPI; 2001-483233/52.

XX N-PSDB; AAB26343.

PT Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,

PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -

XX Claim 10; Page 116-117; 119pp; English.

XX The present sequence is that of a novel human growth regulatory-like  
 CC polypeptide (GRLP). The amino acid sequence is predicted from a  
 CC novel assembled cDNA (see AAB26343) based on Hyseq clone number  
 CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
 CC belongs to the same protein family as growth regulatory proteins.  
 CC growth factors, human melanoma derived growth regulatory protein,  
 CC precursor (64% similarity and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRLP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polypeptides, which include the GRLP mature protein,  
 CC may also have nutritional uses, cytokine and cell proliferation  
 CC or differentiation activity, stem cell growth factor activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC immunosuppressive or immunostimulant activity, activin/inhibin  
 CC activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, use in cancer diagnosis and therapy,  
 CC drug screening, receptor/ligand activity, antiinflammatory  
 CC activity, and treatment of leukaemia, nervous system disorders,  
 CC arthritis and inflammation.

SQ Sequence 128 AA;

Query Match 100.0%; Score 590; DB 22; Length 128;

Best Local Similarity 100.0%; Pred. No. 2e-68;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 60

Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSLVKENGA 78

QY 61 GEFWAGSVYGDQDEMVGVPFPRNLVKEQRYQATKEVPTDIDFFCE 110

Db 79 GEFWAGSVYGDQDEMVGVPFPRNLVKEQRYQATKEVPTDIDFFCE 128

RESULT 3

AAB69123

ID AAB69123 standard; Protein; 128 AA.

XX AAB69123;

DT 23-APR-2001 (first entry)

XX Human MLP protein sequence SEQ ID NO.6.

XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor.

OS Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 DR N-PSDB; AAF59065.  
 XX  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 XX Claim 2; Page 91-92; 111pp; Japanese.  
 XX  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 XX Sequence 128 AA;

Query Match 100.0%; Score 590; DB 22; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68; Indels 0; Gaps 0;  
 Matches 110; Conservative 0; Mismatches 0;  
 QY 1 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQQIYVYVKLVKNGA 60  
 DB 19 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQQIYVYVKLVKNGA 78  
 QY 61 GEFWAGSVYGDQDGVGVYPRNLVKEQRYQVQATKEVPTDIDPFCE 110  
 DB 79 GEFWAGSVYGDQDGVGVYPRNLVKEQRYQVQATKEVPTDIDPFCE 128

RESULT 4  
 ABB95602  
 ID ABB95602 standard; Protein; 128 AA.  
 XX  
 XX ABB95602;  
 AC  
 AC  
 DT 19-JUL-2002 (first entry)  
 XX  
 XX Human angiogenesis related protein PRO9873 SEQ ID NO: 360.  
 DE  
 XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 XW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 XW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;  
 XW antiarteriosclerotic.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WC200208284-A2.  
 DN  
 XX  
 XX 31-JAN-2002.  
 PD  
 XX  
 XX 09-JUL-2001; 2001WO-US21735.  
 PF  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 PR 25-JUL-2000; 2000US-220654P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 02-AUG-2000; 2000US-222695P.  
 PR 17-AUG-2000; 2000US-0643657.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000US-233328.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 18-SEP-2000; 2000US-0665350.  
 PR 24-OCT-2000; 2000US-242922P.

PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 01-MAR-2001; 2001WO-US06520.  
 PR 09-MAR-2001; 2001WO-US06666.  
 PR 14-MAR-2001; 2001US-0802706.  
 PR 22-MAR-2001; 2001US-0808689.  
 PR 05-APR-2001; 2001US-0818744.  
 PR 10-MAY-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 25-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 01-JUN-2001; 2001WO-US17443.  
 PR 20-JUN-2001; 2001WO-US17800.  
 PR 28-JUN-2001; 2001WO-US19692.  
 PR 28-JUN-2001; 2001WO-US00000.  
 XX (GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERRITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANG/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX  
 XX WPI; 2002-171999/22.  
 DR N-PSDB; ABL95740.  
 XX  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 XX Claim 11; Fig 360; 567pp; English.  
 PS  
 XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a PRO protein of the invention.  
 XX  
 SQ Sequence 128 AA;  
 Query Match 100.0%; Score 590; DB 23; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68; Indels 0; Gaps 0;  
 Matches 110; Conservative 0; Mismatches 0;  
 QY 1 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQQIYVYVKLVKNGA 60  
 DB 19 HGIFMDRLASKKLCADDECVYITISLASAQEDYNAPDCRFINVKKGQQIYVYVKLVKNGA 78



PR 28-JUL-2000; 2000WO-US20710.  
 PR 23-AUG-2000; 2000WO-US23522.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 15-SEP-2000; 2000US-000000P.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 28-NOV-2000; 2000US-253646P.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 28-FEB-2001; 2000WO-US34956.  
 PR 10-MAY-2001; 2000US-0854280.  
 PR 25-MAY-2001; 2001WO-US17092.  
 XX (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;  
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WT;  
 XX  
 DR WPI; 2002-172001/22.  
 DR N-PSDB; ABK33571.  
 XX  
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,  
 PT useful for treating a PRO related disorder and for diagnosing tumours  
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal  
 PT tumour or liver tumour -  
 XX  
 PS Claim 1; Figure 72; 359pp; English.  
 XX  
 CC The invention relates to one hundred and twenty two nucleic acids  
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides  
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,  
 CC agonists and antagonists are useful for treating a PRO related disorder.  
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
 CC protein sequences of the invention.  
 XX  
 SQ Sequence 128 AA;  
 Query Match 100.0%; Score 590; DB 23; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKGGQIYVYSLVKVNGA 60  
 DB 19 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKGGQIYVYSLVKVNGA 78  
 QY 61 GEFWAGSVYGDQDGMGVGVPFPRNLVKEQRVYQATKEVPTTIDIFFCE 110  
 DB 79 GEFWAGSVYGDQDGMGVGVPFPRNLVKEQRVYQATKEVPTTIDIFFCE 128  
 RESULT 7  
 AAU09871  
 ID AAU09871 standard; Protein; 128 AA.  
 XX  
 AC AAU09871;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE Novel human secreted protein #12.  
 XX  
 KW Secreted protein; cytostatic; immunosuppressive; vulneryary; vaccine;  
 KW antinflammatory; neuroprotective; nephrotropic; cardiovascular;  
 KW human; cancer; autoimmune disease; wound healing disorder; infection;

KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal.  
 XX  
 OS Homo sapiens.  
 XX WO200179454-A1.  
 PN  
 PD 25-OCT-2001.  
 XX  
 PF 11-APR-2001; 2001WO-US11797.  
 XX  
 PR 13-APR-2000; 2000US-196603P.  
 PR 24-APR-2000; 2000US-199417P.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PA  
 FI Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 XX  
 DR WPI; 2002-061975/08.  
 DR N-PSDB; AAS17583.  
 XX  
 XX New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, neurological and  
 PT renal diseases, or gastrointestinal diseases. These may also be used to  
 PT treat diseases, abnormalities and disorders caused by abnormal  
 XX expression, production, function and/or metabolism of the genes, as  
 XX vaccines for inducing immunological response in a mammal, and in  
 XX screening methods for detecting the effect of added compounds on the  
 XX production of mRNA and polypeptide in cells. The polypeptides can be used  
 XX as immunogens to produce antibodies immunospecific for the polypeptides,  
 XX and to identify membrane-bound or soluble receptors. The polynucleotides  
 XX may be used as diagnostic reagents, in chromosome localisation studies,  
 XX and in tissue expression studies. The present sequence represents the  
 XX amino acid sequence of novel human secreted protein #12.  
 SQ Sequence 128 AA;  
 Query Match 100.0%; Score 590; DB 23; Length 128;  
 Best Local Similarity 100.0%; Pred. No. 2e-68;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKGGQIYVYSLVKVNGA 60  
 DB 19 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKGGQIYVYSLVKVNGA 78  
 QY 61 GEFWAGSVYGDQDGMGVGVPFPRNLVKEQRVYQATKEVPTTIDIFFCE 110  
 DB 79 GEFWAGSVYGDQDGMGVGVPFPRNLVKEQRVYQATKEVPTTIDIFFCE 128  
 RESULT 8  
 AAB82672  
 ID AAB82672 standard; Protein; 105 AA.  
 XX  
 AC AAB82672;  
 XX  
 DT 02-OCT-2001 (first entry)  
 XX  
 DE Human growth regulatory-like polypeptide (mature protein).  
 XX  
 KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.



XX OS Homo sapiens.	XX 23-APR-2001 (first entry)
XX PN WO200155332-A2.	XX Mouse MLP protein sequence SEQ ID NO:26.
XX PD 02-AUG-2001.	XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX PF 25-JAN-2001; 2001WO-US02455.	XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX PR 25-JAN-2000; 2000US-0491404.	XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX PR 02-MAY-2000; 2000US-0563786.	XX inhibitor.
XX PA (HYSE-) HYSEQ INC.	XX Mus musculus.
XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;	XX WO200102564-A1.
XX PI Dmanac RT;	XX 11-JAN-2001.
XX XX WPI; 2001-483233/52.	XX 29-JUN-2000; 2000WO-JP04278.
XX DR N-PSDB; AAH26343.	XX 30-JUN-1999; 99JP-0186718.
XX XX Isolated human growth regulatory-like polypeptide useful for treating	XX (TAKE ) TAKEDA CHEM IND LTD.
XX PT e.g. Alzheimer's disease, cancer, autoimmune disorders,	XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX PT hyperproliferative disorders, coagulation disorders, and nervous system	XX Tanaka H;
XX PT disorders -	XX WPI; 2001-159271/16.
XX XX Claim 10; Page 117; 119pp; English.	XX N-PSDB; AAF59080.
XX XX The present sequence is that of a novel human growth regulatory-like	XX Safe, low-toxicity secretory cell function-regulatory protein and
XX CC polypeptide (GRLP) mature protein. The sequence is predicted from	XX encoded DNA, applicable as drugs, in diagnosis and development of
XX CC a novel assembled cDNA (see AAH26343) based on Hyseq clone number	XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX CC 1637272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP	XX diseases -
XX CC belongs to the same protein family as growth regulatory proteins,	XX Claim 3; Page 98-99; 111pp; Japanese.
XX CC growth factors, human melanoma derived growth regulatory protein	XX The present invention describes novel MLP proteins and their encoding
XX CC precursor (64% similarity and 45% identity over 111 amino acids)	XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX CC or melanoma inhibitory activity, cattle cartilage-derived	XX activities, and can be used in gene therapy and as secretory cell
XX CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%	XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX CC similarity over 126 amino acids) and other retinoic acid-sensitive	XX the diagnosis and development of promoters and inhibitors for preventing
XX CC proteins. GRLP polypeptides and polynucleotides of the invention	XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX CC and diagnosis of disorders and diseases caused by, or involving,	XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX CC cartilage development and maintenance, inhibition of melanoma cell	XX in the exemplification of the present invention.
XX CC growth and tumours, including neuroectodermal tumours such as	XX SQ Sequence 110 AA;
XX CC gliomas. The polypeptides, which include the GRLP mature protein,	XX Query Match 92.7%; Score 547; DB 22; Length 110;
XX CC may also have nutritional uses, cytokine and cell proliferation,	XX Best Local Similarity 90.0%; Pred. No. 6.3e-63;
XX CC or differentiation activity, stem cell growth factor activity,	XX Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
XX CC haematopoiesis regulating activity, tissue growth activity,	QY 1 HGIEMDLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 60
XX CC immunosuppressive or immunostimulant activity, activin/inhibin	DB 1 HGVFMDKLSSKKLCADDECVYTISLASAQEDYNAPDCRFIDVKKGQIYVYSKLVTEGA 60
XX CC activity, chemotactic/chemokinetic activity, haemostatic and	QY 61 GEFWAGSVYGDQDGMGVGYPFRLNVLKQRVYQATKEVPTTIDDFCE 110
XX CC thrombolytic activity, use in cancer diagnosis and therapy,	DB 61 GEFWAGSVYGDQDGMGVGYPFRLNVLKQRVYQATKEVPTTIDDFCE 110
XX CC drug screening, receptor/ligand activity, antiinflammatory	RESULT 10
XX CC activity, and treatment of leukaemia, nervous system disorders,	AAB69125
XX CC arthritis and inflammation.	ID AAB69125 standard; Protein; 128 AA.
XX XX Sequence 105 AA;	XX AAB69125;
XX Query Match 95.1%; Score 561; DB 22; Length 105;	XX 23-APR-2001 (first entry)
XX Best Local Similarity 100.0%; Pred. No. 8.9e-65;	XX Mouse MLP protein sequence SEQ ID NO:12.
XX Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
QY 6 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 65	XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
DB 1 DRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 60	XX cardiant; gene therapy; secretory cell function regulator; promoter;
QY 66 GSVYGDQDGMGVGYPFRLNVLKQRVYQATKEVPTTIDDFCE 110	XX inhibitor.
DB 61 GSVYGDQDGMGVGYPFRLNVLKQRVYQATKEVPTTIDDFCE 105	
RESULT 9	
AAB69127	
ID AAB69127 standard; Protein; 110 AA.	
XX AAB69127;	

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XX Mus musculus.
OS WO200102564-A1.
PN 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX N-PSDB; AAF59068.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
XX Claim 4; Page 93-94; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
XX Sequence 128 AA;
XX
XX Query Match 92.7%; Score 547; DB 22; Length 128;
XX Best Local Similarity 90.0%; Pred. No. 7.8e-63;
XX Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYKLVKNGA 60
XX 19 HGVFMDKLSKKLCADDECVYTISLASAQEDYNAPDCRFIDVKKGQIYVYKLVKNGA 78
XX
XX 61 GEFWAGSVYGDGQDEMGVYGPRLNIVKEQRYQATKEVPTTDDIFDCE 110
XX 79 GEFWAGSVYGDQDEMGVYGPRLNIVKEQRYQATKEIPTTDDIFDCE 128
XX
XX RESULT 11
XX AAB69131
XX ID AAB69131 standard; Protein; 110 AA.
XX
XX AC AAB69131;
XX
XX 23-APR-2001 (first entry)
XX
XX Rat MLP protein sequence SEQ ID NO:49.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.
XX
XX Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX

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PR 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX N-PSDB; AAF59099.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
XX Claim 5; Page 107; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
XX Sequence 110 AA;
XX
XX Query Match 91.7%; Score 541; DB 22; Length 110;
XX Best Local Similarity 89.1%; Pred. No. 3.8e-62;
XX Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
XX
XX 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYKLVKNGA 60
XX 1 HGVFMDKLSKKLCADDECVYTISLASAQEDYNAPDCRFIDVKKGQIYVYKLVKNGA 60
XX
XX 61 GEFWAGSVYGDGQDEMGVYGPRLNIVKEQRYQATKEVPTTDDIFDCE 110
XX 61 GAFWAGSVYGDQDEMGVYGPRLNIVKEQRYQATKEIPTTDDIFDCE 110
XX
XX RESULT 12
XX AAB69130
XX ID AAB69130 standard; Protein; 128 AA.
XX
XX AC AAB69130;
XX
XX 23-APR-2001 (first entry)
XX
XX Rat MLP protein sequence SEQ ID NO:47.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.
XX
XX Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX N-PSDB; AAF59098.
XX

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XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint  
PT diseases -  
XX  
PS Claim 6; Page 106; 111pp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 128 AA;  
Query Match 91.7%; Score 541; DB 22; Length 128;  
Best Local Similarity 89.1%; Pred. No. 4.7e-62;  
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;  
QY 1 HGFNDRLASKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGA 60  
DB 19 HGFMDKLSKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGA 78  
QY 61 GEFWAGSVYGDQDEMGVYFPFNLVKEQRYQVQATKEVPTDIDFFCE 110  
DB 79 GAFWAGSVYGDQDEMGVYFPFNLVKEQRYQVQATKEIPTDIDFFCE 128  
RESULT 13  
AAB69129  
ID AAB69129 standard; Protein; 87 AA.  
XX  
AC AAB69129;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Rat MLP protein sequence SEQ ID NO:39.  
XX  
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor.  
XX  
OS Rattus sp.  
XX  
PN WO200102564-A1.  
XX  
PD 11-JAN-2001.  
XX  
PF 29-JUN-2000; 2000WO-JP04278.  
XX  
PR 30-JUN-1999; 99JP-0186718.  
XX  
PA (TAKE ) TAKEDA CHEM IND LTD.  
XX  
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;  
DR WPI; 2001-159271/16.  
XX  
CC Safe, low-toxicity secretory cell function-regulatory protein and  
CC encoded DNA, applicable as drugs, in diagnosis and development of  
CC promoters and inhibitors for preventing or treating e.g. bone and joint  
CC diseases -  
XX  
PS Example 9; Page 103; 111pp; Japanese.  
XX  
CC The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant

CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.  
XX  
SQ Sequence 87 AA;  
Query Match 70.7%; Score 417; DB 22; Length 87;  
Best Local Similarity 88.5%; Pred. No. 3.8e-46;  
Matches 77; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 6 DRLASKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGAGFWA 65  
DB 1 DKLSSKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYVKLVKNGAGFWA 60  
QY 66 GSVYGDQDEMGVYFPFNLVKEQRY 92  
DB 61 GSVYGDQDEMGVYFPFNLVKEQRY 87  
RESULT 14  
AAR69811  
ID AAR69811 standard; Protein; 131 AA.  
XX  
AC AAR69811;  
XX  
DT 25-MAR-2003 (updated)  
DT 26-OCT-1995 (first entry)  
XX  
DE Melanoma inhibiting protein (human).  
XX  
KW Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;  
KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;  
KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;  
KW probe; fusion protein.  
XX  
OS Homo sapiens.  
XX  
PN WO9503328-A2.  
XX  
PD 02-FEB-1995.  
XX  
PF 19-JUL-1994; 94WO-EP02369.  
XX  
PR 20-JUL-1993; 93DE-4324247.  
XX  
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.  
XX  
PI Bogdahn U, Buettner R, Kaluza B;  
PI  
DR WPI; 1995-075191/10.  
DR N-PSDB; AAQ84050, AAQ84051.  
XX  
PT New melanoma inhibiting protein and related nucleic acid -  
PT vectors, transformed cells, antibodies etc., useful for treating  
PT tumours and as immunosuppressant e.g. by gene therapy  
XX  
PS Claim 1; Page 54; 85pp; German.  
XX  
CC This protein has melanoma-inhibiting activity and can be used to  
CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell  
CC lung cancer, neuroectodermal tumours) or as an immunosuppressant  
CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of  
CC peripheral blood lymphocytes). Antibodies raised against the  
CC protein can be used to detect cell producing the protein and also  
CC for protein purification. Probes derived from DNA encoding the  
CC protein (AAQ84050, AAQ84051) can be used to detect sequences encoding  
CC the protein or related proteins. The protein may be expressed as  
CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).  
CC (Updated on 25-MAR-2003 to correct PN field.)  
XX

SQ Sequence 131 AA;  
 Query Match 43.0%; Score 253.5; DB 16; Length 131;  
 Best Local Similarity 45.4%; Pred. No. 1.3e-24;  
 Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;  
 QY 5 MDRASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYVKLVKENGAGE-F 63  
 Db 27 MPKLAADRLKCADQECSPISMAVALQDYMAPDCRFILIHKGQVYVFSKL---KGRGLF 83  
 QY 64 WAGSVYGDQDEMGV-VGYFPRNLVKQRYOEATKEVPTTDDIFFCE 110  
 Db 84 WGGSVQGDYDGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYQ 131

RESULT 15  
 AAG65614  
 ID AAG65614 standard; Protein; 131 AA.

XX AAG65614;  
 AC  
 XX 07-JAN-2002 (first entry)  
 DE Human MIA protein sequence.  
 XX  
 KW MIA; melanoma inhibiting activity protein; antiinflammatory; human;  
 KW antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;  
 KW immunosuppressive; ophthalmological; dermatological; antidiabetic;  
 KW neuroprotective; immune tolerance; T-cell tolerance.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200170253-A1.  
 XX  
 XX 27-SEP-2001.  
 XX  
 XX 15-MAR-2001; 2001WO-EP02991.  
 XX  
 XX 23-MAR-2000; 2000EP-0201063.  
 XX  
 XX (ALKU ) AKZO NOBEL NV.  
 XX  
 XX Nelissen RLH, Verheijden GFM;  
 XX  
 XX WPI; 2001-611446/70.  
 DR N-PSDB; AAH47783.  
 XX  
 PT Use of melanoma inhibiting activity protein or its derivatives as  
 PT immune modulatory agents for the treatment of inflammatory diseases,  
 PT specifically rheumatoid arthritis -  
 XX  
 PS Example 4; Page 34; 4lpp; English.  
 XX  
 CC The invention relates to the use of melanoma inhibiting activity (MIA)  
 CC protein and/or its fragments that have anti-inflammatory effects and  
 CC induce systemic immune tolerance or specific T-cell tolerance to MIA  
 CC antigen, for manufacturing a preparation against inflammatory diseases  
 CC and for induction of systemic immune tolerance or specific T-cell  
 CC tolerance in patients suffering from or susceptible to inflammatory  
 CC diseases. A fragment of MIA is useful as a therapeutic substance and is  
 CC useful for manufacture of pharmaceutical preparations against  
 CC inflammatory diseases such as an immune-cell mediated cartilage  
 CC destruction disease, specifically rheumatoid arthritis, autoimmune  
 CC diseases like Graves' disease, juvenile arthritis, primary  
 CC glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,  
 CC myasthenia gravis, Addison's disease, primary biliary sclerosis,  
 CC uveitis, systemic lupus erythematosus, inflammatory bowel disease,  
 CC multiple sclerosis or diabetes. The MIA polypeptides have specific  
 CC effect on the autoreactive T-cells thus leaving the other components of  
 CC the immune system intact as compared to the non-specific suppressive  
 CC effect of immunosuppressive drugs. The present sequence represents a  
 CC human MIA protein.  
 XX

SQ Sequence 131 AA;  
 Query Match 43.0%; Score 253.5; DB 22; Length 131;  
 Best Local Similarity 45.4%; Pred. No. 1.3e-24;  
 Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;  
 QY 5 MDRASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYVKLVKENGAGE-F 63  
 Db 27 MPKLAADRLKCADQECSPISMAVALQDYMAPDCRFILIHKGQVYVFSKL---KGRGLF 83  
 QY 64 WAGSVYGDQDEMGV-VGYFPRNLVKQRYOEATKEVPTTDDIFFCE 110  
 Db 84 WGGSVQGDYDGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYQ 131

Search completed: December 29, 2003, 16:09:03  
 Job time : 22.5686 secs



16	590	100.0	128	12	US-10-219-532-72	Sequence 72, Appl
17	590	100.0	128	12	US-10-219-533-72	Sequence 72, Appl
18	590	100.0	128	12	US-10-223-081-360	Sequence 360, Appl
19	590	100.0	128	12	US-10-230-437-72	Sequence 72, Appl
20	590	100.0	128	12	US-10-232-228-72	Sequence 72, Appl
21	590	100.0	128	12	US-10-232-082-360	Sequence 360, Appl
22	590	100.0	128	15	US-10-227-884-72	Sequence 72, Appl
23	590	100.0	128	15	US-10-230-163-72	Sequence 72, Appl
24	590	100.0	128	15	US-10-230-338-72	Sequence 72, Appl
25	590	100.0	128	15	US-10-218-631-72	Sequence 72, Appl
26	590	100.0	128	15	US-10-230-414-72	Sequence 72, Appl
27	590	100.0	128	15	US-10-216-159A-72	Sequence 72, Appl
28	590	100.0	128	15	US-10-218-849-72	Sequence 72, Appl
29	590	100.0	128	15	US-10-227-873-72	Sequence 72, Appl
30	590	100.0	128	15	US-10-227-883-72	Sequence 72, Appl
31	590	100.0	128	15	US-10-219-076-72	Sequence 72, Appl
32	590	100.0	128	15	US-10-230-434-72	Sequence 72, Appl
33	590	100.0	128	15	US-10-219-003-72	Sequence 72, Appl
34	590	100.0	128	15	US-10-219-075-72	Sequence 72, Appl
35	590	100.0	128	15	US-10-219-464-72	Sequence 72, Appl
36	590	100.0	128	15	US-10-219-466-72	Sequence 72, Appl
37	590	100.0	128	15	US-10-219-479-72	Sequence 72, Appl
38	590	100.0	128	15	US-10-219-481-72	Sequence 72, Appl
39	590	100.0	128	15	US-10-230-260-72	Sequence 72, Appl
40	590	100.0	128	15	US-10-232-231-72	Sequence 72, Appl
41	590	100.0	128	15	US-10-232-233-72	Sequence 72, Appl
42	590	100.0	128	15	US-10-216-165-72	Sequence 72, Appl
43	590	100.0	128	15	US-10-218-956-72	Sequence 72, Appl
44	590	100.0	128	15	US-10-219-468-72	Sequence 72, Appl
45	590	100.0	128	15	US-10-219-478-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-10-216-163-72  
; Sequence 72, Application US/10216163  
; Publication No. US20030149239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530PIC3  
; CURRENT APPLICATION NUMBER: US/10/216,163  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656

OM protein - protein search, using sw model  
Run on: December 29, 2003, 16:09:08 ; Search time 15.098 Seconds  
(without alignments)  
1449.984 Million cell updates/sec  
Title: US-10-019-455A-24  
Perfect score: 590  
Sequence: 1 HGIFMDRLASKKLCADCEV.....RVYQATKEVPTTIDIFFCE 110  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 724715 seqs, 199017464 residues  
Total number of hits satisfying chosen parameters: 724715  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	128	12	US-10-216-163-72
2	590	100.0	128	12	US-10-218-785-72
3	590	100.0	128	12	US-10-219-063-72
4	590	100.0	128	12	US-10-219-066-72
5	590	100.0	128	12	US-10-219-067-72
6	590	100.0	128	12	US-10-219-068-72
7	590	100.0	128	12	US-10-219-069-72
8	590	100.0	128	12	US-10-219-073-72
9	590	100.0	128	12	US-10-219-475-72
10	590	100.0	128	12	US-10-219-480-72
11	590	100.0	128	12	US-10-219-483-72
12	590	100.0	128	12	US-10-219-525-72
13	590	100.0	128	12	US-10-219-526-72
14	590	100.0	128	12	US-10-219-530-72
15	590	100.0	128	12	US-10-219-531-72

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-72

Query Match          100.0%; Score 590; Dh 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 60
    |||||
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKNGA 78
    |||||

QY 61 GEFWAGSVYGDQDEMGVGVFPRLVKEQRYQVQATKEVPTTDDFFCE 110
    |||||
Db 79 GEFWAGSVYGDQDEMGVGVFPRLVKEQRYQVQATKEVPTTDDFFCE 128
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RESULT 2
US-10-218-765-72
; Sequence 72, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT APPLICATION NUMBER: US/10/218,765
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
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; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085579
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; PRIOR APPLICATION NUMBER: 60/090472
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; PRIOR APPLICATION NUMBER: 60/106178
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; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: 60/106248
; PRIOR FILING DATE: 1998-10-29
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; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106905
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; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64; 0; Indels 0; Gaps 0;
Matches 110; Conservative 0; Mismatches 0;

QY 1 HGIFMDRLASKKLCADDECVCYTISLASAQEDYNAPCRFINVKKGQIYVYKLVKNGA 60
Db 19 HGIFMDRLASKKLCADDECVCYTISLASAQEDYNAPCRFINVKKGQIYVYKLVKNGA 78
QY 61 GEFWAGSVYGDGDGVGVYPRNLVKEQRYVQATKEVPTTDDIDFFCE 110
Db 79 GEFWAGSVYGDGDGVGVYPRNLVKEQRYVQATKEVPTTDDIDFFCE 128

RESULT 3
US-10-219-063-72
; Sequence 72. Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: F3530PIC24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-063-72

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Best Local Similarity 100.0%; Pred. No. 5e-64; 0; Indels 0; Gaps 0;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-219-067-72  
; Sequence 72, Application US/10219067  
; Publication No. US20030187204A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C51  
; CURRENT APPLICATION NUMBER: US/10/219,067  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-067-72  
Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGIFMDRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60  
DB 19 HGIFMDRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78  
QY 61 GEFWAGSVYGDQDEMGVYGFPRNLVKEQRVYQATKEVPTTIDDFCE 110  
DB 79 GEFWAGSVYGDQDEMGVYGFPRNLVKEQRVYQATKEVPTTIDDFCE 128  
RESULT 6  
US-10-219-068-72  
; Sequence 72, Application US/10219068  
; Publication No. US20030187205A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.

US-10-219-066-72  
; Sequence 72, Application US/10219066  
; Publication No. US20030187203A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C27  
; CURRENT APPLICATION NUMBER: US/10/219,066  
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; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
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; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-066-72  
Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGIFMDRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60  
DB 19 HGIFMDRLASKKLCADDECVYVITSLASAEQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78  
QY 61 GEFWAGSVYGDQDEMGVYGFPRNLVKEQRVYQATKEVPTTIDDFCE 110  
DB 79 GEFWAGSVYGDQDEMGVYGFPRNLVKEQRVYQATKEVPTTIDDFCE 128  
RESULT 5



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; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-073-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 60
Db 19 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 78

Qy 61 GEFWAGSVYGGQDEMGMVGVFPNRLVKEQRYQATKEVPTTIDIDFFCE 110
Db 79 GEFWAGSVYGGQDEMGMVGVFPNRLVKEQRYQATKEVPTTIDIDFFCE 128

RESULT 9
US-10-219-475-72
; Sequence 72, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC49
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-475-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 60
Db 19 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 78

Qy 61 GEFWAGSVYGGQDEMGMVGVFPNRLVKEQRYQATKEVPTTIDIDFFCE 110
Db 79 GEFWAGSVYGGQDEMGMVGVFPNRLVKEQRYQATKEVPTTIDIDFFCE 128

RESULT 9
US-10-219-475-72
; Sequence 72, Application US/10219475
; Publication No. US20030187208A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC49
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-475-72
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; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-475-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 60
Db 19 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 78

Qy 61 GEFWAGSVYGGQDEMGMVGVFPNRLVKEQRYQATKEVPTTIDIDFFCE 110
Db 79 GEFWAGSVYGGQDEMGMVGVFPNRLVKEQRYQATKEVPTTIDIDFFCE 128

RESULT 10
US-10-219-480-72
; Sequence 72, Application US/10219480
; Publication No. US20030187209A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC38
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-219-480-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 60
Db 19 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYYVYSLVKVNGA 78
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QY 61 GEFWAGSVYGDQDGMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 110  
Db 79 GEFWAGSVYGDQDGMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 128

## RESULT 11

US-10-219-483-72  
; Sequence 72, Application US/10219483  
; Publication No. US20030187210A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3530P1C43  
; CURRENT APPLICATION NUMBER: US/10/219,483  
; CURRENT FILING DATE: 2002-08-13  
; PRIOR APPLICATION NUMBER: 10/119,480  
; PRIOR FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063549  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/064103  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/069873  
; PRIOR FILING DATE: 1997-12-17  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079656  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 246  
; SEQ ID NO 72  
; LENGTH: 128  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-219-525-72

Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 60  
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 78  
QY 61 GEFWAGSVYGDQDGMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 110  
Db 79 GEFWAGSVYGDQDGMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 128

## RESULT 13

US-10-219-526-72  
; Sequence 72, Application US/10219526  
; Publication No. US20030187212A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stephan, Jean-Philippe F.  
; APPLICANT: Watanabe, Colin L.  
; APPLICANT: Wood, William I.

Query Match 100.0%; Score 590; DB 12; Length 128;  
Best Local Similarity 100.0%; Pred. No. 5e-64;  
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 60  
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKGQOIYVYSLVKENGA 78

QY 61 GEFWAGSVYGDQDGMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 110  
Db 79 GEFWAGSVYGDQDGMGVGFPRNLVKEQRYVQYQATKEVPTTDDIFFCE 128

## RESULT 12

US-10-219-525-72  
; Sequence 72, Application US/10219525  
; Publication No. US20030187211A1  
; GENERAL INFORMATION:

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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC41
; CURRENT APPLICATION NUMBER: US/10/219,526
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-526-72

Query Match          100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYVQATKEVPTTIDIDFCE 110
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 79 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYVQATKEVPTTIDIDFCE 128
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RESULT 14
US-10-219-530-72
; Sequence 72, Application US/10219530
; Publication No. US20030187213A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC54
; CURRENT APPLICATION NUMBER: US/10/219,530
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1997-10-17
```

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; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-530-72

Query Match          100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 60
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 19 HGIFMDRLASKKLCADDECVYTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKNGA 78
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYVQATKEVPTTIDIDFCE 110
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 79 GEFWAGSVYGDQDEMGVGVYFPRNLVKEQRYVQATKEVPTTIDIDFCE 128
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RESULT 15
US-10-219-531-72
; Sequence 72, Application US/10219531
; Publication No. US20030187214A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC66
; CURRENT APPLICATION NUMBER: US/10/219,531
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1997-10-17
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Tue Dec 30 10:20:40 2003

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; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 72
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-531-72

Query Match      100.0%; Score 590; DB 12; Length 128;
Best Local Similarity 100.0%; Pred. No. 5e-64;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKNGA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      19 HGIFMDRLASKKLCADDECVYTTISLASAQEDYNAPDCRFINVKKGQQIYVYSKLVKNGA 78

Qy      61 GEFWAGSYVGDQDEMGMVGVGFPRNLVKEQRYQEATKEVPTTIDIDFFCE 110
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      79 GEFWAGSYVGDQDEMGMVGVGFPRNLVKEQRYQEATKEVPTTIDIDFFCE 128
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Search completed: December 29, 2003, 16:26:15  
Job time : 15.098 secs







Tue Dec 30 10:20:40 2003

Db 27 MPKLADKLCADQBCSHPI5MAVALQDYMADPCRFLLTHRGQVVVFSKL---KGRGRLF 83

QY 64 WAGSVYGGQDGMGV-VGYEPRNLVKEQRYVQEQATKEVPTTIDIFFCE 110

Db 84 WGSVQGDYGDLAARLGYFPSSIVREDQTLKPGKVDKTKDWDYFCQ 131

RESULT 2

US-08-578-649-5

; Sequence 5, Application US/08578649

; Patent No. 5770366

; GENERAL INFORMATION:

; APPLICANT: Ulrich Bogdan

; APPLICANT: Reinhard Buttner

; APPLICANT: Brigitte Kaluza

; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN

; NUMBER OF SEQUENCES: 24

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Felfe & Lynch

; STREET: 805 Third Avenue

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10022

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: Wordperfect

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/578,649

; FILING DATE: 29-July-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: DE P 43 24 247.2

; FILING DATE: 20-July-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Andrew L. Tiajolo

; REGISTRATION NUMBER: 31,575

; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 688-9200

; TELEFAX: (212) 838-3884

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 130 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-578-649-5

Query Match 39.2%; Score 231.5; DB 1; Length 130;

Best Local Similarity 43.5%; Pred. No. 2.2e-22;

Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADECVYTTISLASAQSDYNAPDCRFNLVKKGGQIYVYKLVKENGAGE-F 63

Db 26 MPKLADWKLCADECSHPISMAVALQDYMADPCRFLLTHRGQVVVFSKL---KGRGRLF 82

QY 64 WAGSVYGGQDGMGV-VGYEPRNLVKEQRYVQEQATKEVPTTIDIFFCE 110

Db 83 WGSVQGDYGDLAARLGYFPSSIVREDLNSKPGKIDMKTDQWDYFCQ 130

RESULT 3

US-07-646-537B-2

; Sequence 2, Application US/07646537B

; Patent No. 5348864

; GENERAL INFORMATION:

; APPLICANT: Barbacid, Mariano

; TITLE OF INVENTION: Vav Proto-Oncogene Protein

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

Query Match 13.8%; Score 81.5; DB 3; Length 54;

Best Local Similarity 32.3%; Pred. No. 0.0023;

Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;

QY 28 AQEDYNAPDCRFNLVKKGGQIYVYKLVKENGAGEFWAGSVYGGQDGMGVVGYFPRNLV 87

Db 1 ARYDFCARDRSELSLKEGDII---KILNKGQGGQWWRGEIYGR-----VGWFFPANYV 49

; ADDRESSEE: Bristol-Myers Squibb Company

; STREET: P.O. Box 4000

; CITY: Princeton

; STATE: New Jersey

; COUNTRY: U.S.A.

; ZIP: 08543-4000

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/646,537B

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Gaul, Timothy J.

; REGISTRATION NUMBER: 33,111

; REFERENCE/DOCKET NUMBER: DC10

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (609) 921-5901

; TELEFAX: (609) 921-4526

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 844 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-646-537B-2

Query Match 14.5%; Score 85.5; DB 1; Length 844;

Best Local Similarity 31.4%; Pred. No. 0.032;

Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFNLVKKGGQIYVYKLVKENGAGEFWAGSVYGGQDGMGVVGYFPRN 85

Db 786 AKARYDFCARDRSELSLKEGDII---KILNKGQGGQWWRGEIYGR-----ICWFFPSN 834

QY 86 LVKEQRYVQEQ 95

Db 835 YVEED--YSE 842

RESULT 4

US-09-346-510B-21

; Sequence 21, Application US/09346510B

; Patent No. 6281014

; GENERAL INFORMATION:

; APPLICANT: O'Brien, Timothy J.

; APPLICANT: Wang, Yinxiang

; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof

; FILE REFERENCE: D6221C1P

; CURRENT APPLICATION NUMBER: US/09/346,510B

; CURRENT FILING DATE: 1999-07-01

; PRIOR APPLICATION NUMBER: 08/871,732

; PRIOR FILING DATE: 1997-06-09

; NUMBER OF SEQ ID NOS: 32

; SEQ ID NO 21

; LENGTH: 54

; TYPE: PRT

; ORGANISM: unknown

; FEATURE:

; NAME/KEY: Domain

; OTHER INFORMATION: amino acid sequence of Vav SH3 domain

US-09-346-510B-21

Query Match 13.8%; Score 81.5; DB 3; Length 54;

Best Local Similarity 32.3%; Pred. No. 0.0023;

Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;

QY 28 AQEDYNAPDCRFNLVKKGGQIYVYKLVKENGAGEFWAGSVYGGQDGMGVVGYFPRNLV 87

Db 1 ARYDFCARDRSELSLKEGDII---KILNKGQGGQWWRGEIYGR-----VGWFFPANYV 49



```

CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
;
CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
;
INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-09-134-078-25
;
Query Match 11.9%; Score 70.5; DB 4; Length 680;
Best Local Similarity 27.6%; Pred. No. 2.1;
Matches 32; Conservative 12; Mismatches 37; Indels 35; Gaps 6;
;
QY 25 LASAQEDYNAPDCRFINVKKQOI-----YVYSK-----LVKENGAGEF 63
Db 404 LFNTEGDIREDTCSFILPKDGMIEIKKTVVRAGVDFYNTFEKLSVKVEDLVFENEIHL 463
;
QY 64 WAGSVYG-----DQDEMGVVGYPFRNLVKEQ---RVYQEAATKEVPTTDDIF 107
Db 464 GYG-IYGFDLDTTRIPDGEHEMFLEGHFOGKTVKDSIKAKVVNEA-RVYLAEEVDF 517
;
RESULT 10
US-08-630-915A-135
; Sequence 135, Application US/08630915A
; Patent No. 6309820
;
GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLAKES, Dana M.
; APPLICANT: MCCONNELL, Stephen J.
; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
; TITLE OF INVENTION: USING SAME
; NUMBER OF SEQUENCES: 227
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,915A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-174
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
;
;
CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
;
CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
;
INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
;
US-09-134-078-61
;
Query Match 11.9%; Score 70.5; DB 4; Length 663;
Best Local Similarity 27.6%; Pred. No. 2.1;
Matches 32; Conservative 12; Mismatches 37; Indels 35; Gaps 6;
;
QY 25 LASAQEDYNAPDCRFINVKKQOI-----YVYSK-----LVKENGAGEF 63
Db 387 LFNTEGDIREDTCSFILPKDGMIEIKKTVVRAGVDFYNTFEKLSVKVEDLVFENEIHL 446
;
QY 64 WAGSVYG-----DQDEMGVVGYPFRNLVKEQ---RVYQEAATKEVPTTDDIF 107
Db 447 GYG-IYGFDLDTTRIPDGEHEMFLEGHFOGKTVKDSIKAKVVNEA-RVYLAEEVDF 500
;
RESULT 9
US-09-134-078-25
; Sequence 25, Application US/09134078
; Patent No. 6368844
;
GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
;

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; INFORMATION FOR SEQ ID NO: 135:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 62 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-630-915A-135

Query Match 11.3%; Score 66.5; DB 4; Length 62;  
Best Local Similarity 26.6%; Pred. No. 0.25;  
Matches 17; Conservative 11; Mismatches 29; Indels 7; Gaps 2;

Qy 25 LASAQEDYNADCRFINVKKGQOIYVSKLVKENGAGFEFWAGSVYGGODEMGVGYEPR 84  
Db 4 IAQVIASYTATGPOLTLAPGQLI-----LIRKKNPGWGEGLQARKKRQ--IGWFFA 56

Qy 85 NLVK 88  
Db 57 NYVK 60

RESULT 11  
US-08-245-511-48  
; Sequence 48, Application US/08245511  
; Patent No. 5928900  
; GENERAL INFORMATION:  
; APPLICANT: Masure, H Robert  
; APPLICANT: Pearce, Barbara J  
; APPLICANT: Tuomanen, Elaine  
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
; TITLE OF INVENTION: ACCELLULAR VACCINES BASED THEREON  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/245,511  
; FILING DATE: 18-MAY-1994  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/116,541  
; FILING DATE: 01-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-069 CIP  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 642 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; IMMEDIATE SOURCE:  
; CLONE: amia  
; FEATURE:

; OTHER INFORMATION: NOTE: the reference contains a  
; OTHER INFORMATION: sequence error; the correct sequence shown below is obtained  
; PUBLICATION INFORMATION:  
; AUTHORS: Allouing, et al.  
; JOURNAL: Mol. Microbiol.  
; VOLUME: 4  
; PAGES: 633-644  
; DATE: 1990  
US-08-245-511-48

Query Match 11.3%; Score 66.5; DB 2; Length 642;  
Best Local Similarity 22.5%; Pred. No. 6.5;  
Matches 27; Conservative 20; Mismatches 44; Indels 29; Gaps 4;

Qy 6 DRLASKKLCADCECVYTISLASAQEDYNAPDCRFINVKKGQOIYVSKLVKEN-----58  
Db 309 EKVATKKALLNKDFRQALNFALDRSAYSAQ-----INGKDGAAALAVRNLFVKPDPFVSAGEK 364

Qy 59 -----GAGEFWAGSVYGGODEMGVGYEPRNLVKEQRYQEATKEVPTTIDF 107  
Db 365 TFGDLVAAQLPAYGDWKGVNLADQD-----GLF--NADKAKAEFRKAKKALEADGVQF 417

RESULT 12  
US-08-600-993A-48  
; Sequence 48, Application US/08600993A  
; Patent No. 5981229  
; GENERAL INFORMATION:  
; APPLICANT: Masure, H Robert  
; APPLICANT: Pearce, Barbara J  
; APPLICANT: Tuomanen, Elaine  
; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND  
; TITLE OF INVENTION: ACCELLULAR VACCINES BASED THEREON  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/600,993A  
; FILING DATE: 1-MAR-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/245,511  
; FILING DATE: 18-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/116,541  
; FILING DATE: 01-SEP-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-069 US  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 48:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 642 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO

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; MOLECULE TYPE: peptide
US-08-630-915A-40

Query Match      11.2%; Score 66; DB 4; Length 248;
Best Local Similarity 30.4%; Pred. No. 2;
Matches 24; Conservative 7; Mismatches 24; Indels 24; Gaps 3
Qy 28 AQEDYNAPDCRFNIVKKGQGIYYVYSKLIVKENGAGEFWAGSYVYGQDQEMGVVGYFPRNLV 87
Db 190 AMYDYAANNEDELSFSKQILNVNWK-----DQPDWVWQGEI-----NGVTGLFPSNYV 237

Qy 88 KEQRYQEAATKEVPTTID 106
Db 238 K-----MTTDS 244

```

RESULT 14  
US-08-434-255-8  
: Sequence 8, Application US/08434255  
: Patent No. 5621089  
: GENERAL INFORMATION:  
: APPLICANT: Sloma, Alan P.  
: APPLICANT: Outtrup, Helle  
: APPLICANT: Danbmann, Claus  
: APPLICANT: Aaslytg, Dorrit  
: TITLE OF INVENTION: ALKALINE PROTEASE  
: NUMBER OF SEQUENCES: 27  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: No. 5621089 No. 5621089disk of No. 5621089th America, Inc.  
: STREET: 405 Lexington Avenue, 64th Floor  
:

```

ADDRESS: NO. 36210890 NO. 36210890 DISK 01 NO. 36210890CII AMERICA, INC.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agris Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 280 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-434-255-8

Query Match          11.2%; Score 66; DB 1; Length 280;
Best Local Similarity 29.8%; Pred.No. 2.;
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

QY 22 TISLASAQEDYNAPDCRFNVKKGQOIYYVSKLVKENGAGEFWAGSYVGQDQDEMGVVGY 81
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 34 TVAVLDSGDVDYNHPDLARKVIKGYPDFIDRDNPNMDLNGHGTGHVAGTVAADTNNGIGVAGM 93
   |:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      82 FERNLYKEQRV 92
Db      94 APDTKILAVRV 104

RESULT 15
US-08-459-967-8
```

```
; Sequence 8, Application US/08459967
; Patent No. 5622841
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dammann, Claus
; APPLICANT: Aaslyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5622841o No. 5622841disk of No. 5622841th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,967
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,255
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-967-8

Query Match      11.2%; Score 66; DB 1; Length 280;
Best Local Similarity 25.6%; Pred. No. 2.4;
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

QY      22 TISLASAQEDYNAPDCRFINVKGCQIYVYISKLVKENGAGEFWAGSVYGDQDEMGVVGY 81
Db      34 TVAVLDGVDYNHFDLARKVIKGYDFIDRDNPNPMDLNGHGHVAGTVAADTNNIGIVAGM 93

QY      82 PPNLVKEQRV 92
Db      94 APDTKILAVRV 104

Search completed: December 29, 2003, 16:11:50
Job time : 8.0112 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:11:59 ; Search time 1810.69 Seconds  
(without alignments)  
2485.278 Million cell updates/sec

Title: US-10-019-455a-24  
Perfect score: 590  
Sequence: 1 HGIPMDRLASKKLCADDECV.....RVYQEATKEVPTTIDIFFCE 110

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/cgn2\_1/USPTO.spool/US10019455/runat\_29122003\_160347\_240/app\_query.fasta\_1.1770  
-DB=GenEmbl -Qfmt=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10019455 @CGN\_1\_1\_6034 @runat\_29122003\_160347\_240 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*  
15: em\_ba.\*  
16: em\_fun.\*  
17: em\_hum.\*  
18: em\_in.\*  
19: em\_mu.\*  
20: em\_om.\*  
21: em\_or.\*  
22: em\_ov.\*  
23: em\_pat.\*  
24: em\_ph.\*  
25: em\_pl.\*  
26: em\_ro.\*  
27: em\_sts.\*  
28: em\_un.\*

29: em\_vi.\*  
30: em\_htg\_hum.\*  
31: em\_htg\_inv.\*  
32: em\_htg\_other.\*  
33: em\_htg\_mus.\*  
34: em\_htg\_pln.\*  
35: em\_htg\_rod.\*  
36: em\_htg\_mam.\*  
37: em\_htg\_vrt.\*  
38: em\_sy.\*  
39: em\_htgo\_hum.\*  
40: em\_htgo\_mus.\*  
41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	590	100.0	330	6	BD010816 Novel pol
2	590	100.0	330	6	BD093117 Novel pol
3	590	100.0	384	6	BD010802 Novel pol
4	590	100.0	384	6	BD093103 Novel pol
5	590	100.0	521	6	AX358818 Sequence
6	590	100.0	521	6	AX362311 Sequence
7	590	100.0	521	6	AX454774 Sequence
8	590	100.0	521	6	AX491252 Sequence
9	590	100.0	846	9	AF233261 Homo sapi
10	590	100.0	865	9	AF243505 Homo sapi
11	590	100.0	923	6	BD010820 Novel pol
12	590	100.0	923	6	BD093121 Novel pol
13	590	100.0	1422	9	HS4242552 Homo sapi
14	547	92.7	330	6	BD010817 Novel pol
15	547	92.7	330	6	BD093118 Novel pol
16	547	92.7	384	6	BD010805 Novel pol
17	547	92.7	384	6	BD093106 Novel pol
18	547	92.7	929	10	AF243504 Mus muscu
19	547	92.7	947	6	BD010821 Novel pol
20	547	92.7	947	6	BD093122 Novel pol
21	547	92.7	958	10	MMU243939 Mus muscu
22	547	92.7	1054	10	AF233333 Mus muscu
23	541	91.7	330	6	BD010836 Novel pol
24	541	91.7	330	6	BD093137 Novel pol
25	541	91.7	384	6	BD010835 Novel pol
26	541	91.7	384	6	BD093136 Novel pol
27	477.5	80.9	484	5	AF233518 Gallus ga
28	471	79.8	307	6	BD010830 Novel pol
29	471	79.8	307	6	BD093131 Novel pol
30	413	70.0	261	6	BD010829 Novel pol
31	413	70.0	261	6	BD093130 Novel pol
32	390	66.1	466	5	AF233519 Rana cate
33	269	45.6	121151	9	HS705D16 Human DNA
34	266.5	45.2	144765	2	EX510362 Mus muscu
C 35	285.5	45.0	215581	2	AC106161 Rattus no
C 36	254.5	43.1	442	6	AX331430 Sequence
C 37	254.5	43.1	442	6	AX331840 Sequence
38	253.5	43.0	330	6	A42959 Sequence 18
39	253.5	43.0	330	6	AX016802 Sequence
40	253.5	43.0	396	9	BT007044 Homo sapi
41	253.5	43.0	396	12	BT007775 Synthetic
42	253.5	43.0	459	6	A42942 Sequence 1
43	253.5	43.0	459	6	AX016785 Sequence
C 44	253.5	43.0	459	6	AX252508 Sequence
C 45	253.5	43.0	459	6	AX287209 Sequence

ALIGNMENTS

RESULT 1



BD010816	BD010816	330 bp	DNA	linear	PAT 31-JAN-2002
LOCUS	Novel polypeptide and DNA thereof.				
DEFINITION	BD010816				
ACCESSION	BD010816.1	GI:18639189			
VERSION	JP 2001069994-A/17.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 330)				
AUTHORS	Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y., Yoshimura,K. and Tanaka,H.				
TITLE	Novel polypeptide and DNA thereof				
JOURNAL	Patent: JP 2001069994-A 17 21-MAR-2001;				
	TAKEDA CHEMICAL INDUSTRIES LTD				
COMMENT	OS Homo sapiens (human)				
	PN JP 2001069994-A/17				
	PD 21-MAR-2001				
	PF 29-JUN-2000 JP 2000195911				
	PR				
	PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI SHINICHI MOGI,				
	PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC A61P19/08,				
	PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC G01N33/53//				
	CC C12P21/08, C12N15/00, A61K37/02, C12N5/00				
	CH				
	FH Key	Location/Qualifiers			
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	FT /organism='Homo sapiens (human)'				
FEATURES	Location/Qualifiers				
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BASE COUNT	91 a 60 c 91 g 88 t				
ORIGIN					
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Score:	590.00	Matches:	110		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	6	Gaps:	0		
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Db 1	CATGGAATATTATTATGGACCGCTAGCTTCCAAGAGCTCTGTGCAGATGATGAGTGTCTC 60				
Qy 21	TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40				
Db 61	TATTACTATTCTCTGGCTAGTGTCTCAGAAGATTATATGCCCGAGCTGTAGATTCAATT 120				
Qy 41	AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyVala 60				
Db 121	AACGTTAAAAAAGGCGCAGCATCTATGTGTACTCAAAAGCTGGTAAAGAAAAATGGAGCT 180				
Qy 61	GlyGluPheTTPAlaGlySerValTyrClyAspGlyGlnAspGluMetGlyValValcIy 80				
Db 181	GGAGAAATTTTGGCTGGCAGTGTTATGTGTATGCCGAGGACGAGATGGGAGTCGTGGGT 240				
Qy 81	TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100				
Db 241	TATTTCCCGAGAACTTGGTCAAGGAACAGCGTGTGTACCGAGAGCTACCAAGAGATT 300				
Qy 101	ProThrThrAspIleAspPheCysGlu 110				

Qy	81	TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal	100
Db	295	TATTTCCTCCAGGAACCTTGGTCAAGGAACAGCGTGTGTACCCAGGAAGCTACCAAGAAAGTT	354
Qy	101	ProThrThrAspIleAspPhePheCysGlu	110
Db	355	CCACACAGGATATTGACTTCTCTCTCGAG	384
RESULT 4			
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LOCUS	BD093103	384 bp	DNA
DEFINITION	Novel polypeptide and its DNA.		linear
ACCESSION	BD093103		
VERSION	BD093103.1	GI:22638691	
KEYWORDS	WO 0102564-A/3.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	1 (bases 1 to 384)		
	Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,		
	Yoshimura, K. and Tanaka, H.		
TITLE	Novel polypeptide and its DNA		
JOURNAL	Patent: WO 0102564-A 3 11-JAN-2001;		
	TAKEEDA CHEMICAL INDUSTRIES LTD, YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO		
	HIGEY, SHOICHI OKUBO, SHINICHI MOGI, YUKO NOGUCHI, KOJI YOSHIMURA,		
COMMENT	HIDEYUKI TANAKA		
	OS Homo sapiens (human)		
	PN WO 0102564-A/3		
	PD 11-JAN-2001		
	PF 29-JUN-2000 WO 2000JP004278		
	PR 30-JUN-1999 JP 93P 186718		
	PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, SHINICHI		
	PI MOGI,		
	PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA		
	PC C12N15/12, C12N5/10, C12P21/02, C07K14/47, C07K16/18, A61K45/00, PC		
	A61K38/17,		
	PC A61K39/395, A61K49/16, A61P19/02, A61P19/08, A61K31/7088//C12P21/		
	PC 02, C12R1:19)		
CC			
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FEATURES	source	Location/Qualifiers	
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	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
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ORIGIN			109 t
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Pred. No.:	7.69e-66	Length:	384
Score:	590.00	Matches:	110
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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Qy	21	TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle	40
Db	115	TATACATATTCTCTGCTAGTGTGCTCAAGAAGATATATATGCCCCGACTGTAGATTCAAT	174
Qy	41	AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla	60
Db	175	AACGTTAAAAAGCGCAGCATCTATGTACTCAAGCTGTGTAAAGAAAATGGAGCT	234
Qy	61	GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly	80

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Db      235 GGAGAAATTTGGCTGGCAGGTTTATGGTGATGCCAGGACGAGATGGGAGTCGTGGGT 294
Qy      81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db      295 TATTTCCCGAGAACTTGGTCAAGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTT 354
Qy      101 ProThrThrAspIleAspPheCysGlu 110
Db      355 CCCACCGGATATTGACTTCTTCTGCGAG 384

RESULT 5
AX358818
LOCUS      AX358818
DEFINITION Sequence 71 from Patent WO0193983.
ACCESSION  AX358818
VERSION     AX358818.1
KEYWORDS    GI:18675310
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
            Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
            Patent: WO 0193983-A 71 13-DEC-2001;
            Genentech Inc. (US)
FEATURES    Location/Qualifiers
             source
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               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
BASE COUNT 167 a 86 c 131 g 137 t
ORIGIN

Alignment Scores:
Pred. No.:      1..65      Length:      521
Score:          590.00     Matches:    110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels: 0
DB:             6         Gaps: 0

US-10-019-455A-24 (1-110) x AX358818 (1-521)
Qy      1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
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Qy      21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db      152 TATACTATTTCTCTGGCTAGTGTCTCAAGAAAGATTATAATGCCCGGAGCTGTAGATTCA 211
Qy      41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db      212 AACGTTAAAAAAGGCGACGAGATCTATGTCTCAAAAGCTGTGTAAGAAAGAAATGGAGCT 271
Qy      61 GlyCluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db      272 GGAGAATTTTGGCTGGCAGTGTATGTTATGGTGATGCCAGGACGAGATGGGAGTCGTGGGT 331
Qy      81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db      332 TATTTCCCGAGAACTTGGTCAAGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTT 391
Qy      101 ProThrThrAspIleAspPheCysGlu 110
Db      392 CCCACCGGATATTGACTTCTTCTGCGAG 421

RESULT 6
AX358818
LOCUS      AX358818
DEFINITION Sequence 71 from Patent WO0193983.
ACCESSION  AX358818
VERSION     AX358818.1
KEYWORDS    GI:18675310
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
            Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
            Patent: WO 0193983-A 71 13-DEC-2001;
            Genentech Inc. (US)
FEATURES    Location/Qualifiers
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               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"
BASE COUNT 167 a 86 c 131 g 137 t
ORIGIN

Alignment Scores:
Pred. No.:      1..65      Length:      521
Score:          590.00     Matches:    110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels: 0
DB:             6         Gaps: 0

US-10-019-455A-24 (1-110) x AX358818 (1-521)
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Qy      21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db      152 TATACTATTTCTCTGGCTAGTGTCTCAAGAAAGATTATAATGCCCGGAGCTGTAGATTCA 211
Qy      41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db      212 AACGTTAAAAAAGGCGACGAGATCTATGTCTCAAAAGCTGTGTAAGAAAGAAATGGAGCT 271
Qy      61 GlyCluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db      272 GGAGAATTTTGGCTGGCAGTGTATGTTATGGTGATGCCAGGACGAGATGGGAGTCGTGGGT 331
Qy      81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db      332 TATTTCCCGAGAACTTGGTCAAGAACAGCGTGTGTACCAAGGAAGCTACCAAGGAAGTT 391
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Db      392 CCCACCGGATATTGACTTCTTCTGCGAG 421

RESULT 7
AX454774
LOCUS      AX454774
DEFINITION Sequence 359 from Patent WO0208284.
ACCESSION  AX454774
VERSION     AX454774.1
KEYWORDS    GI:21714011
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
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AX362311
LOCUS      AX362311
DEFINITION Sequence 71 from Patent WO0208288.
ACCESSION  AX362311
VERSION     AX362311.1
KEYWORDS    GI:18694613
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
            Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
            Watanabe,C.K. and Wood,W.I.
            Secreted and transmembrane polypeptides and nucleic acids encoding
            the same
            Patent: WO 0208288-A 71 31-JAN-2002;
            Genentech, Inc. (US)
FEATURES    Location/Qualifiers
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BASE COUNT 167 a 86 c 131 g 137 t
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Alignment Scores:
Pred. No.:      1..65      Length:      521
Score:          590.00     Matches:    110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00% Indels: 0
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Qy      21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db      152 TATACTATTTCTCTGGCTAGTGTCTCAAGAAAGATTATAATGCCCGGAGCTGTAGATTCA 211
Qy      41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db      212 AACGTTAAAAAAGGCGACGAGATCTATGTCTCAAAAGCTGTGTAAGAAAGAAATGGAGCT 271
Qy      61 GlyCluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db      272 GGAGAATTTTGGCTGGCAGTGTATGTTATGGTGATGCCAGGACGAGATGGGAGTCGTGGGT 331
Qy      81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
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Qy      101 ProThrThrAspIleAspPheCysGlu 110
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RESULT 7
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LOCUS      AX454774
DEFINITION Sequence 359 from Patent WO0208284.
ACCESSION  AX454774
VERSION     AX454774.1
KEYWORDS    GI:21714011
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
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Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.  
Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis  
Patent: WO 0208284-A 359 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

**TITLE**  
Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

**JOURNAL**  
Patent: WO 0208284-A 359 31-JAN-2002;  
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone (US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard, Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ; Hillan, Kenneth J. (US) ; Marsters, Scott A. (US) ; Pan, James (US) ; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ; Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William I. (US)

**FEATURES**  
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BASE COUNT 167 a \_ 86 c 131 g 137 t  
ORIGIN

Alignment Scores:  
Pred. No.: 11e-65 Length: 521  
Score: 590.00 Matches: 110  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-019-455A-24 (1-110) x AX454774 (1-521)

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QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
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Db 152 TATACATTTCTCTGGCTAGTCTCAAGAAGATTATAATGCCCGGACTGTAGATTCATT 211  
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Db 332 TATTTCCCGAGGAACCTGGTCAAGGAACAGCGTGTACCAAGAGCTACCAAGGAAGTT 391  
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QY 101 ProThrThrAspIleAspPheCysGlu 110  
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Db 392 CCCACCACGGATATTGACTTCTTCGCGAG 421  
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RESULT 8  
AX491252  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 846)  
Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.  
A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping  
Genomics 66 (3), 242-248 (2000)  
JOURNAL  
MEDLINE  
PUBMED  
20334619  
10873378  
2 (bases 1 to 846)  
Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.  
Direct Submission  
Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA  
Location/Qualifiers  
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**TITLE**  
Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

**JOURNAL**  
Patent: WO 020690-A 359 03-JAN-2002;  
Genentech, Inc. (US)

**FEATURES**  
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Location/Qualifiers  
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BASE COUNT 167 a \_ 86 c 131 g 137 t  
ORIGIN

Alignment Scores:  
Pred. No.: 11e-65 Length: 521  
Score: 590.00 Matches: 110  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-019-455A-24 (1-110) x AX491252 (1-521)

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1 (bases 1 to 846)  
Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S., Denis, C.S., Bell, A.M., Hudspeth, A.J. and Morton, C.C.  
Direct Submission  
Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA  
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DEFINITION Homo sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.
ACCESSION AF243505
VERSION AF243505.1 GI:11991843
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 865)
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
TITLE Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an
in vitro effect on the early differentiation of the inner ear
mesenchyme
JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)
MEDLINE 20568254
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2 (bases 1 to 865)
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
du Dr. Roux, Paris 75015, France
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DEFINITION Novel polypeptide and DNA thereof.
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VERSION BD010820.1 GI:18639193
KEYWORDS JP 2001069994-A/21.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 923)
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AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,  
Yoshimura,K. and Tanaka,H.  
TITLE Novel polypeptide and DNA thereof  
JOURNAL TAKEDA CHEMICAL INDUSTRIES LTD  
COMMENT CS Homo sapiens (human)  
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PF 21-JAN-2001  
PD 21-JUN-2000 JP 2000195911  
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PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA  
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DEFINITION Novel polypeptide and its DNA.  
ACCESSION BD093121  
VERSION BD093121.1 GI:22638709  
KEYWORDS WO 0102564-A/21.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 923)  
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,  
Yoshimura,K. and Tanaka,H.  
TITLE Novel polypeptide and its DNA  
JOURNAL TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO  
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HIDEYUKI TANAKA  
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Qy 101 ProThrThrAspIleAspPheCysGlu 110  
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DEFINITION Homo sapiens mRNA for melanoma inhibitory activity like protein  
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ACCESSION AJ242552



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DEFINITION         Novel polypeptide and its DNA.
ACCESSION          BD093118
VERSION            BD093118.1 GI:22638706
KEYWORDS           WO 0102564-A/18.
SOURCE             Mus sp.
ORGANISM           Mus sp.
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                  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE
AUTHORS            Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
                  Yoshimura,K. and Tanaka,H.
TITLE              Novel polypeptide and its DNA
JOURNAL            Patent: WO 0102564-A 18 11-JAN-2001;
                  TAKEDA CHEMICAL INDUSTRIES LTD,YASUAKI ITO,KAZUNORI NISHI, KAZUHIRO
                  OGI, SHOICHI OKUBO, SHINICHI MOGI,YUKO NOGUCHI,KOJI YOSHIMURA,
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COMMENT            OS Mus sp. (mouse)
                  PN WO 0102564-A/18
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GenCore version 5.1.6  
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Run on: December 29, 2003, 16:23:14 ; Search time 1138.05 Seconds  
(without alignments)  
2349.180 Million cell updates/sec

Title: US-10-019-455a-24

Perfect score: 590

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Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	547	92.7	608	13	BQ564944	BQ564944 gi27g09.y
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35	233.5	43.0	609	12	BM791767	BM791767 K-EST0071
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37	233.5	43.0	1140	12	BG765502	BG765502 602739414
38	232.5	42.8	437	9	AV592759	AV592759 AV592759
39	232.5	42.8	453	9	AA627297	AA627297 nq68g01.s
40	252.5	42.8	517	10	BE665724	BE665724 154861 MA
41	251	42.5	544	13	BQ208982	BQ208982 UI-R-DY1-
42	250.5	42.5	594	14	CA509768	CA509768 UI-R-PS0-
43	249.5	42.3	381	9	AI620915	AI620915 tu05e09.x
44	249.5	42.3	430	10	BF439750	BF439750 nad13c10.
45	247.5	41.9	678	10	BB647928	BB647928 BB647928

# ALIGNMENTS

RESULT 1  
BQ570035  
LOCUS  
DEFINITION  
BQ570035  
ACCSSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE

BQ570035  
gi143b10.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gi143b10 5', mRNA sequence.  
BQ570035  
BQ570035.1 GI:21473352  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 398)

## AUTHORS

Kachar,B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

## JOURNAL

Unpublished

## COMMENT

Contact: Kachar,B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765

Email: kacharbenid@nih.gov

Plate: 143 row: b column: 10

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

## FEATURES

source

1..398

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="gii43b10"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti cDNA pBluescript"

/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bulla capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning Kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold end, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACACCTATGACC) and 25<sup>+</sup> strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster

City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 105 a 69 c 116 g 108 t

## ORIGIN

## Alignment Scores:

Pred. No.:	1.2e-64	Length:	398
Score:	547.00	Matches:	99
Percent Similarity:	96.36%	Conservative:	7
Best Local Similarity:	90.00%	Mismatches:	4
Query Match:	92.71%	Indels:	0
DB:	13	Gaps:	0

US-10-019-455A-24 (1-110) x BQ570035 (1-398)

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 Db 67 CATGGTGATTATGGATAAACTTTCTTAAGAAGTTGTGGGATGAGGAGTGTC 126

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 Db 127 TATATCTATTCTCTGGCAAGAGCACAGAGATTACATGCCCCAGACTGTAGGTTTCATC 186

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 Db 187 GATGTCAAGAAGGCGACAGATCTATGTTACTCCAAGCTGGTAAACAGAAACCGAGCT 246

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 Db 247 GGAGAGTTTTGGCTGGCAGTGTTTATGTGCACCACAGGATGAGATGGGATTGTAGGT 306

QY 81 TyrPheProArgAnLeuValLysGluGlnArgValTyrGlnGluAlaThylLysGluVal 100  
 Db 307 TATTTCCCAAGCAACTTGTGAAGAGCAGCGTGATACAGGAGGCCACCAAGAGATC 366

QY 101 ProThrThrAspIleAspPhePheCysGlu 110

Db 367 CCAACACCGGATATTGACTTCTCTGTGAA 396

## RESULT 2

BQ564607

LOCUS

DEFINITION BQ564607 488 bp mRNA linear EST 19-JUN-2002  
 gi19h02.yl Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 Clone gi19h02.5', mRNA sequence.

ACCESSION

BQ564607

VERSION

BQ564607.1

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Mus musculus

REFERENCE

1 (bases 1 to 488)

TITLE

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL

Unpublished

COMMENT

Contact: Kachar,B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kacharbenid@nih.gov

Plate: 19 row: h column: 02

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1..488

/organism="Mus musculus"

/mol\_type="mRNA"



(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 147 a 85 c 143 g 139 t  
ORIGIN

Alignment Scores:  
Pred. No.: 1,71e-64 Length: 514  
Score: 547.00 Matches: 99  
Percent Similarity: 96.36% Conservative: 7  
Best Local Similarity: 90.00% Mismatches: 4  
Query Match: 92.71% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x BQ568498 (1-514)

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Db      119 TATACTATTCTCTGGCAAGACAGACAGAGAAATTACAAATGCCCACTGTAGTTTCATC 178

QY      41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyVala 60
Db      179 GATGTCAGAAGAGGGCAGCAGACTATGTTTACTCCAGCTGTTACACAGAAACCGAGCT 238

QY      61 GlyGluPheTrpIaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db      239 GGAGAGTTTGGGCTGGCAGTGTATGTTATGGTGACCAACAGCATGAGATGGGAATTTAGCT 298

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QY      81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGlnAlaThrLysGluVal 100
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QY      101 ProThrThrAspIleAspPhePheCysGlu 110
Db      359 CCAACACCGGATATTGACTTCTTCTCTGTAA 388

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#### RESULT 4

##### LOCUS

##### DEFINITION

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

BQ564134 534 bp mRNA linear EST 19-JUN-2002  
gill1d01.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gill1d01 5', mRNA sequence.

BQ564134

BQ564134.1 GI:21467451

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 534)

Kachar, B.

EST analysis of gene expression in the mouse Organ of Corti at the  
onset of hearing

Unpublished

Contact: Kachar, B.

National Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kacharbenidcd.nih.gov

Plate: 11 row: d column: 01

Seq primer: M13RPI reverse primer (ABI).

Location/Qualifiers

1. .534

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="gill1d01"

/sex="male and female"

/dev\_stage="Post natal day 5 to 13"

/clone\_lib="Mouse Organ of Corti; Vector: pBluescript; The  
organ of Corti (OC) was fine dissected from a total of 386  
OC as follows: 102 samples from post-natal (P) day 5; 72  
from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;  
14 from P12 and 24 from P13. After killing animals by  
cervical dislocation followed by decapitation, the bulla  
was removed and opened in Leibowitz medium. The bony  
capsule of the cochlea was chipped away, stria vascularis  
and spiral ligament were removed and the sensory  
epithelium was carefully dissected out of the modiolus.

Total RNA was extracted using the micro Fasttrack kit  
(catalog # K1593-02; Invitrogen, Carlsbad, CA), according  
to manufacturer's instructions. Reverse transcription and  
library construction were carried out with the Uni-Zap XR  
vector kit (catalog # 237211, Stratagene) and Uni-Zap XR  
Gigapack III Gold Cloning kit (catalog # 237612), both  
from Stratagene (La Jolla, CA, USA), according to  
manufacturer's instructions. Briefly: 1.5 ug mRNA was  
reverse transcribed using a hybrid oligo(dT) linker-primer  
that contains an Xho I site. First strand synthesis was  
primed with the linker-primer and transcribed using  
Moloney murine leukemia virus reverse transcriptase  
(MMLV-RT) and 5-methyl dCTP. The second strand was  
synthesized with DNA polymerase and RNase H. Complementary  
DNA was blunt ended with Pfu DNA polymerase, ligated with  
EcoR I adapters in the presence of ligase and digested  
with Xho I. The cDNA was sequentially size fractionated  
over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

#### FEATURES

source



strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 160 a 92 c 154 g 153 t

ORIGIN

#### Alignment Scores:

Pred. No.: 1.92e-64 Length: 560  
Score: 547.00 Matches: 99  
Percent Similarity: 96.36% Conservative: 7  
Best Local Similarity: 90.00% Mismatches: 4  
Query Match: 92.71% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x BQ569741 (1-560)

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QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
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QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
DB 180 GATGTCAAGAAAGGCGAGCAGATCATGTGTCTCAAGCTGGTAACAGAAAACGGAGCT 239  
QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValGly 80  
DB 240 GGAGAGTTTGGCGTGGCAGTGTATGTGTACCCAGAGTGGATGGGAATTGTAGGT 299  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
DB 300 TATTTCGCCAGCACTTGGTGAAGAGCAGCGGTATATCCAGGAGGCCACCAAGGAGATC 359  
QY 101 ProThrThrAspIleAspPheCysGlu 110  
DB 360 CAACACCGGATATTGACTTCTTCTGTGAA 389

#### RESULT 6

BQ564944  
LOCUS BQ564944 608 bp mRNA linear EST 19-JUN-2002  
DEFINITION gi27909.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gi27909 5', mRNA sequence.

ACCESSION BQ564944

VERSION BQ564944.1 GI:21468261

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Kachar.B. (bases 1 to 608)

TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

JOURNAL Unpublished

COMMENT Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 27 row: g column: 09

Seq primer: M13RPI reverse primer (ABI).

FEATURES  
source

1. 608  
/organism="Mus musculus"  
/mol\_type="mRNA"  
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/dev\_stage="Post natal day 5 to 13"  
/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on Xli Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 169 a 107 c 166 g 166 t

ORIGIN

Alignment Scores:

Pred. No.: 2.15e-64 Length: 608  
Score: 547.00 Matches: 99





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Qy 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
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 Db 247 GGAGAGTTTGGCGTGGCAGTGTATGTTGGTGGACCCACGAGTGGAGTGGGAATTGTAGGT 306  
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Qy 81 TyrPheProArgAsnLeuVallysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
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 Db 307 TATTTCCCGAGCACTTGGTGAAGAGCAGCGGTATACCGAGGAGGCCACCAAGGAGATC 366  
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Qy 101 ProThrThrAspIleAspPheCysGlu 110  
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Db 367 CCAACCCAGGATATTGACTTCTTCTGTGAA 396  
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## RESULT 8

BO563768 684 bp mRNA linear EST 19-JUN-2002  
 LOCUS gi06c09.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
 DEFINITION clone gi06c09 5', mRNA sequence.

ACCESSION BO563768  
 VERSION 1  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 684)  
 AUTHORS Kachar B.  
 TITLE EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
 JOURNAL Unpublished  
 COMMENT Contact: Kachar, B.  
 Structural Cell Biology  
 National Institute of Deafness and other Communication Disorders  
 50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
 Tel: 301-402-1599  
 Fax: 301-402-1765  
 Email: kachar@nidcd.nih.gov  
 Plate: 06 row: C column: 09  
 Seq primer: M3RPI reverse primer (ABI).  
 Location/Qualifiers

## FEATURES

source

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 /dev\_stage="Post natal day 5 to 13"  
 /clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
 /note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was

synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLi Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 194 a 120 c 178 g 192 t  
 ORIGIN

## Alignment Scores:

Pred. No.: 2,548-64 Length: 684  
 Score: 547.00 Matches: 99  
 Percent Similarity: 96.36% Conservative: 7  
 Best Local Similarity: 90.00% Mismatches: 4  
 Query Match: 92.71% Indels: 0  
 DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x BQ563768 (1-684)

Qy 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20  
 |||||  
 Db 67 CATGTTGTTATTTATGGATAAACTTTCTTCTAAGAAGTTGTGTGGATGAGGAGTGTGTC 126  
 |||||

Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 |||||  
 Db 127 TATACTATTTCTCTGGCAGAGACACAGGAAGATTACATGCCCCAGACTGTAGGTTCATC 186  
 |||||

Qy 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 |||||  
 Db 187 GATGTCAAGAAAGGCGAGCATCTATGTTTACTCCAGCTGGTAACAGAAAACGAGCT 246  
 |||||

Qy 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 |||||  
 Db 247 GGAGAGTTTGGCGTGGCAGTGTATTGTTGGTCCACCAGGATGAGTGGGAATTGTAGGT 306  
 |||||

Qy 81 TyrPheProArgAsnLeuVallysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
 |||||  
 Db 307 TATTTCCCGAGCACTTGGTGAAGAGCAGCGGTATACCGAGGAGGCCACCAAGGAGATC 366  
 |||||

Qy 101 ProThrThrAspIleAspPheCysGlu 110  
 |||||

Db 367 CCAACCCAGGATATTGACTTCTTCTGTGAA 396  
 |||||

## RESULT 9

BB611549 696 bp mRNA linear EST 31-AUG-2001  
 LOCUS BB611549

transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 50.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGATTATTAATATCCCTCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI."

BASE COUNT 204 a 122 c 176 g 194 t  
ORIGIN

Alignment Scores:  
Pred. No.: Length: 696  
Score: 547.00 Matches: 99  
Percent Similarity: 96.36% Conservative: 7  
Best Local Similarity: 90.00% Mismatches: 4  
Query Match: 92.71% Indels: 0  
Gaps: 0  
DB: 10

US-10-019-455A-24 (1-110) x BB611549 (1-696)

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QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
DB 138 TATTAATATTTCTTGGCAAGAGCAGAGATACATGCCAGACTGTAGGTTTCATC 197  
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLysLeuValLysGluAsnGlyAla 60  
DB 198 GATGTCAGAAAGGCGCAGCAGATCTATGTTTACTCCAAAGCTGGTAAACAGAAACGAGCT 257  
QY 61 GlyGluPheTTPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
DB 258 GGAGAGATTTGGGCTGGCAGTGTATTGTTGGTCCAGCAGGATGATGAGTGGAAATTTAGCT 317  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
DB 318 TATTTCCCACTTGGTGAAGAGCAGCGTGTATACCAGGAGGCCACCAAGGAGATC 377  
QY 101 ProThrThrAspIleAspPhePheCysGlu 110  
DB 378 CCAACCGGATATTGACTTCTTCTGTGAA 407

RESULT 10  
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LOCUS gi42903.y1 Mouse Organ of Corti cDNA pBlueScript Mus musculus cDNA  
DEFINITION clone gi42903 5', mRNA sequence.  
ACCESSION BQ565637  
VERSION BQ565637.1 GI:21468954  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Kachar.B.  
REFERENCE 1 (bases 1 to 474)  
AUTHORS EST analysis of gene expression in the mouse Organ of Corti at the  
TITLE onset of hearing  
JOURNAL Unpublished  
COMMENT Contact: Kachar.B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 42 row: g column: 03  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
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/mol\_type="mRNA"

FEATURES  
source

BB611549 RIKEN full-length enriched, 13 days embryo head Mus  
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BB611549  
EST. BQ611549.1 GI:15393547  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 696)  
Arakawa, K., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.,  
Hiramoto, K., Ishii, Y., Ito, M., Kawai, J., Kono, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H.,  
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,  
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Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,  
Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)  
Unpublished  
Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gsc.riken.go.jp/  
URL: http://genome.gsc.riken.go.jp/  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new  
genes. Genome Res. 10 (10), 1617-1630 (2000)  
wagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,  
Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and  
Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Kono, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shingawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T.,  
Ishii, Y. and Hayashizaki, Y.  
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.  
Funct. Genomics 2 pre, 172-186 (2001)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.  
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Location/Qualifiers  
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/clone\_lib="RIKEN full-length enriched, 13 days embryo  
head"  
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Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGATCTCGATTATTAATATCCCTCCCCCCCCCCC 3']. cDNA was  
prepared by using trehalose thermo-activated reverse

/db\_xref="taxon:10090"  
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/sex="male and female"  
/dev stage="Post natal day 5 to 13"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR GigaPack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

145 a 78 c 131 g 120 t  
BASE COUNT  
ORIGIN

Alignment Scores:  
Pred. No.: 7,386-64 Length: 474  
Score: 542.00 Matches: 98  
Percent Similarity: 95.45% Conservative: 7  
Best Local Similarity: 89.09% Mismatches: 5  
Query Match: 91.86% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x BQ565637 (1-474)  
QY 1 HisGlyIlePheMetAspArgLeuAlaSerIysLysLeuCysAlaAspAspGluCysVal 20  
Db 68 CATGGTGTATTATGGATAAAGTCTTCTTAATAAGTGTGTGGGATGAGGAGTGTGTC 127  
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
Db 128 TATATCTATTCTCTGGCAGAGACACAGGAGATTACATGCCAGACTGTAGGTTTCATC 187  
QY 41 AsnValLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
Db 188 GATGTCAAGAAAGGGCAGCAGATCTATGTTTCTCAAGCTGTATCAAGAAACCGAGCT 247  
QY 61 GlyGluPheThrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValGly 80  
Db 248 GGAGAGTTTGGCTGGCAGTGTATTATGTGACCCAGGATGAGATGGGAATTAGTGT 307  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
Db 308 TATTTCCTCCAGCAACTTGTGTAAGGAGCAGCGTGTATACAGGAGGCCACCAAGGAGATC 367  
QY 101 ProThrThrAspIleAspPheCysGlu 110  
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RESULT 11  
BQ566932  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source

BQ566932 409 bp mRNA linear EST 19-JUN-2002  
gi73909.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA  
clone gi73909 5', mRNA sequence.  
BQ566932  
VERSION BQ566932.1 GI:21470249  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Rodentia; Sciurognathi; Muridae; Mus.  
Kachar, B.  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
Unpublished  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kachar@nidcd.nih.gov  
Plate: 73 row: 9 column: 09  
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/dev stage="Post natal day 5 to 13"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit

(catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-Zap XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapack III Gold and upon titration on XL1 Blue MRF' cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's EXassist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

BASE COUNT 102 a 75 c 121 g 111 t

# Alignment Scores:

Pred. No.: 4,5e-61 Length: 409  
Score: 521.00 Matches: 97  
Percent Similarity: 94.55% Conservative: 7  
Best Local Similarity: 88.18% Mismatches: 5  
Query Match: 88.31% Indels: 1  
DB: 13 Gaps: 0

US-10-019-455a-24 (1-110) x BQ566932 (1-409)

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Db 81 CATGGTGATTATGGATAAACITTCCTCTAAGAGTGTGTGCTTGATGAGAGGTGTG 140  
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Db 141 CTATACTATTCTCTGGCAAGACACAGGAGATTACATGCCACGACTGTAGTTTCAT 200  
Qy 40 aAsnValIlyslsGlyGlnIlelTyrValTyrSerIlyslsLeuValIlyslsGlnAl 60  
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Db 261 TGGAGAGTTTGGGCTGGCAGTGTATTATGGTACCACCGAGATGAGATGGGAATTGTAGG 320

Qy 80 YTYrPheProArgAsnLeuValIlyslsGluGlnArgValTyrGlnGluAlaThrIlyslsGluVa 100  
Db 321 TTTATTTCCCGAGCACTGTGTGAAGGAGCAGCGTGTATACCGAGGAGGCCACCAAGAGAT 380  
Qy 100 lProThrThrAspIleAspPhePheCys 109  
Db 381 CCCAACACGCGCTATTGACTTCTTCTGT 408  
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LOCUS  
DEFINITION  
gi37b12.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA clone gi37b12 5', mRNA sequence.  
ACCESSION  
BQ565411  
VERSION  
BQ565411.1 GI:21468728  
KEYWORDS  
EST.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
REFERENCE  
1 (bases 1 to 490)  
AUTHORS  
Kachar, B.  
TITLE  
EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing  
JOURNAL  
Unpublished  
COMMENT  
Contact: Kachar, B.  
Structural Cell Biology  
National Institute of Deafness and other Communication Disorders  
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA  
Tel: 301-402-1599  
Fax: 301-402-1765  
Email: kacharben@nid.nih.gov  
Plate: 37 row: b column: 12  
Seq primer: M13RP1 reverse primer (ABI).  
FEATURES  
Location/Qualifiers  
1..490  
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/clone\_lib="Mouse Organ of Corti cDNA pBluescript"  
/note="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapack III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker-primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden)

and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25% strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

```

BASE COUNT      191 a   77 c   109 g   112 t   1 others
ORIGIN
Alignment Scores:
Pred. No.:      3,82e-60      Length:      490
Score:          515.00      Matches:      94
Percent Similarity: 94.55%      Conservative: 10
Best Local Similarity: 85.45%      Mismatches:   6
Query Match:      87.29%      Indels:       0
DB:              13          Gaps:          0
US-10-019-455a-24 (1-110) x BQ565411 (1-490)

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```

QY      1  HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
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QY      21  TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
      201 TATACATATTCTCTGGCAGAGACAGACAGAAAATTTACAAATGCCCAACTGTAGTTCATC 260
QY      41  AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
      261 GATGTCAAAAAGGGCAGCAATCTATGTTTACTCCAGCTGTTACAAAAACGGAGCT 320
QY      61  GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
      321 GGAAGTTTGGGCTGCGAGTGTATTATGGGACACACAGGATGAAATGGGAATTGTAGGT 380
QY      81  TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
      381 TATTTCCTCCACCAACTGGTGTGAAGGAGACGCGTGTATACCAGAGGCCCAACAGGAGATC 440
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```

RESULT 13
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DEFINITION gi88408.y1 Mouse Organ of Corti cDNA pBluescript Mus musculus cDNA
clone gi88408 5', mRNA sequence.
ACCESSION BQ567343
VERSION   BQ567343.1 GI:21470660
KEYWORDS  EST.

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## SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 604)

Kachar, B.

EST analysis of gene expression in the mouse Organ of Corti at the onset of hearing

Unpublished

## JOURNAL

Unpublished

Contact: Kachar, B.

Structural Cell Biology

National Institute of Deafness and other Communication Disorders

50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA

Tel: 301-402-1599

Fax: 301-402-1765

Email: kachar@nidcd.nih.gov

Plate: 88 row: d column: 08

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1. 604

## FEATURES

source

/organism="Mus musculus"

/mol type="mRNA"

/strain="BALB/c"

/db\_xref="taxon:10090"

/clone="gi88408"

/sex="male and female"

/dev stage="Post natal day 5 to 13"

/clone lib="Mouse Organ of Corti cDNA pBluescript"

/notes="Organ: Organ of Corti; Vector: pBluescript; The organ of Corti (OC) was fine dissected from a total of 386 OC as follows: 102 samples from post-natal (P) day 5; 72 from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10; 14 from P12 and 24 from P13. After killing animals by cervical dislocation followed by decapitation, the bulla was removed and opened in Leibowitz medium. The bony capsule of the cochlea was chipped away, stria vascularis and spiral ligament were removed and the sensory epithelium was carefully dissected out of the modiolus. Total RNA was extracted using the Micro Fasttrack kit (catalog # K1593-02; Invitrogen, Carlsbad, CA), according to manufacturer's instructions. Reverse transcription and library construction were carried out with the Uni-Zap XR vector kit (catalog # 237211, Stratagene) and Uni-Zap XR Gigapak III Gold Cloning kit (catalog # 237612), both from Stratagene (La Jolla, CA, USA), according to manufacturer's instructions. Briefly: 1.5 ug mRNA was reverse transcribed using a hybrid oligo(dT) linker-primer that contains an Xho I site. First strand synthesis was primed with the linker- primer and transcribed using Moloney murine leukemia virus reverse transcriptase (MMLV-RT) and 5-methyl dCTP. The second strand was synthesized with DNA polymerase and RNase H. Complementary DNA was blunt ended with Pfu DNA polymerase, ligated with EcoR I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-1000 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with EcoR I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XLI Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200 ul of saturated culture with the Concert96(TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACAGCTATGACC) and 25%

strength BigDye terminator sequencing chemistry (Applied Biosystems Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Watlham, MA), and analyzed on 3700 automated capillary sequencers using POP5 polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in GenBank and have known function; 23% have hits in GenBank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified.

BASE COUNT 178 a 108 c 152 g 166 t

## ORIGIN

Alignment Scores:  
Pred. No.: 3 08e-58 Length: 604  
Score: 502.00 Matches: 92  
Percent Similarity: 96.00% Conservatives: 4  
Best Local Similarity: 92.00% Mismatches: 4  
Query Match: 85.08% Indels: 0  
DB: 13 Gaps: 0

US-10-019-455A-24 (1-110) x B0567343 (1-604)

QY 11 LysLysLeuCysAlaAspAspGluCysValTyrThrIleSerLeuAlaSerIadnGlu 30  
Db 1 AAGAAGTTGTGTCGGATGAGGAGTGTCTATCTATCTCTGCGAAGACGACAGAA 60  
QY 31 AspTyrAsnAlaProAspCysArgPheIleAsnValLysGlyGlnIleTyrVal 50  
Db 61 GATTACATGCCACGACGTAGTTTCATCGATGTCACAGAGGCGCAGATCTATGTT 120  
QY 51 TyrSerLysLeuValLysGlnLysGlyAlaGlyGluPheTyrPalaGlySerValTyrGly 70  
Db 121 TACTCCAGCTGTTAACAAGAAACGAGCTGGAGAGTTTGGCGTGGCAGTCTTATGCT 180  
QY 71 AspGlyGlnAspGluMetGlyValGlyTyrPheProArgAsnLeuValLysGluGln 90  
Db 181 GACCACAGATGAGATGGGAATGTAGATTATTTCCAGCACTTGTGTGAAGAGCAG 240  
QY 91 ArgValTyrGlnGluAlaThrLysGluValProThrAspIleAspPheCysGlu 110  
Db 241 CGTGTTATACAGAGGCCACCAAGAGAGATCCCAACCGATATTGACTTCTCTGTGAA 300

## RESULT 14

BY232622 365 bp mRNA linear EST 10-DEC-2002  
LOCUS BY232622 RIKEN full-length enriched, adult inner ear Mus musculus  
DEFINITION cDNA clone F930026720 5', mRNA sequence.

ACCESSION BY232622

VERSION 1

KEYWORDS

SOURCE Mus musculus (house mouse)

## ORGANISM

REFERENCE  
AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H.,  
Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C.,  
Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A.,  
Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S.,  
Reisel, K. W., Blake, J. A., Bratt, D., Brusic, V., Chothia, C., Corbani,  
L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest,  
A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A.,  
Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J.,  
Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M.,  
King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons,  
P. A., Maglott, D. R., Maitais, L., Marchionni, L., McKenzie, L., Miki,  
H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Portea, G.,  
Pessole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D.,  
Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring,  
B. Z., Ringwald, M., Sandelin, A., Schneider, C., Sempile, C. A., Setou

M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale,  
R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y.,  
Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa,  
M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A.,  
Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura,  
M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii,  
Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata,  
K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander,  
E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## CONTACT

## LABORATORY

## SCIENCE

## THE INSTITUTE

## 1-7-22

## Tel:

## Fax:

## Email:

## URL:

## Alzawa, K.,

## T., Imotani, K.,

## Murata, M.,

## Sakazume, N.,

## M., Waki, K.,

## Submission

## Computational

## Human Genome

## Normalization

## Prepare full-length

## genes. Genome

## RIKEN integrated

## sequencing pipeline

## 10 (11), 1757-1771

## Computer-based

## encyclopedia: real-time

## nonredundant cDNA

## cDNA library was

## Encyclopedia Project

## Genomic Sciences

## Division of Experimental

## prepare mouse tissues.

## Tissues were provided

## Research Hospital 555

## assistance we gratefully

## (http://genome.gsc.riken.go.jp)

## FEATURES

## source

## 1. 365

## /organism="Mus musculus"

## /mol\_type="mRNA"

## /strain="C57BL/6J"

## /db\_xref="taxon:10090"

## /clone="F930026720"

## /tissue\_type="inner ear"

## /dev\_stage="adult"

## /clone\_lib="RIKEN full-length enriched, adult inner ear"

## BASE COUNT 97 a 60 c 110 g 98 t

## ORIGIN

## Alignment Scores:

## Pred. No.:

## Score:

## Percent Similarity:

## Best Local Similarity:

## Query Match:

## DB:

## US-10-019-455A-24 (1-110) x BY232622 (1-365)

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QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
Db 78 CATGGTGTATTTATGATAAACTTTCTTAAAGAGTTGTGCGGATGAGAGTGTGTC 137
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 138 TATACTATTTCCTGCGACAGACAGAGAGATTACAATGCCACAGCTGTAGTTTCATC 197
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db 198 GATGTCACAGAAAGGGCAGCAGATCTATGTTTACTCCAAGCTGTGTAACAGAAAACCGAGCT 257
QY 61 GlyGluPheThrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db 258 GGAGAGTTTGGGCTGGCGTGTGTTATGTTGTCACACAGATGAGATGGGAATTGTAGGT 317
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAla 96
Db 318 TATTTCCCCAGCAACTTGTGTGAAGGAGCAGCGTGTATACCAGGAGGCC 365

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## RESULT 15

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BE236443
LOCUS BE236443 527 bp mRNA linear EST 25-APR-2001
DEFINITION 144645 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE236443
VERSION BE236443.1 GI:9021161
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

```

```

REFERENCE 1 (bases 1 to 527)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrrenkrug,S.C., Bennett
,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
Keele,J.W.
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
JOURNAL Genome Res. 11 (4), 626-630 (2001)
MEDLINE 21180013
PUBMED 11282978
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCAGCAGC
Plate: 54 row: C column: 18
Seq primer: ATTAGGTGACACTATAG.

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## FEATURES

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/lab_host="DH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from day 20 and day 40
embryos."
BASE COUNT 173 a 94 c 126 g 134 t
ORIGIN

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## Alignment Scores:

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Pred. No.: 4.17e-50 Length: 527

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Score: 442.00 Matches: 87
Percent Similarity: 81.08% Conservative: 3
Best Local Similarity: 78.38% Mismatches: 7
Query Match: 74.92% Indels: 14
DB: 10 Gaps: 2

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US-10-019-455A-24 (1-1110) x BE236443 (1-527)

```

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QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20
Db 89 CATGGATATTTATGACAGACACTTGGTTCAGAAAGCTGTGTGCAGATGATGATGTGC 148
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40
Db 149 TATACTATTTCCTGCGCAGAGCTCAAGAAGATTACAATGCTCCGCACTGTAGATTCAT 208
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60
Db 209 AACGTTAAAAAGGACAGTGGATCTATGTTTACTCAAGCTG----- 250
QY 61 GlyGluPheThrAlaGlySerValTyrGlyAsp---GlyGlnAspGluMetGlyValVal 79
Db 251 -----GTCATATGGCAATCAGTCTGAGAGTGAATGGAAACCGTG 289
QY 80 GlyTyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGlu 99
Db 290 GGTATATTTCCAGCAACTTGGTCCAGGAACAACATGTGTACCAAGAAGCCACCAAGGAA 349
QY 100 ValProThrThrAspIleAspPhePheCysGlu 110
Db 350 GTTCCTACCACGGATATTGACTTTTTCGCGAG 382

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Search completed: December 29, 2003, 22:00:48

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Job time : 1140.05 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 29, 2003, 16:10:49 ; Search time 132.647 Seconds  
(without alignments)  
2238.558 Million cell updates/sec

Title: US-10-019-455a-24

Perfect score: 590

Sequence: 1 HGIFMDRLASKKLCADCEV.....RVQEQATKEVPTDIDFFCE 110

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPRO\_pool/US10019455/runat\_29122003\_160347\_230/app\_query.fasta\_1.1770  
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	590	100.0	330	22	AAF59079	Human MLP nucleoti
2	590	100.0	384	22	AAF59065	Human MLP nucleoti
3	590	100.0	387	24	AA517583	DNA encoding novel
4	590	100.0	426	22	AAH26341	Human growth regul
5	590	100.0	521	24	ABL95740	Human angiogenesis
6	590	100.0	521	24	ABL82521	Human PRO9873 cDNA
7	590	100.0	521	24	ABK33571	cDNA encoding huma
8	590	100.0	891	22	AAH98228	Human EST-derived
9	590	100.0	891	22	AAH26342	Human growth regul
10	590	100.0	923	22	AAF59083	Human MLP nucleoti
11	590	100.0	1201	22	AAH26343	Human growth regul
12	547	92.7	330	22	AAF59080	Mouse MLP nucleoti
13	547	92.7	384	22	AAF59068	Mouse MLP nucleoti
14	547	92.7	947	22	AAF59084	Mouse MLP nucleoti
15	541	91.7	330	22	AAF59099	Rat MLP nucleotide
16	541	91.7	384	22	AAF59098	Rat MLP nucleotide
17	471	79.8	307	22	AAF59093	Rat MLP nucleotide
18	413	70.0	261	22	AAF59092	Rat MLP nucleotide
C 19	254.5	43.1	442	24	ABL63602	Breast cancer rela
C 20	254.5	43.1	442	24	ABL64012	Breast cancer rela
21	253.5	43.0	330	16	AAQ84061	Sequence encoding
22	253.5	43.0	459	16	AAQ84050	Sequence encoding
C 23	253.5	43.0	459	22	AAI70083	Melanoma inhibitor
C 24	253.5	43.0	459	22	AAI18732	Human antisense ol
25	253.5	43.0	555	23	ABV59229	Human prostate exp
26	251.5	42.6	433	22	AAH47783	Recombinant human
27	231.5	39.2	581	16	AAQ84052	Sequence encoding
28	226.5	38.4	417	22	AAH99775	Human proteinenco
29	225.5	38.2	884	22	AA522459	Human cDNA encodi
30	225.5	38.2	1230	24	ABQ79850	Human TANGO 130 pa
31	225.5	38.2	1263	21	AAZ51245	Human TANGO 130 cd
32	225.5	38.2	1263	24	ABQ79849	Human TANGO 130 po
33	225.5	38.2	4409	23	ABV21035	Human prostate exp
34	225.5	38.2	4409	23	ABV23751	Human prostate exp
35	225.5	38.2	4409	23	ABV26878	Human prostate exp
36	225.5	38.2	4409	23	ABV29625	Human prostate exp
37	225.5	38.2	5724	24	ABQ79852	Human TANGO 130 po
38	225.5	38.2	8121	24	ABQ79851	Human TANGO 130 po
39	217	36.8	2037	22	AA546220	Human DNA encoding
40	217	36.8	2037	25	ACA57978	Human PRO20088 cDN
41	217	36.8	2037	25	ABX98448	Human cDNA encodi
42	217	36.8	2037	25	ABX98950	Novel human secret
43	217	36.8	2037	25	ACA05995	Human secreted/tra
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ALIGNMENTS

RESULT 1  
AAF59079  
ID AAF59079 standard; DNA; 330 BP.  
XX  
AC AAF59079;  
XX  
DT 23-APR-2001 (first entry)  
XX  
DE Human MLP nucleotide sequence SEQ ID NO:23.  
XX

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
XX cardiant; gene therapy; secretory cell function regulator; promoter;  
XX inhibitor; ds.  
OS Homo sapiens.  
XX



PN WO200102564-A1.  
 XX 11-JAN-2001.  
 XX 29-JUN-2000; 2000WO-JP04278.  
 XX 30-JUN-1999; 99JP-0186718.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 DR P-PSDB; AAB69126.  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX Claim 8; Page 97; 111pp; Japanese.  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX Sequence 330 BP; 91 A; 60 C; 91 G; 88 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: Length: 1-95e-75 330  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-019-455A-24 (1-110) x AAF59079 (1-330)  
 QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysVal 20  
 DB 1 CATGGAAATATTATGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 60  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheile 40  
 DB 61 TATACCTATTCTCTGGCTAGTGTCTCAAGAAGATTATATGCTCCCGGACTGTAGATTTCATT 120  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 DB 121 AACGTTAAAGAGGGGAGGAGAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 180  
 QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 DB 181 GGAGATTTTGGCTGGCAGTGTCTATGTGTATGTCAGGAGAGATGGAGTCTGTGGGT 240  
 QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
 DB 241 TATTTCCCGGAGAACTTGGTCAAGGAAACAGCGTGTGTACAGGAGACTACCAAGGAAGTT 300  
 QY 101 ProThrThrAspIleAspPheCysGlu 110  
 DB 301 CCCACCCAGGATATTGACTTCTCTCGGAG 330  
 RESULT 2  
 AAF59065  
 ID AAF59065 standard; DNA; 384 BP.  
 XX  
 AC AAF59065;

XX 23-APR-2001 (first entry)  
 DE Human MLP nucleotide sequence SEQ ID NO:4.  
 XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiant; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
 XX Homo sapiens.  
 XX WO200102564-A1.  
 XX 11-JAN-2001.  
 XX 29-JUN-2000; 2000WO-JP04278.  
 XX 30-JUN-1999; 99JP-0186718.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 XX WPI; 2001-159271/16.  
 DR P-PSDB; AAB69123.  
 XX Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX Example 1; Page 91; 111pp; Japanese.  
 XX The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX Sequence 384 BP; 99 A; 70 C; 106 G; 109 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: Length: 2.41e-75 384  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-019-455A-24 (1-110) x AAF59065 (1-384)  
 QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLeuCysAlaAspGluCysVal 20  
 DB 55 CATGGAAATATTATGGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 114  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheile 40  
 DB 115 TATACCTATTCTCTGGCTAGTGTCTCAAGAAGATTATATGCTCCCGGACTGTAGATTTCATT 174  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 DB 175 AACGTTAAAGAGGGGAGGAGAGATCTATGTGTACTCAAGCTGGTAAAGAAATGGAGCT 234  
 QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 DB 235 GGAGATTTTGGCTGGCAGTGTCTATGTGTATGTCAGGAGAGATGGAGTCTGTGGGT 294  
 QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100

Db 295 TATTCCCAAGAACTGGTCAAGAACAGCGTGTGTACCAAGAGCTACCAAGGAAGTT 354  
 QY 101 ProThrThrAspPhePheCysGlu 110  
 Db 355 CCCACCACGGATATTGACTTCTTCTGCGAG 384

RESULT 3  
 AAS17583  
 ID AAS17583 standard; cDNA; 387 BP.  
 AC AAS17583;  
 XX  
 DT 26-FEB-2002 (first entry)  
 DE DNA encoding novel secreted protein #12.  
 XX Secreted protein; cytostatic; immunosuppressive; vulnary; vaccine;  
 KW antiinflammatory; neuroprotective; nephrotropic; cardiovascular;  
 KW human; cancer; autoimmune disease; wound healing disorder; infection;  
 KW haematopoietic disorder; inflammatory disorder; infertility;  
 KW neurological disease; psychiatric disease; cardiovascular disease;  
 KW respiratory disease; renal; gastrointestinal; ss.  
 XX Homo sapiens.  
 OS  
 XX  
 PH Key Location/Qualifiers  
 CDS 1..387  
 FT /\*tag= a  
 FT /product= "Human secreted protein"  
 FT  
 PN WO200179454-A1.  
 XX  
 XX 25-OCT-2001.  
 XX  
 XX 11-APR-2001; 2001WO-US11797.  
 XX  
 XX 13-APR-2000; 2000US-196503P.  
 PR 24-APR-2000; 2000US-199417P.  
 XX  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;  
 XX  
 DR WPI; 2002-061975/08.  
 DR P-PSDB; AAU09671.  
 XX  
 PT New secreted proteins or polypeptides, useful for treating e.g. cancer,  
 PT autoimmune diseases, wound healing disorder, infections, haematopoietic  
 PT disorders, inflammatory disorders, infertility, cancer -  
 XX  
 PS Claim 2; Page 44; 92pp; English.  
 XX  
 CC The invention relates to an isolated novel secreted polypeptide (I) and  
 CC polynucleotide (II). (I) and (II) are useful for treating cancer,  
 CC autoimmune diseases, wound healing disorder, infections, haematopoietic  
 CC disorders, inflammatory disorders, infertility, neurological and  
 CC psychiatric diseases, cardiovascular diseases, respiratory diseases,  
 CC renal diseases, or gastrointestinal diseases. These may also be used to  
 CC treat diseases, abnormalities and disorders caused by abnormal  
 CC expression, production, function and/or metabolism of the genes, as  
 CC vaccines for inducing immunological response in a mammal, and in  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and polypeptide in cells. The polypeptides can be used  
 CC as immunogens to produce antibodies immunospecific for the polypeptides,  
 CC and to identify membrane-bound or soluble receptors. The polynucleotides  
 CC may be used as diagnostic reagents, in chromosome localisation studies,  
 CC and in tissue expression studies. The present sequence represents the  
 CC coding sequence of novel human secreted protein #12.  
 XX  
 SQ Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;

Alignment Scores:  
 Pred. No.: 2.44e-75 Length: 387  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0

US-10-019-455a-24 (1-110) x AAS17583 (1-387)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspAspGluCysVal 20  
 Db 55 CATGGAATATTATGACCGCTAGCTTCCAGAAAGCTCTGTGAGATGATGAGTGTGTC 114  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 Db 115 TATACTATTCTCTGGCTAGTGTCTCAAGAGATTATAATATATATATATATATATAT 174  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 Db 175 AACGTAAAGGAGGAGCAGATCTATGTGTACTCAAGAGCTGTAAAGAAATGGAGCT 234  
 QY 61 GlyGluPheTyrAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 Db 235 CGAGATTTTGGCTGGCAGTGTATGTATGTCAGGAGGAGATGGAGTGTGTGGT 294  
 QY 81 TyrPheProArgAsnLeuValLysGlnGlnArgValTyrGlnGluAlaThrLysGluVal 100  
 Db 295 TATTTCCCGAGAACTTGTGTCAAGGAGCAGGCTGTGTACCGAGAGCTACCAAGGAAGTT 354  
 QY 101 ProThrThrAspPhePheCysGlu 110  
 Db 355 CCCACCACGGATATTGACTTCTTCTGCGAG 384

RESULT 4  
 AAH26341  
 ID AAH26341 standard; cDNA; 426 BP.  
 XX  
 AC AAH26341;  
 XX  
 DT 02-OCT-2001 (first entry)  
 XX  
 DE Human growth regulatory-like polypeptide clone 16372272.  
 XX  
 KW Growth regulatory-like polypeptide; human; cartilage; melanoma;  
 KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
 KW ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200155332-A2.  
 XX  
 PD 02-AUG-2001.  
 XX  
 XX 25-JAN-2001; 2001WO-US02455.  
 XX  
 XX 25-JAN-2000; 2000US-0491404.  
 PR 02-MAY-2000; 2000US-0563786.  
 XX  
 XX (HYSE-) HYSEQ INC.  
 PA  
 XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;  
 XX  
 XX WPI; 2001-483233/52.  
 XX  
 PT Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -  
 XX  
 PS Example 1; Page 114; 119pp; English.

CC The present sequence is that of Hyseq clone identification number  
 CC 16372272, which was obtained from a human thymus cDNA library  
 CC using standard PCR with primers specific for vector sequence  
 CC flanking the inserts, sequencing by hybridisation sequence  
 CC signature analysis, and Sanger sequencing techniques. This  
 CC expressed sequence tag was used in the assembly of a full-length  
 CC cDNA sequence (see AAB26343) encoding a novel human growth  
 CC regulatory-like polypeptide (GRLP, see AAB2671). The GRLP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 43% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRLP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.

XX SQ Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;

#### Alignment Scores:

Pred. No.: 2.79e-75 Length: 426  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservativity: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAB26341 (1-426)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerIlyLysLeuCysAlaAspGluCysVal 20  
 Db CATGGAATATTTATGGACCGCTAGCTTCCAAGAAGCTCTGTCAGATGATGAGTGTGTC 132  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 Db TATACATATTTCTCTGGCTAGTGTCTCAAGAAGATTATTAATGCCCGGACTGTAGATTCAAT 192  
 QY 41 AsnValIlyLysGlyGlnGlnIleTyrValTyrSerIlyLysLeuValIlyGluAsnGlyAla 60  
 Db AAGCTTAAAAAGGAGCAGACGATCTATGCTACTCAAAAGCTGGTAAAGAAATGGAGCT 252  
 QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 Db GGAGAATTTTGGCTGGCAGTGTATGTTGATGGCCAGCAGATGGGAGTCGTGGT 312  
 QY 81 TyrPheProArgAsnLeuValIlyGlnArgValTyrGlnGluAlaThrIlyLysGluVal 100  
 Db TATTTCCCGAGGAACCTGGTCAAGGAACACGCTGTGTACCAAGAGCTACCAAGGAAGTT 372  
 QY 101 ProThrThrAspIleAspPhePheCysGlu 110  
 Db CCCACACGAGATATTGACTTCTTCTCGGAG 402

#### RESULT 5

ABL95740  
 ID ABL95740 standard; cDNA; 521 BP.

XX ABL95740;

XX 19-JUL-2002 (first entry)

DE Human angiogenesis related cDNA PRO9873 SEQ ID NO: 359.

XX Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;  
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;

KW antiarteriosclerotic; gene; ss.  
 OS Homo sapiens.  
 XX WO200208284-A2.  
 XX 31-JAN-2002.  
 XX 09-JUL-2001; 2001WO-US21735.  
 XX 20-JUL-2000; 2000US-219556P.  
 XX 25-JUL-2000; 2000US-220624P.  
 XX 25-JUL-2000; 2000US-220664P.  
 XX 28-JUL-2000; 2000WO-US20710.  
 XX 02-AUG-2000; 2000US-222695P.  
 XX 17-AUG-2000; 2000US-064357.  
 XX 23-AUG-2000; 2000WO-US23522.  
 XX 24-AUG-2000; 2000WO-US23328.  
 XX 07-SEP-2000; 2000US-230978P.  
 XX 15-SEP-2000; 2000US-000000P.  
 XX 18-SEP-2000; 2000US-0664610.  
 XX 18-SEP-2000; 2000US-0665350.  
 XX 24-OCT-2000; 2000US-242922P.  
 XX 08-NOV-2000; 2000US-0709238.  
 XX 10-NOV-2000; 2000WO-US30952.  
 XX 10-NOV-2000; 2000WO-US30873.  
 XX 20-DEC-2000; 2000WO-US32678.  
 XX 20-DEC-2000; 2000US-0747259.  
 XX 22-JAN-2001; 2000WO-US34956.  
 XX 28-FEB-2001; 2001US-076709.  
 XX 28-FEB-2001; 2001US-0796498.  
 XX 01-MAR-2001; 2001WO-US06520.  
 XX 09-MAR-2001; 2001WO-US06666.  
 XX 14-MAR-2001; 2001US-0802706.  
 XX 22-MAR-2001; 2001US-0806889.  
 XX 05-APR-2001; 2001US-0828366.  
 XX 10-MAY-2001; 2001US-0854208.  
 XX 25-MAY-2001; 2001US-0854280.  
 XX 25-MAY-2001; 2001US-0866028.  
 XX 25-MAY-2001; 2001US-0866034.  
 XX 30-MAY-2001; 2001WO-US17092.  
 XX 30-MAY-2001; 2001US-0870574.  
 XX 30-MAY-2001; 2001WO-US17443.  
 XX 01-JUN-2001; 2001WO-US17800.  
 XX 28-JUN-2001; 2001WO-US19692.  
 XX 28-JUN-2001; 2001WO-US00000.

(GETH ) GENENTECH INC.

(BAKE/) BAKER K P.

(FERR/) FERRARA N.

(GERB/) GERBER H.

(GERB/) GERRITSEN M E.

(GODD/) GODDARD A.

(GODO/) GODOWSKI P J.

(GURN/) GURNEY A L.

(HILL/) HILLAN K J.

(MARS/) MARSTERS S A.

(PANG/) PAN J.

(PAON/) PAONI N F.

(STEP/) STEPHAN J P.

(WATA/) WATANABE C K.

(WILL/) WILLIAMS P M.

(WOOD/) WOOD W I.

(BAKE/) BAKER K P.

(GERB/) GERBER H.

(GODD/) GODDARD A.

(GODD/) GODOWSKI P J.

(HILL/) HILLAN K J.

(MARS/) MARSTERS S A.

(PANG/) PAN J.

(PAON/) PAONI N F.

(STEP/) STEPHAN J P.

(WATA/) WATANABE C K.

(WILL/) WILLIAMS P M.

(WOOD/) WOOD W I.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 Stephan JF, Watanabe CK, Williams PW, Wood WI, Ye W;

WPI; 2002-171999/22.  
 P-PSDB; ABB95602.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,

PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX  
 XX  
 PS Claim 1; Fig 359; 567pp; English.  
 XX  
 XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a coding sequence of the invention.  
 XX  
 SQ Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:  
 Pred. No.: 3,71e-75 Length: 521  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0

US-10-019-455A-24 (1-110) x ABL95740 (1-521)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20  
 Db 92 CATGGAATATTTATGACCGCTAGCTTCCAGAGAGCTCTGTGCAGATGATGAGTGTGTC 151  
 QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 Db 152 TATACATTTCTCTGGCTAGTGTCTCAAGAGATTAATATGCCCCGAGCTGTAGATTTCATT 211  
 QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 Db 212 AACGTTAAAAAGGCGACAGATCATGTGTACTCAAGAGCTGGTAAAAAGAAATGGAGCT 271  
 QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 Db 272 GGAGAAATTTTGGCGTGGCAGTGTATTATGTTGATGCCAGGACGAGATGGGAGTCTGGGT 331  
 QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
 Db 332 TATTTCCCGAGAACTTGGTCAAGGACAGCGGTGTGTACCAAGAGAGCTACCAAGAGATT 391  
 QY 101 ProThrThrAspIleAspPheCysGlu 110  
 Db 392 CCCACACGAGATATTGACTTCTTCTGCGAG 421

# RESULT 6

ABL88251

ID ABL88251 standard; cDNA; 521 BP.

AC ABL88251;

XX

DT 16-MAY-2002 (first entry)

XX

DE Human PRO9873 cDNA sequence SEQ ID NO:359.

XX

KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; Gene mapping; Gene; ss.

OS Homo sapiens.

XX

PN WO200200690-A2.

XX

PD 03-JAN-2002.  
 XX  
 PF 20-JUN-2001; 2001WO-US19692.  
 XX  
 PR 23-JUN-2000; 2000US-213637P.  
 PR 20-JUL-2000; 2000US-219556P.  
 PR 25-JUL-2000; 2000US-220624P.  
 PR 28-JUL-2000; 2000US-220664P.  
 PR 02-AUG-2000; 2000WO-US20710.  
 PR 17-AUG-2000; 2000US-222695P.  
 PR 23-AUG-2000; 2000US-0643657.  
 PR 24-AUG-2000; 2000WO-US23522.  
 PR 07-SEP-2000; 2000US-230978P.  
 PR 18-SEP-2000; 2000US-0664610.  
 PR 24-OCT-2000; 2000US-0665350.  
 PR 08-NOV-2000; 2000US-0709238.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 10-NOV-2000; 2000WO-US30873.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000US-0747259.  
 PR 20-DEC-2000; 2000WO-US34956.  
 PR 22-JAN-2001; 2001US-0767609.  
 PR 28-FEB-2001; 2001US-0796498.  
 PR 28-FEB-2001; 2001WO-US06520.  
 PR 01-MAR-2001; 2001WO-US06666.  
 PR 09-MAR-2001; 2001US-0802706.  
 PR 14-MAR-2001; 2001US-0808689.  
 PR 22-MAR-2001; 2001US-0816744.  
 PR 05-APR-2001; 2001US-0828366.  
 PR 10-MAY-2001; 2001US-0854208.  
 PR 10-MAY-2001; 2001US-0854280.  
 PR 25-MAY-2001; 2001US-0866028.  
 PR 25-MAY-2001; 2001US-0866034.  
 PR 30-MAY-2001; 2001WO-US17092.  
 PR 30-MAY-2001; 2001US-0870574.  
 PR 01-JUN-2001; 2001WO-US17443.  
 XX  
 XX (GETH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.

P-PSDB; ABB84996.

One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 infarction), endothelial or angiogenic disorders in a mammal -

Claim 2; Fig 359; 565pp; English.

ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 antiangiogenic, hypotensive, vulnery and antiarteriosclerotic  
 activities, and can be used in gene therapy. The PRO polynucleotides,  
 proteins, agonists and antagonists are useful for treating or diagnosing  
 a cardiovascular, endothelial or angiogenic disorder in a mammal,  
 e.g. cardiac hypertrophy, trauma, cancer, age-related macular  
 degeneration, atherosclerosis, hypertension, arterial restenosis,  
 rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,  
 lymphangitis, tumour angiogenesis (such as breast carcinoma and liver  
 carcinoma) and wound healing. The PRO polynucleotides have applications  
 in molecular biology, including use as hybridisation probes, and in  
 chromosome and gene mapping. ABL88259 to ABL88267 represent primers and  
 probes used in the exemplification of the present invention.

Sequence 521 BP; 167 A; 86 C; 131 G; 137 T; 0 other;

Alignment Scores:



```

RESULT 8
AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX
AC AAH98228;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 85.
XX
DE Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder;
XX biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
XX 03-AUG-2000; 2000US-0631451.
XX 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
XX
DR P-ESDB; AAM23569.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 236; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics.
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Alignment Scores:
Pred. No.: 7,92e-75 Length: 891
Score: 590.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAH98228 (1-891)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20
Db 73 CATGGAATATTATGGACCGCTAGCTTCCAAAGAGCTCTGTGCAGATGATGAGTGTC 132
QY 21 TyrThrIleSerLeuAlaSerAlaGluAspTyrRnaAlaProAspCysArgPheIle 40
Db 133 TATCTATTCTCTGGCTAGTGCTCAGAGATTTATATGCCCGGAGCTAGATTCATT 192
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyVala 60
Db 193 AACGTTAAAAAAGGCGACAGATCTATCTGTACTCAAAGCTGGTAAAGAAATGGAGCT 252

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QY 61 GlyGluPheTIPAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80
Db 253 GGAGAAATTTGGGCTGGCAGTGTTTATGGTGATGCCAGGACGAGATGGGAGTCTGTGGGT 312
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100
Db 313 TATTTCCCGCAGAACTTGGTCAAGGAACAGCGTGTGTACCGAGGAGCTTACCAAGGAAGTT 372
QY 101 ProThrThrAspIleAspPhePheCysGlu 110
Db 373 CCACACACGGATATTGACTTCTTCTGGCAG 402
RESULT 9
AAH26342
ID AAH26342 standard; cDNA; 891 BP.
XX
AC AAH26342;
XX
DT 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide partial cDNA clone.
XX
KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200155332-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02455.
XX
PR 25-JAN-2000; 2000US-0491404.
XX 02-MAY-2000; 2000US-0563786.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX
DR WPI; 2001-483233/52.
XX
PT Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
PT hyperproliferative disorders, coagulation disorders, and nervous system
PT disorders -
XX
PS Claim 1; Page 115; 119pp; English.
XX
CC The present sequence is that of a novel nucleic acid that was
CC assembled from human thymus cDNA library-derived Hyseq clone
CC identification number 16372272 (see AAH26341). A recursive
CC algorithm was used to extend the clone by pulling additional
CC sequences from different databases. A full-length sequence (see
CC AAH26343) encoding novel human growth regulatory-like polypeptide
CC (GRIP, see AAB82671) was subsequently obtained. Human GRIP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein,
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRIP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and

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CC peptide-nucleic acid molecules, and to produce transgenic animals.

SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

#### Alignment Scores:

Pred. No.: 7.92e-75 Length: 891  
Score: 590.00 Matches: 110  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAH26342 (1-891)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20  
DB 73 CATGGAATATTATGGACCGCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGATGTGTC 132  
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
DB 133 TATACATATTTCTGTGGCTAGTGTCTCAAGAAGATTATATGCCCGGACTGTAGATTCATT 192  
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
DB 193 AACGTTAAAAAAGCGCAGCAGATCTATGTCTACTCAAAAGCTGGTAAAGAAATGGAGCT 252  
QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
DB 253 GGAGAATTTTGGGCTGGCAGTGTATGTTGGTGGCCAGGACGAGATGGGAGTCGTGGGT 312  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
DB 313 TATTTCCCAAGAACTTGGTCAAGGACACGGTGTGTACCAAGAGCTACCAAGGAAGTT 372  
QY 101 ProThrThrAspIleAspPheCysGlu 110  
DB 373 CCCACCACGGATATTGACTTCTTCTCGCAG 402

#### RESULT 10

AAF59083  
ID AAF59083 standard; DNA; 923 BP.

XX AAF59083;

DT 23-APR-2001 (first entry)

DE Human MLP nucleotide sequence SEQ ID NO:29.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
KW Joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
KW cardiant; gene therapy; secretory cell function regulator; promoter;  
KW inhibitor; ds.

XX Homo sapiens.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
PI Tanaka H;

XX WPI; 2001-159271/16.

XX Safe, low-toxicity secretory cell function-regulatory protein and  
PT encoded DNA, applicable as drugs, in diagnosis and development of  
PT promoters and inhibitors for preventing or treating e.g. bone and joint

#### PT diseases -

XX Example 1; Page 99-100; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding  
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant  
CC activities, and can be used in gene therapy and as secretory cell  
CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
CC the diagnosis and development of promoters and inhibitors for preventing  
CC or treating bone and joint diseases as well as pathologic angiogenesis.  
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
CC in the exemplification of the present invention.

SQ Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

#### Alignment Scores:

Pred. No.: 8.32e-75 Length: 923  
Score: 590.00 Matches: 110  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 22 Gaps: 0

US-10-019-455A-24 (1-110) x AAF59083 (1-923)

QY 1 HisGlyIlePheMetAspArgLeuAlaSerLysLysLeuCysAlaAspGluCysVal 20  
DB 88 CATGGAATATTATGGACCGCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGATGTGTC 147  
QY 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
DB 148 TATACATATTTCTGTGGCTAGTGTCTCAAGAAGATTATATGCCCGGACTGTAGATTCATT 207  
QY 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
DB 208 AACGTTAAAAAAGCGCAGCAGATCTATGTTGGTGGCCAGGACGAGATGGGAGTCGTGGGT 267  
QY 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
DB 268 GGAGAATTTTGGGCTGGCAGTGTATGTTGGTGGCCAGGACGAGATGGGAGTCGTGGGT 327  
QY 81 TyrPheProArgAsnLeuValLysGluGlnArgValTyrGlnGluAlaThrLysGluVal 100  
DB 328 TATTTCCCAAGAACTTGGTCAAGGACACGGTGTGTACCAAGAGCTACCAAGGAAGTT 387  
QY 101 ProThrThrAspIleAspPheCysGlu 110  
DB 388 CCCACCACGGATATTGACTTCTTCTCGCAG 417

#### RESULT 11

AAH26343  
ID AAH26343 standard; cDNA; 1201 BP.

XX AAH26343;

XX 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide cDNA.

XX Growth regulatory-like polypeptide; human; cartilage; melanoma;  
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;  
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 33..419

FT /\*tag= a

FT sig\_peptide 33..101

FT /\*tag= b

FT mat\_peptide 102..416

FT /\*tag= c

PN W0200155332-A2.  
 XX 02-AUG-2001.  
 XX 25-JAN-2001; 2001WO-US02455.  
 PF 25-JAN-2000; 2000US-0491404.  
 FR 02-MAY-2000; 2000US-0563786.  
 XX (HYSE-) HYSEQ INC.  
 XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;  
 PI Drmanac RT;  
 XX WPI; 2001-483233/52.  
 DR P-PSDB; AAB82671.  
 XX Isolated human growth regulatory-like polypeptide useful for treating  
 PT e.g. Alzheimer's disease, cancer, autoimmune disorders,  
 PT hyperproliferative disorders, coagulation disorders, and nervous system  
 PT disorders -  
 XX Claim 1; Page 115-116; 119pp; English.  
 XX The present sequence is that of a novel nucleic acid encoding  
 CC human growth regulatory-like polypeptide (GRLP, see AAB82671).  
 CC The sequence was assembled using human thymus cDNA library-derived  
 CC Hyseq clone identification number 16372272 (see AAB82671) as seed,  
 CC using software programs to pull additional sequences from Hyseq's  
 CC proprietary database containing expressed sequence tag sequences,  
 CC and by gel sequencing using primers to extend both 5' and 3' ends.  
 CC The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP  
 CC belongs to the same protein family as growth regulatory proteins,  
 CC growth factors, human melanoma derived growth regulatory protein  
 CC precursor (64% similarity) and 45% identity over 111 amino acids)  
 CC or melanoma inhibitory activity, cattle cartilage-derived  
 CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%  
 CC similarity over 126 amino acids) and other retinoic acid-sensitive  
 CC proteins. GRLP polypeptides and polynucleotides of the invention  
 CC can be used in the prophylaxis, treatment (including gene therapy)  
 CC and diagnosis of disorders and diseases caused by, or involving,  
 CC cartilage development and maintenance, inhibition of melanoma cell  
 CC growth and tumours, including neuroectodermal tumours such as  
 CC gliomas. The polynucleotides can also be used to design probes  
 CC and primers, for chromosome and gene mapping, in the recombinant  
 CC production of protein, in the generation of antisense, ribozyme and  
 CC peptide-nucleic acid molecules, and to produce transgenic animals.  
 CC They may also have cytokine and cell proliferation or  
 CC differentiation activity, stem cell growth factor activity,  
 CC haematopoiesis regulating activity, tissue growth activity,  
 CC immunosuppressive or immunostimulant activity, activin/inhibin  
 CC activity, chemotactic/chemokinetic activity, haemostatic and  
 CC thrombolytic activity, use in cancer diagnosis and therapy,  
 CC drug screening, receptor/ligand activity, antiinflammatory,  
 CC activity, and treatment of leukaemia, nervous system disorders,  
 CC arthritis and inflammation.  
 XX Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1-21e-74 Length: 1201  
 Score: 590.00 Matches: 110  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 22 Gaps: 0  
 US-10-019-455A-24 (1-110) x AAB26343 (1-1201)  
 Qy 1 HisGlyLePheMetAspArgLeuAlaSerIysLysLeuCysAlaAspGluCysVal 20  
 Db 87 CATGGAATATTTATGGACCGTCTAGCTCCAAAGAGCTCTGCGAGATGATGATGCTGTC 146  
 Qy 21 TyrThrIleSerLeuAlaSerAlaGlnGluAspTyrAsnAlaProAspCysArgPheIle 40  
 Db 147 TATACTATTCTCTGGCTAGTGTCTCAAGAGATTATATAATGCCCGAGCTGTAGATTCAAT 206  
 Qy 41 AsnValLysLysGlyGlnGlnIleTyrValTyrSerLysLeuValLysGluAsnGlyAla 60  
 Db 207 AACGTTTAAAAAGGCGACGAGATCTATGTGTACTCAAGCTGGTAAAGAAAATGGAGCT 266  
 Qy 61 GlyGluPheTrpAlaGlySerValTyrGlyAspGlyGlnAspGluMetGlyValValGly 80  
 Db 267 GGAGAAATTTGGCTGGCAGTGTATGTGTATGATGCCAGGACGAGATGGAGTCTGTGGGT 326  
 Qy 81 TyrPheProArgAsnIleValLysGluGlnArgValTyrGlnGluAlaThrIysGluVal 100  
 Db 327 TATTTCCCGAGAACTTGGTCAAGGAAACAGCGTGTGTACCGAGGAAGCTACCAAGGAAGT 386  
 Qy 101 ProThrThrAspIleAspPhePheCysGlu 110  
 Db 387 CCACACCGGATATTGACTTCTTCTGCGAG 416  
 RESULT 12  
 AAF59080  
 ID AAF59080 standard; DNA; 330 BP.  
 XX  
 AC AAF59080;  
 XX 23-APR-2001 (first entry)  
 DT  
 DE Mouse MLP nucleotide sequence SEQ ID NO:25.  
 XX  
 KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;  
 KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;  
 KW cardiac; gene therapy; secretory cell function regulator; promoter;  
 KW inhibitor; ds.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO200102564-A1.  
 XX 11-JAN-2001.  
 PD  
 XX 29-JUN-2000; 2000WO-JP04278.  
 PF  
 XX 30-JUN-1999; 99JP-0186718.  
 PR  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 PA  
 XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;  
 PI Tanaka H;  
 PI WPI; 2001-159271/16.  
 DR P-PSDB; AAB69127.  
 XX  
 PT Safe, low-toxicity secretory cell function-regulatory protein and  
 PT encoded DNA, applicable as drugs, in diagnosis and development of  
 PT promoters and inhibitors for preventing or treating e.g. bone and joint  
 PT diseases -  
 XX  
 PS Claim 10; Page 98; 111pp; Japanese.  
 XX  
 CC The present invention describes novel MLP proteins and their encoding  
 CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiac  
 CC activities, and can be used in gene therapy and as secretory cell  
 CC function regulators. The MLP proteins and DNAs can be used in drugs, in  
 CC the diagnosis and development of promoters and inhibitors for preventing  
 CC or treating bone and joint diseases as well as pathologic angiogenesis.  
 CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used  
 CC in the exemplification of the present invention.  
 XX  
 SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 2.97e-69 Length: 330